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Handling changes in MRI acquisition parameters in modeling whole brain lesion volume and atrophy data in multiple sclerosis subjects: Comparison of linear mixed-effect models

Alicia S. ChuaMS\textsuperscript{a}, Svetlana EgorovaMD, PhD\textsuperscript{a,b}, Mark C. AndersonMS\textsuperscript{a}, Mariann Polgar-TurcsanyiMS\textsuperscript{a}, Tanuja ChitnisMD\textsuperscript{a,b}, Howard L. WeinerMD\textsuperscript{a,b}, Charles R.G. GuttmannMD\textsuperscript{a,d}, Rohit BakshiMD\textsuperscript{a,b,d}, Brian C. HealyPhD\textsuperscript{a,b,c,*}

*Corresponding author at: Partners Multiple Sclerosis Center, 1 Brookline Place, Suite 602, Brookline, MA 02445, USA.
E-mail address: bcchealy@partners.org (B.C. Healy).

1. Introduction

Multiple sclerosis (MS) is a chronic inflammatory disease of the central nervous system (CNS) that results in impairment of a range of functions, including physical disability and cognitive dysfunction (Krupp et al., 1989; Rao et al., 1991; Steinman, 2001). Magnetic resonance imaging (MRI) of the brain is an established tool to monitor disease activity and progression in MS subjects. Two common measures derived from brain MRI scans are the brain parenchymal fraction (BPF) and T2 hyperintense lesion volume (T2LV), and these measures are routinely assessed longitudinally in clinical trials and observational studies. When measuring each outcome longitudinally, observed changes may be potentially confounded by variability in MRI acquisition parameters between scans. In order to accurately model longitudinal change, the acquisition parameters should thus be considered in statistical models. In this paper, several models for including protocol as well as individual MRI acquisition parameters in linear mixed models were compared using a large dataset of 3453 longitudinal MRI scans from 1341 subjects enrolled in the CLIMB study, and model fit indices were compared across the models. The model that best explained the variance in BPF data was a random intercept and random slope with protocol specific residual variance along with the following fixed-effects: baseline age, baseline disease duration, protocol and study time. The model that best explained the variance in T2LV was a random intercept and random slope along with the following fixed-effects: baseline age, baseline disease duration, protocol and study time. In light of these findings, future studies pertaining to BPF and T2LV outcomes should carefully account for the protocol factors within longitudinal models to ensure that the disease trajectory of MS subjects can be assessed more accurately.

Magnetic resonance imaging (MRI) of the brain provides important outcome measures in the longitudinal evaluation of disease activity and progression in MS subjects. Two common measures derived from brain MRI scans are the brain parenchymal fraction (BPF) and T2 hyperintense lesion volume (T2LV), and these measures are routinely assessed longitudinally in clinical trials and observational studies. When measuring each outcome longitudinally, observed changes may be potentially confounded by variability in MRI acquisition parameters between scans. In order to accurately model longitudinal change, the acquisition parameters should thus be considered in statistical models. In this paper, several models for including protocol as well as individual MRI acquisition parameters in linear mixed models were compared using a large dataset of 3453 longitudinal MRI scans from 1341 subjects enrolled in the CLIMB study, and model fit indices were compared across the models. The model that best explained the variance in BPF data was a random intercept and random slope with protocol specific residual variance along with the following fixed-effects: baseline age, baseline disease duration, protocol and study time. The model that best explained the variance in T2LV was a random intercept and random slope along with the following fixed-effects: baseline age, baseline disease duration, protocol and study time. In light of these findings, future studies pertaining to BPF and T2LV outcomes should carefully account for the protocol factors within longitudinal models to ensure that the disease trajectory of MS subjects can be assessed more accurately.

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observational studies typically involve variations in scanner platform and acquisition protocol to meet the demands of routine clinical care and ever-changing acquisition platforms and protocols. Therefore, there is an unmet need to consider what statistical approaches may be necessary to address the challenge of providing unbiased estimates of intra-subject and inter-subject changes with time in the face of heterogeneously obtained MRI data.

Linear mixed-effect (LME) models (Fitzmaurice et al., 2012; Verbeke and Molenberghs, 2009) have been shown to be efficient in performing group-based inference for neuroimaging data, as shown in studies analyzing both functional MRI (fMRI) and structural MRI data (Bernal-Rusiel et al., 2013; Bowman, 2014; Lange, 1999). LME models account for both between-subject and within-subject variance components, enabling researchers to obtain subject-specific estimated means and account for unbalanced data due to measurements at irregular time points of observation (Fitzmaurice et al., 2012; Verbeke and Molenberghs, 2009). Within the past decade, several MS researchers have aimed to study subject-specific atrophy rates via the mixed-effect modeling framework (Anderson et al., 2007; Jones et al., 2013; Luguridi et al., 2011). More recently, Jones et al. demonstrated that a mixed-effect model is superior to a linear regression model in explaining the brain atrophy rate. These investigators proposed including acquisition protocol in LME models using a categorical variable for protocol (Jones et al., 2013). Despite this initial investigation of the impact of protocol on modeling disease course in MS, a comprehensive evaluation of the possible fixed and random effects including those associated with acquisition parameters has not been completed. Such assessment is warranted to appropriately identify the mean response trajectory for MRI data such as BPF and T2LV. The aim of this study was to build a comprehensive model for the BPF and T2LV including subject-specific (random) effects and MRI acquisition parameter (individually or combined) (fixed) effects.

2. Methods

2.1. Subjects

Longitudinal MRI scans from 1341 subjects were selected from the Comprehensive Longitudinal Investigation of Multiple Sclerosis at the Brigham and Women’s Hospital, Partners MS Center (CLIMB), an ongoing prospective observational cohort study that began enrolling subjects in 2000 (Gauthier et al., 2006). Inclusion criteria for the CLIMB study are age ≥18 years and a clinically isolated syndrome (CIS) or diagnosis of MS according to the revised McDonald criteria (Polman et al., 2005). Subjects have clinical visits every 6 months that include complete neurological examinations and Expanded Disability Status Scale (EDSS) ratings (Kurtzke, 1983). All subjects from the CLIMB cohort with available MRI scans up to 6 years after study entry were included in this study. We limited the follow-up time to 6 years in order to ensure that the subset of subjects followed for much longer periods did not have too much leverage on this analysis. Hence, scans for subjects that are greater than 6 years from their baseline scan were excluded. Demographic and clinical characteristics of subjects are provided in Table 1.

2.2. Image acquisition and processing

BPF and T2LV were calculated by applying an image analysis pipeline to dual-echo, conventional spin-echo images (DE-CSE). Over the years, some acquisition parameter variations were included in the DE-CSE pulse sequence. All MRI scans were acquired on various 1.5 T Signa GE scanners at the Brigham and Women’s Hospital (BWH), Boston, Massachusetts, using at times a standard quadrature head coil, and at other times a multichannel head coil (8 Channel High Resolution Brain Array (BHR BRAIN)). DE-CSE MRI protocols were acquired axially with pulse sequences including various combinations of following parameter ranges: TR = 2216–3000 ms, TE1/TE2 30/80 ms, slice thickness 3 mm, with no interslice gaps, resulting in a pixel size of 0.7813–0.9375 mm. In this study, nineteen unique DE-CSE MRI protocols (i.e., variably parameterized DE-CSE MRI pulse sequences) were used as detailed in Table 2. The original standard protocol in the CLIMB study was protocol A. Over the years, this protocol had to be adapted because of operational considerations, resulting in the 19 distinct protocols in Table 2. Quantitative image analysis was performed from the dual-echo images using an automated template-driven segmentation pipeline with partial volume effect correction (TDS+) (Wei et al., 2002) followed by manual editing of output segmentation maps by an experienced observer. Large scale data management and analysis was enabled by an image analysis workflow management system linked to our Image Centered Oracle MS Database (Liu et al., 2005). The pipeline involves a semi-automated skull-stripping editing procedure to derive the intracranial volume (ICV) followed by automated segmentation of gray matter (GM), CSF, white matter (WM), and white matter lesions through TDS+ (Wei et al., 2002). BPF was calculated by the following formula: BPF = \((GM + WM + lesions) / ICC\) (Wei et al., 2004), where ICC is the volume of the intracranial cavity serving as reference for individual head size (Kikinis et al., 1992). After the pipeline was completed, all of the MRI scans reported in this study (N = 3453) underwent manual correction of automatically generated segmentation maps of T2 lesions, brain parenchymal compartments and CSF by expert readers using 3D Slicer software (Liu et al., 2005). We note that no correction for misclassification of T1 hypointensities was performed in our pipeline, but recent work from our group has demonstrated that these hypointensities have a limited impact on measures of BPF (Dell’Oglio et al., 2015).

2.3. Statistical analysis

Statistical analyses were conducted using the MIXED procedure in the Statistical Analysis System (SAS) version 9.3 (Cary, NC). A cube
root transformation was applied to T2LV prior to analysis to avoid violation of model assumptions. In addition, BPF was modeled as a percent to allow easier interpretation of the model coefficients. Since the goal of our analysis was the estimation of both the mean BPF and T2LV trajectories over time with a set of serial measurements from subjects, an LME model was used. In the process of model selection, several models were proposed and investigated, but two main considerations were of interest. First, using the most complex mean model, several potential models for the covariance/random effect structures were compared. Once the covariance/random effects structures were compared, several models for the impact of protocol parameterization on the fixed effects were assessed (Diggle et al., 2002).

For the assessment of the covariance structure, the model included protocol, baseline age, baseline disease duration, study time and an interaction term between protocol and study time. In terms of covariance structure/random effects, we compared three models: (A1) subject-specific random intercept only, (A2) subject-specific random intercept and study time effect, and (A3) subject-specific intercept and study time effect with protocol specific residual variance. Although assessment of protocol specific random study time effects was of interest, many protocols failed to have multiple observations on the same subject so these variance components were not estimable in our dataset. Therefore, model (Model A2) was the chosen covariance structure. Using this covariance structure, the fitting of the model with the specified fixed effects were shown in Table 3; additional statistics from each of the models are presented in Supplementary Table 1. The random intercept and slope model (Model A2) was superior to the random intercept only model (Model A1), and the improvement was substantial. Further, the random intercept and slope model with protocol specific residual variance (Model A3) was superior to the random intercept and slope model. Therefore, Model A3 was the chosen covariance structure.

Using this covariance structure, the fit of the model with the specified fixed effects are shown in Table 3; additional statistics from each of the models are presented in Supplementary Table 2. The results show that the lowest AIC was attained with Model B2. This model includes separate estimates for cross-sectional effect of age and the

Table 2

<table>
<thead>
<tr>
<th>Protocol</th>
<th>N scans</th>
<th>Coil</th>
<th>Pixel spacing (mm)</th>
<th>Pixel bandwidth (mm)</th>
<th>Repetition time (ms)</th>
<th>Scanner Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>2125</td>
<td>Head</td>
<td>0.9375</td>
<td>84.9219</td>
<td>3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>B</td>
<td>41</td>
<td>Head</td>
<td>0.9375</td>
<td>84.9219</td>
<td>3000</td>
<td>BWH: Pike 2 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>C</td>
<td>210</td>
<td>Head</td>
<td>0.9375</td>
<td>81.4062</td>
<td>3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>D</td>
<td>63</td>
<td>Head</td>
<td>0.9375</td>
<td>84.9219</td>
<td>&lt;3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>E</td>
<td>75</td>
<td>8 HR Brain</td>
<td>0.9375</td>
<td>84.9219</td>
<td>3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>F</td>
<td>31</td>
<td>8 HR Brain</td>
<td>0.9375</td>
<td>81.4062</td>
<td>3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>G</td>
<td>104</td>
<td>8 HR Brain</td>
<td>0.8594</td>
<td>84.9219</td>
<td>3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>H</td>
<td>30</td>
<td>8 HR Brain</td>
<td>0.8594</td>
<td>81.4062</td>
<td>3000</td>
<td>BWH: Pike 1 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
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<tr>
<td>I</td>
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<td>8 HR Brain</td>
<td>0.8594</td>
<td>81.4062</td>
<td>3000</td>
<td>BWH: Pike 2 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>J</td>
<td>181</td>
<td>8 HR Brain</td>
<td>0.8594</td>
<td>84.9219</td>
<td>3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>K</td>
<td>13</td>
<td>8 HR Brain</td>
<td>0.8594</td>
<td>81.4062</td>
<td>&lt;3000</td>
<td>BWH: Pike 1 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>L</td>
<td>47</td>
<td>8 HR Brain</td>
<td>0.8594</td>
<td>81.4062</td>
<td>&lt;3000</td>
<td>BWH: Pike 2 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>M</td>
<td>225</td>
<td>8 HR Brain</td>
<td>0.7813</td>
<td>84.9219</td>
<td>3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
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<tr>
<td>N</td>
<td>89</td>
<td>8 HR Brain</td>
<td>0.7813</td>
<td>81.4062</td>
<td>3000</td>
<td>BWH: Pike 1 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>O</td>
<td>19</td>
<td>8 HR Brain</td>
<td>0.7813</td>
<td>81.4062</td>
<td>3000</td>
<td>BWH: Pike 2 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
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<tr>
<td>P</td>
<td>136</td>
<td>8 HR Brain</td>
<td>0.7813</td>
<td>84.9219</td>
<td>&lt;3000</td>
<td>BWH: 221 Longwood Ave., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>Q</td>
<td>16</td>
<td>8 HR Brain</td>
<td>0.7813</td>
<td>81.4062</td>
<td>&lt;3000</td>
<td>BWH: Pike 1 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>R</td>
<td>12</td>
<td>8 HR Brain</td>
<td>0.7813</td>
<td>81.4062</td>
<td>&lt;3000</td>
<td>BWH: Pike 2 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
<tr>
<td>S</td>
<td>12</td>
<td>8 HR Brain</td>
<td>0.8203</td>
<td>81.4062</td>
<td>3000</td>
<td>BWH: Pike 1 — 75 Francis St., Boston, MA (1.5 T Scanner)</td>
</tr>
</tbody>
</table>

Notes:

-Column 1, Protocol: Protocol sequence.
-Column 2, N scans: Number of scans.
-Column 3, Coil: Type of coil.
-Column 4, Pixel spacing (mm): Pixel spacing in mm.
-Column 5, Pixel bandwidth (mm): Pixel bandwidth in mm.
-Column 6, Repetition time (ms): Repetition time in milliseconds.
-Column 7, Scanner Name: Name and details of the scanner.

Table 3

<table>
<thead>
<tr>
<th>Model comparison</th>
<th>Smaller model AIC</th>
<th>Larger model AIC</th>
<th>Preferred model</th>
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<tbody>
<tr>
<td>Covariance models</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A1 vs. A2</td>
<td>14,390.1</td>
<td>14,149.4</td>
<td>A2</td>
</tr>
<tr>
<td>A1 vs. A3</td>
<td>14,390.1</td>
<td>13,995.4</td>
<td>A3</td>
</tr>
<tr>
<td>A2 vs. A3</td>
<td>14,149.4</td>
<td>13,995.4</td>
<td>A3</td>
</tr>
<tr>
<td>Mean models</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B1 vs. B2</td>
<td>14,009.7</td>
<td>13,992.1</td>
<td>B2</td>
</tr>
<tr>
<td>B2 vs. B3</td>
<td>14,048.5</td>
<td>13,983.0</td>
<td>B2</td>
</tr>
<tr>
<td>B3 vs. B4</td>
<td>13,992.1</td>
<td>13,983.0</td>
<td>B3</td>
</tr>
<tr>
<td>B4 vs. B5</td>
<td>14,004.5</td>
<td>14,009.7</td>
<td>B4</td>
</tr>
</tbody>
</table>

Legend: AIC: Akaike Information Criterion; for full description of models A1–A3 and models B1–B5, please refer to the Statistical analysis section.

3. Results

3.1. BPF

Comparison of models for the selection of covariance parameters is presented in at the top of Table 3; additional statistics from each of the models are presented in Supplementary Table 1. The random intercept and slope model (Model A2) was superior to the random intercept only model (Model A1), and the improvement was substantial. Further, the random intercept and slope model with protocol specific residual variance (Model A3) was superior to the random intercept and slope model. Therefore, Model A3 was the chosen covariance structure.

Using this covariance structure, the fit of the model with the specified fixed effects are shown in Table 3; additional statistics from each of the models are presented in Supplementary Table 2. The results show that the lowest AIC was attained with Model B2. This model includes separate estimates for cross-sectional effect of age and the
longitudinal change with age, demonstrating the potential problems associated with using age at the MRI visit as the time metric in longitudinal models for BPF. Further, a protocol by study time interaction was not found to add significantly to the model since Model B3 did not lead to improvement over Model B2. Finally, the model including fixed effects for each of the components of the protocol provided an inferior fit compared to a model with a protocol specific effect, demonstrating that the parameters for the protocols do not have simple additive effects on BPF, as might have been expected, given that individual protocol parameters might have complex interactions towards the resulting image contrast and noise characteristics. The final parameter estimates from model B2 are shown in Supplementary Table 3.

3.2. T2LV

Comparison of models for the selection of covariance parameters is presented at the top of Table 4; additional statistics for each of the fixed effects models are shown in Supplementary Table 4. The random intercept and slope model (Model A2) was superior to the random intercept only model (Model A1), and the improvement was substantial. For T2LV, the random intercept and slope model with protocol specific residual variance (Model A3) could not be fit because the residual variance associated with one of the protocols was estimated to be equal to 0. Given the inability to estimate some of the parameters, Model A2 was chosen for further analysis.

Using this covariance structure, the fit of the model with the specified fixed effects are shown in Table 4; additional statistics for each of the fixed effects models are shown in Supplementary Table 5. The results show that the lowest AIC was attained with Models B2 and B5. As for BPF, the results show that including separate estimates for cross-sectional effect of age at study entry and the within subject longitudinal change provided a superior fit compared to a model with a single parameter for age.

Within the analysis of the BPF, the residual variability associated with each of the protocols was found to differ, demonstrated by the improvement in model fit comparing Models A2 and A3. This result indicates that the homoscedasticity assumption of many commonly used models may be inefficient when subjects are measured using different scanning protocols. When the estimated residual variances were investigated in Supplementary Table 3, the protocols with the largest deviations from protocol A had the largest difference in terms of residual variability. These results show that accounting for heteroscedasticity due to protocol may be an important consideration in modeling BPF data from multiple protocols. In addition to the impact of protocol on residual variance, protocol was found to have an impact on the intercept (p < 0.001 for overall effect of protocol in Model B2), but there was no protocol by study time interaction (p = 0.06 from Model B3). Further, including the components of the protocol as additive fixed effects failed to improve model relative to including protocol specific fixed effects.

Within the analysis of the cube root transformation of T2LV, the model with protocol specific residual variance failed to converge because the residual variance for one of the protocols was found to be equal to 0. Therefore, estimating the change with age using a single parameter for age in T2LV would underestimate the change with time for a specific subject. Therefore, estimating the change with age using a single parameter would underestimate the change with time for a specific subject. Further work assessing the impact of age may provide more insight regarding this finding.

For both outcome measures, separate parameters for the cross-sectional effect of age and the within subject change with age were found to lead to an improved fit relative to a single parameter for the effect of age. In both models, the within subject change in the outcomes with age was found to be larger than the cross-sectional effect of age. Therefore, estimating the change with age using a single parameter would underestimate the change with time for a specific subject.

Further work assessing the impact of age may provide more insight regarding this finding.

For this analysis, model selection was based on the AIC. The AIC includes a penalty for model complexity, but an alternative measure for model selection is the Bayesian Information Criterion (BIC). The BIC has a larger penalty for model complexity compared to the AIC; therefore, models with fewer parameters are favored by the BIC more than the AIC. The BIC for each of the model compared in this paper are also provided in the supplementary tables. When the BIC is used for model selection, the same variance components were chosen, but Model B4 was found to be superior to Model B2 in each case. This result is driven by the fact that Model B4 required fewer parameters. At the same time, we prefer Model B2 because we had sufficient sample size to estimate all of the parameters in our model so choosing the model with fewer parameters was not viewed as an advantage.

Our study has several limitations that warrant further discussion. First, our results are based on a specific MRI processing pipeline. In
particular, the reported results regarding brain atrophy are based on analysis of BPF measured two channel (PD/T2 weighted MRI) pipeline in which two variables (lesion volume and brain atrophy) are measured simultaneously, while other pipelines measure normalized brain volume using alternative approaches. To assess whether these results apply to other brain atrophy measures and processing pipelines, similar analyses must be completed. Second, we were unable to assess the impact of protocol on the random effect variances due to the limited number of subjects who had repeated observations on the many protocols. Furthermore, we did not assess the potential role of changes in the post-processing pipeline. This may be especially relevant to the combining of existing datasets from multiple centers that have already been processed by different analysis pipelines. Thus, future work will be required to fully assess the range of deviations that may have an impact on the random effect distributions, which includes the inter-rater reliability of scan editing for both ICC and final segmentation correction. Third, the presence of steroid treatment for a relapse at the time of the MRI scan could have impacted the modeling of longitudinal change. Therefore, future work investigating the impact of steroids/relapses at the time of an MRI scan in modeling the longitudinal change of BPF and T2LV is warranted. Finally, we note that this is an observational study following subjects longitudinally. Our analysis only assessed the time of an MRI scan in modeling the longitudinal change of BPF and T2LV outcomes provide a good fit to the data. In light of these findings, future research pertaining to BPF and T2LV outcomes should carefully account for protocol parameters described in Table 2, but other potential sources of variability including scanner changes could have impacted the longitudinal changes. Therefore, the impact of other sources of variability on the modeling of longitudinal changes will be a subject of further research. In conclusion, we believe that our proposed models for both outcomes provide a good fit to the data. In light of these findings, future research pertaining to BPF and T2LV outcomes should carefully account for protocol in the analysis to ensure that the true disease trajectory of MS subjects can be assessed.

Acknowledgments

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Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.nicl.2015.06.009.

References


WNL.33.11.14466585237.
