

A METHOD FOR EXPLORATORY REPEATED-MEASURES ANALYSIS APPLIED TO A BREAST-CANCER SCREENING STUDY

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When a model may be fitted separately to each individual statistical unit, inspection of the point estimates may help the statistician to understand between-individual variability and to identify possible relationships. However, some information will be lost in such an approach because estimation uncertainty is disregarded. We present a comparative method for exploratory repeated-measures analysis to complement the point estimates that was motivated by and is demonstrated by analysis of data from the CADET II breast-cancer screening study. The approach helped to flag up some unusual reader behavior, to assess differences in performance, and to identify potential random-effects models for further analysis.

1. Introduction. In this article we propose an approach for exploratory repeated-measures analysis. The term repeated measures is used in a loose sense to mean that more than one datum is recorded on each individual unit. However, the measurements themselves will be permitted to have any data structure with a likelihood function, perhaps ranging from replicated readings of the same quantity to multivariate measurements of a stochastic process through time. The exploratory method was motivated and is applied to data from the computer aided detection evaluation trial (CADET) II trial, where 27 human readers inspected distinct mammograms (breast x -rays) for cancer screening. Our analysis aim is to determine whether real differences in behavior exist between the individual readers, including whether any might be outliers, and then if heterogeneity is observed, to seek possible groups of similar individuals, and factors that correlate with the differences. The proposal is partly motivated by the difficulty of such an objective when the sample size is 27, even when up to several thousand measurements are observed on each reader. The approach is developed in the next section and then it is demonstrated using the data. Conclusions follow a section discussing the application of the method to other data sets.

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2. Method. The general data structure is first described and the main similarity-matrix idea is defined. Then, some properties of the matrix are recorded and we comment on some ways in which it may be used for exploratory repeated-measures analysis.

2.1. *Setup.* Suppose there are n individual units ($i = 1, \dots, n$) with n_i repeated measurements $\mathbf{y}_i = (y_{i,1}, \dots, y_{i,n_i})$ observed. The application in this paper has the units as humans who interpret mammograms for cancer screening. We assume that there is a suitable model form for the probability mass or density function $p(y|\mathbf{u}_i)$ parametrized by $\mathbf{u}_i = (u_{i1}, \dots, u_{im})$, where m is the dimension of each \mathbf{u}_i . For example, if the results are binary indicators for recall ($y = 1$) or no action ($y = 0$), then $p(y|u_i)$ might be a binomial model ($m = 1$) with parameter u_i interpreted as i 's probability of recall. More generally, $p(y|\mathbf{u}_i)$ could be developed from a data analysis, or knowledge of the problem, but we assume that the \mathbf{u}_i occur in the same form for each individual $p(\mathbf{y}_i|\mathbf{u}_i)$. The statistical modeling goal taken here is to understand variability of the \mathbf{u}_i 's, perhaps through a model for $p(\mathbf{u})$, or $p(\mathbf{u}|\mathbf{x})$ with explanatory variables $\mathbf{x}_i = (x_{i1}, \dots, x_{ir})$. This two-stage model structure taken is also taken in other areas, such as in applications using linear mixed models [Crowder and Hand (1990)].

Note that the setup considered is different to generalized estimating equations (GEE). These are used to estimate marginal (population-averaged) regression coefficients $\boldsymbol{\beta}$ in a repeated measures context where $E(\mathbf{y}_i) = \mu(\mathbf{x}_i; \boldsymbol{\beta})$, but without assuming a full probability model for \mathbf{y}_i or even a "true" covariance structure for \mathbf{y}_i . In this paper we have a full (conditional) probability model for \mathbf{y}_i , $p(\mathbf{y}_i|\mathbf{u}_i)$, that is based on subject-specific parameters (random effects) and the focus is upon their distribution over the population.

2.2. *The similarity matrix.* The exploratory measure that we call a similarity matrix is obtained in two steps:

- (1) Compute consistent $\hat{\mathbf{u}}_i$ for $i = 1, \dots, n$, such as maximum likelihood estimates of \mathbf{u}_i ; then
- (2) calculate the z -matrix with row $i = 1, \dots, n$ and column $j = 1, \dots, n$ entries from

$$(1) \quad z_{ij} = \frac{p(\mathbf{y}_i|\hat{\mathbf{u}}_j)}{\sum_{k=1}^n p(\mathbf{y}_i|\hat{\mathbf{u}}_k)}.$$

A likelihood function $p(\text{data}|\theta)$ reveals the relative plausibilities of different parameter θ -values in the light of the data. Here $z_{ij} \propto p(\mathbf{y}_i|\hat{\mathbf{u}}_j)$ does likewise for the \mathbf{u}_j ($j = 1, \dots, n$) in light of the data \mathbf{y}_i . The z_{ij} quantity thus explores the similarity of the \mathbf{u}_j 's via their estimates, by measuring how close individual j 's parameter fit is to individual i 's data.

If y_{il} is a sequence of $l = 1, \dots, n_i$ binary indicators as above, and a binomial likelihood is assumed for $p(y_i|u_i)$, then using the notation $y_{i+} = \sum_{l=1}^{n_i} y_{il}$, we have

$$(2) \quad z_{ij} = \frac{\hat{u}_j^{y_{i+}} (1 - \hat{u}_j)^{(n_i - y_{i+})}}{\sum_{k=1}^n \hat{u}_k^{y_{i+}} (1 - \hat{u}_k)^{(n_i - y_{i+})}},$$

because $\binom{n_i}{y_{i+}}$ cancels in the numerator and denominator.

2.3. *Some properties of the matrix.*

(1) $0 \leq z_{ij} \leq 1$.

(2) $z_{ij} = O(1/n)$. The practical significance is that larger matrices will have smaller z_{ij} terms.

(3) $z_{i+} = \sum_{j=1}^n z_{ij} = 1$.

(4) $z_{ij} \leq z_{ii}$ for $j \neq i$ if maximum-likelihood estimation is used [because $p(\mathbf{y}_i|\mathbf{u}) \leq p(\mathbf{y}_i|\hat{\mathbf{u}}_i)$ for all \mathbf{u}].

(5) The matrix follows from Bayes' rule

$$p_e(\mathbf{u}|\mathbf{y}_i) \propto p(\mathbf{y}_i|\mathbf{u})p_e(\mathbf{u}),$$

where $p_e(\mathbf{u})$ is a probability mass function that approximates variation of the random effect \mathbf{u} across individuals $p(\mathbf{u})$ by assigning mass $1/n$ to each of the points $(\hat{\mathbf{u}}_1, \dots, \hat{\mathbf{u}}_n)$. The e subscript is used in the notation to make explicit the reference to this *empirical* distribution. That is, $z_{ij} = P_e(\mathbf{u}_i = \hat{\mathbf{u}}_j|\mathbf{y}_i)$, and the z_{ij} quantities are posterior \mathbf{u}_i mass values where the \mathbf{u} distribution has been restricted to the points in $p_e(\mathbf{u})$.

(6) z is not symmetric unless $P_e(\mathbf{u}_j = \hat{\mathbf{u}}_i|\mathbf{y}_j)$ equals $P_e(\mathbf{u}_i = \hat{\mathbf{u}}_j|\mathbf{y}_i)$. Thus, it is not a similarity matrix in the usual sense.

(7) When $z_{ij} = z_{ii}$, then \mathbf{y}_i is equally well conditioned on $\hat{\mathbf{u}}_i$ and $\hat{\mathbf{u}}_j$, and $P_e(\mathbf{u}_i = \hat{\mathbf{u}}_j|\mathbf{y}_i) = P_e(\mathbf{u}_i = \hat{\mathbf{u}}_i|\mathbf{y}_i)$.

(8) $z_{+j} > 1$ means that $\hat{\mathbf{u}}_j$ is very likely the value for many i and/or z_{jj} is relatively large.

(9) An alternative measure z_{+j}/z_{jj} can be used to assess the importance of $\hat{\mathbf{u}}_j$ over the $i \neq j$.

(10) A measure of the overall concentration of the estimates is $\text{trace}(z)/n \in (0, 1)$. Since $z_{++} = n$, $\text{trace}(z)/n$ attains maximum value 1 when $z_{ii} = 1$ for all i .

(11) $(z_{11}, z_{22}, \dots, z_{nn})$, or $\text{diag}(z)$ provides a comparative measure of concentration in the estimates. This is because point estimates $\hat{\mathbf{u}}_i$ with relatively high (or close to 1) z_{ii} entries may be interpreted as good predictions since

$$(3) \quad \begin{aligned} E_e(\mathbf{u}_i|\mathbf{y}_i) &= \sum_{j=1}^n \hat{\mathbf{u}}_j P_e(\mathbf{u}_i = \hat{\mathbf{u}}_j|\mathbf{y}_i) \\ &= \sum_{j=1}^n z_{ij} \hat{\mathbf{u}}_j. \end{aligned}$$

So for z_{ii} close to one (and therefore z_{ij} close to 0 for $j \neq i$), a prediction from (3) is likely to be very close to $\hat{\mathbf{u}}_i$; for z_{ii} not close to 1, the point-estimate $\hat{\mathbf{u}}_i$ may be misleading because a prediction from (3) is subject to nonnegligible averaging (shrinkage).

(12) If the \mathbf{u}_i are distinct, then as $n_i \rightarrow \infty$ for each i the z -matrix will converge to the identity matrix because a consistent estimator of \mathbf{u} is used. In practice, this means that when the \mathbf{u}_i are different, then a data set with large n_i and well-estimated \mathbf{u}_i will have a z -matrix close to the identity matrix. Conversely, little structure is likely to be seen when all the n_i are small, but it may still be worth applying the method to see if this is the case. The most useful case is likely to be when some of the n_i are moderate.

(13) A referee suggested a possible connection with Rubin's propensity score [Rosenbaum and Rubin (1983)]. In that setting individuals are matched (one a case, the other a control) by a propensity score $e(\mathbf{x}_i) = P(c_i = 1|\mathbf{x}_i)$, where c is an indicator of being a case. In our setup individuals are matched to each other through $z_{ij} = P_e(\mathbf{u}_i = \hat{\mathbf{u}}_j|\mathbf{y}_i)$. The propensity score reduces the dimension of multivariate matching on \mathbf{x}_i to a univariate measure; the z -matrix transforms the dimensionality of matching individuals on \mathbf{u}_i to a two-dimensional matrix.

2.4. *Why use the matrix for exploratory analysis?* The first step in the computation of the z -matrix is to obtain point estimates $(\hat{\mathbf{u}}_1, \dots, \hat{\mathbf{u}}_n)$. These might be plotted in exploratory analysis to look for clusters, outliers and other structural relationships or trends across individuals in the data. For example, one can plot the parameter fits $\hat{\mathbf{u}}_i$ against each other, and against other covariates by using a matrix scatter plot. An example demonstrating the use of this approach for exploratory analysis with hierarchical linear models is Bowers and Drake (2005). One issue with the plots is that uncertainty in the point estimates is disregarded and so apparent trends may be less impressive than first appears, or masked by sampling variation.

A first way that the above properties of the z -matrix can be used to add to the information in the plots is by helping to quantify the concentration of each individual's estimate $\hat{\mathbf{u}}_i$ by inspection of $\text{diag}(z)$. A second way is by making comparisons between the estimates $\hat{\mathbf{u}}_i$ and $\hat{\mathbf{u}}_j$ from two individuals i and j , through the z_{ij} and z_{ji} terms. An example of where these properties are useful is when the z_{ij} entries are zero, except for those within an identifiable cluster of \mathbf{u} -values from the plots. This would suggest that the individuals form a fairly homogeneous group. A third way is to improve the point-estimates $\hat{\mathbf{u}}_j$ ($j = 1, \dots, n$) themselves, by using equation (3) to shrink the estimates through $E_e(\mathbf{u}_i|\mathbf{y}_i)$. A fourth way is by using quantities such as $z_{+j} - z_{jj}$ or z_{jj}/z_{+j} for $j = 1, \dots, n$ to show the more important $\hat{\mathbf{u}}_j$, or to identify outliers. Some techniques to draw attention to these and other features are next described.

3. Exploratory analysis with the z -matrix. In this section we propose a number of ways to present the z -matrix. They will be demonstrated using the breast-screening data later on.

3.1. *Tabular presentation of the matrix.* When printing out the matrix it is important to display it in such a way that important aspects of the data are clearly visible. With this in mind we next suggest a way to display the matrix in tabular form:

- Print out the transpose of z , not z . When making comparisons between individuals the main interest is comparing z_{ij} for $j = 1, \dots, n$. The transpose of the z -matrix is better because, as in tables, it is easier to compare down columns than across rows [LGDUW (2004)].
- Multiply the matrix by a power of 10 (e.g., 1,000) and do not display (multiplied) values less than 1. The point here is to focus the eye's attention on the difference between large, small and negligible proportions by using the number of digits displayed in a number. For example, the number 1,000 is seen to be larger than 10 because it has twice the number of digits; it is more difficult to see at first glance that 0.1000 is bigger than 0.0010 because they have the same number of digits. The choice of multiplication factor should depend on n since $z_{ij} = O(1/n)$.
- Experiment with the order of individuals. The order used might be based on an examination of one z -matrix, to regroup similar individuals, or it might be made using the covariate \mathbf{x}_i data. A recommended first order is by one of the \mathbf{u} components, or a function of interest using the \mathbf{u} 's.

3.2. *Graphical presentation of the matrix.* An alternative to printing the matrix is to use a plot. Since $\sum_{j=1}^n z_{ij} = 1$, a recommended display is a histogram variety, where there is one bar for each cell in the matrix. Such a chart can be produced using a symbols plot, with rectangles of area proportional to z_{ij} . It is arguably easier to compare the shape of histograms down a page (one for each of the n units), so it might be better to leave the matrix untransposed in this instance. Use of the transpose for printing and the untransposed matrix for plotting might also help the statistician to see different features.

3.3. *Graphs to assess the number of groups.* For scalar \hat{u}_i (i.e., each component of $\hat{\mathbf{u}}_i$ if a vector) order the individuals by \hat{u}_i . Then a plot of $(\hat{u}_i, i/n)$ provides the estimated distribution function of u , based on the a priori $p_e(u)$. Such an approach uses information in the separate u 's, but due to the equal weights, it might be improved by using the data to change the weights from $1/n$. The proposal is to use an estimate of the density of u_j from $n^{-1}z_{+j}$. If the u_i 's are all well estimated and different, then the weights will not change much from $1/n$. If some are more likely over the sample than others, then they will be up-weighted,

and others will be down-weighted. A related quantity is the distribution function $Z_k = n^{-1} \sum_{j=1}^k z_{+j}$. Plots of the z -matrix density and distribution function can be used to help assess the number of groups in the data.

3.4. *Shrinking parameter fits.* A way to incorporate estimation uncertainty into any exploratory plots involving \mathbf{u} is to use equation (3) to shrink the estimates through $E_e(\mathbf{u}_i | \mathbf{y}_i)$. In this way, outliers might be more reliably identified, as well as possible patterns.

3.5. *Smoothing covariates.* The matching of individuals through the z -matrix may be used to show the average covariates \mathbf{x} for a given $\hat{\mathbf{u}}_i$. This might aid inspection of possible correlations beyond using the observed covariates \mathbf{x}_i recorded for each individual $i = 1, \dots, n$ in plots against (functions of) parameters $\hat{\mathbf{u}}_i$. We next show how $\tilde{\mathbf{x}}_i = \sum_{k=1}^n \mathbf{x}_k z_{ik} / z_{+k}$ can be derived as the expected \mathbf{x} given $\hat{\mathbf{u}}_i$ from the z -approach.

Suppose we have data \mathbf{d} , known to be one of the \mathbf{y}_i , but not which one, and have prior $P(\mathbf{d} = \mathbf{y}_i) = 1/n$ for $i = 1, \dots, n$. If we were interested in the probability that the data $i = 1, \dots, n$ were generated by parameter fit $\hat{\mathbf{u}}_j$, then we could use $P_e(\mathbf{d} = \mathbf{y}_i | \mathbf{u} = \hat{\mathbf{u}}_j) = z_{ij} / z_{+j}$. Now

$$(4) \quad p_e(\mathbf{x} | \mathbf{u}) = \sum_{k=1}^n p(\mathbf{x} | \mathbf{d} = \mathbf{y}_k, \mathbf{u}) P_e(\mathbf{d} = \mathbf{y}_k | \mathbf{u}).$$

In the case where the \mathbf{x}_i are distinct, we model $P(\mathbf{x} = \mathbf{x}_i | \mathbf{d} = \mathbf{y}_k, \mathbf{u})$ by an empirical distribution so that $P(\mathbf{x} = \mathbf{x}_i | \mathbf{d} = \mathbf{y}_k, \mathbf{u}) = 1$ if $i = k$ for $k = 1, \dots, n$, and 0 otherwise, then $P(\mathbf{x} = \mathbf{x}_k | \mathbf{u}) = P(\mathbf{d} = \mathbf{y}_k | \mathbf{u})$, leading to

$$(5) \quad \begin{aligned} E_e(\mathbf{x} | \mathbf{u} = \hat{\mathbf{u}}_i) &= \sum_{k=1}^n \mathbf{x}_k P_e(\mathbf{d} = \mathbf{y}_k | \mathbf{u} = \hat{\mathbf{u}}_i) \\ &= \sum_{k=1}^n \mathbf{x}_k z_{ik} / z_{+k}. \end{aligned}$$

In the case where the \mathbf{x}_i are not distinct, one can still use $\tilde{\mathbf{x}}_i$ as defined above. A crude way to think of the approach is that individuals are locally clustered depending on their $\hat{\mathbf{u}}$'s, and the average covariate at that cluster is obtained. Thus, given $\hat{\mathbf{u}}$, the variation in the $\tilde{\mathbf{x}}$'s is much less than the original \mathbf{x} 's. It is hoped that the process will smooth out some sampling variation, making it easier to assess if there are any real patterns of interest between \mathbf{x} and \mathbf{u} .

3.6. *Graphical testing.* A last exploratory approach is to follow Gelman (2004), Buja et al. (2009) and others by comparing z -matrices or associated plots against null model simulations.

4. Background to application. Two human readers are presently used in England to interpret mammograms (breast x -rays) from the breast-cancer screening program. This regimen is often called double reading, but we will call it dual reading to emphasize that two independent readers inspect each mammogram. If both readers find no abnormalities, the screenee is notified of the negative result and no further action is taken. If both readers find a suspicious abnormality, the screenee is recalled for further investigations. If the readers disagree, one common practice is to have a third reader arbitrate. Typically, for 1,000 women undergoing screening, around 42 might be recalled, of whom 8 are found to have cancer after further investigation [NHS Breast Screening Programme (2009)]. Several studies have shown that two readers can detect more cancers than a single reader [Taylor and Potts (2008)]. The computer aided detection evaluation trial (CADET) II was designed to assess whether a single reader using a computer-aided detection tool could match the performance of two readers.

In the trial 31,057 mammograms were read at three centers in England, such that a ratio of 1 : 1 : 28 were, respectively, dual reading only; single-reading with CAD (computer-aided detection) only; and both dual reading and single reading with CAD. Most of the screens were therefore matched pairs from dual reading and single reading with CAD. The reason why some screens were only read by one of the regimens was to reduce the possibility of bias from readers changing their behavior due to the knowledge that a further reading of the case would take place. Only the 28,204 matched-pair cases are considered from now on. The main detection result was that 199 out of the 227 cancers detected were recalled by dual reading, and 198 by single reading with CAD. 170 of the cases were detected by both, so the single readers with CAD detected 28 cases missed by dual reading; dual reading detected 29 cases missed by the single reader with CAD (and $170 + 28 + 29 = 227$). The overall recall rate for dual reading was 3.4% and for single reading with CAD it was slightly higher at 3.9%. The analysis of the trial in Gilbert et al. (2008) found that single reading with computer-aided detection could be an alternative to dual reading.

The primary analysis published in Gilbert et al. (2008) addressed the question of whether detection and recall rates differ between dual reading versus single reading with CAD. Further questions may be posed of the data to help improve best practice in other areas: if factors can be identified that predict outcomes prior to the screen being read, then steps might be taken to mitigate risks. The aim of the analysis in this article is to assess whether individual readers behaved differently, and to determine if any factors might influence whether a reader missed more cancers, or recalled more often than others. In the data available from the trial we had information on their training (radiologist, radiographer, other) and the number of years they had read mammograms prior to the trial, and we explore whether any differences between them might be related to these two factors. Although there are a large number of screens, the total number of readers involved in the trial was 27, and so drawing inference is more difficult than might appear from consideration of the large number of 28,204 cases.

5. Reader recall and detection rates. In this section we use data from CADET II to demonstrate the z -matrix exploratory analysis as a precursor to model building. The aim of the analysis is to explore the data to assess if and why some readers performed differently to others.

5.1. *Data.* We present two exploratory analyses, one for the first reader in a dual-reader pair, the second for a single reader with CAD. In the case of a first reader i from a dual reading the response is detection of cancer: $y = 1$ when a cancer is detected, 0 otherwise. In the case of a single reader i with CAD the response is recall: $y = 1$ if a case is recalled, 0 if not. There are $k = 1, \dots, n_i$ screens by individual i , and we take

$$p(\mathbf{y}_i | u_i) \propto u_i^{y_i+} (1 - u_i)^{n_i - y_i+},$$

thus assuming that the y_{ik} are conditionally independent with $P(y_{ik} = 1) = u_i$. These data are shown in Tables 1 and 2. The total number of readers in both regimens differs partly due to not all of them being trained to used CAD. Further details about the data are in Gilbert et al. (2008).

Exploratory analyses were also conducted on other combinations of interest, such as on detection rate for single readers with CAD and for second readers in a dual-reader pair. The two presented are chosen because they show how the z -matrix can help to identify similar groups of readers.

5.2. *Exploratory analysis with similarity matrix.* For detection rate the point estimates \hat{u}_i in Table 1 show a group of three individuals with much higher detection rates than the others. Although these readers saw a relatively small number of cases, and the numbers detected are not larger than other readers, the z -matrix [Supplementary Table 1, Brentnall et al. (2011)] suggests the differences are not due to chance. The z -matrix has a block structure with one block corresponding to the 3 outlying readers, and the other block to everyone else. This can also be seen in Figure 1, which contains plots introduced in Section 3.1. The charts suggest that the results might be too extreme to be due to random variation, and that there are two groups. Further evidence of this is seen in the z_{ii} measures of concentration for first dual reader detection rate, shown in Table 1: are all low.

For single-readers with CAD the z -matrix based on data in Table 2 is shown in Table 3. The number of digits reading down each column gives an impression of the size of each z_{ij} for $j = 1, \dots, 18$, and the table shows a center effect where the clearest difference is between centers 2 and 3, with readers from center 1 straddling the two.

5.3. *Model.* The exploratory analysis suggests that a continuous model of $p(u)$ might be inappropriate because there appear to be clusters, or at least there is not enough information to separate individuals within the clusters. Therefore, a more plausible approach than a continuous distribution is to take a discrete

TABLE 1
Number of cases detected and recalled by first 26 dual readers. Analysis is undertaken for detection rate u_i

Center	Cancers y_{i+}	Recalls	Screens n_i	MLE (%) $\hat{u}_i = y_{i+}/n_i$	Concentration ($z_{ii} \times 1,000$)
2	2	10	18	11.1	290
2	8	26	92	8.7	375
2	4	19	53	7.5	363
3	5	11	355	1.4	108
1	5	16	394	1.3	92
3	9	27	805	1.1	103
2	11	36	1,022	1.1	109
1	15	62	1,412	1.1	124
1	6	24	628	1.0	73
2	18	76	1,922	0.9	124
2	11	46	1,384	0.8	83
2	14	67	2,128	0.7	82
1	8	62	1,221	0.7	68
3	5	25	769	0.7	60
1	1	3	160	0.6	47
3	6	29	997	0.6	64
3	12	61	2,002	0.6	76
2	7	34	1,180	0.6	66
3	5	23	906	0.6	63
3	7	27	1,312	0.5	69
1	8	51	1,571	0.5	74
1	10	57	2,132	0.5	86
2	7	40	1,556	0.4	82
1	3	21	735	0.4	72
3	8	48	2,166	0.4	124
1	4	46	1,284	0.3	127
OVERALL	199	947	28,204	0.7	—

distribution for u , with unknown locations u_j and masses θ_j for $j = 1, \dots, k$, where $k \leq n$. That is, $P(u = u_j; \theta) = \theta_j$. The nonparametric maximum likelihood (NPML) estimate of $p(u)$ is a discrete distribution and has the benefit of not requiring specification of the form of $p(u)$. An expectation-maximization (EM) algorithm is used to next obtain the NPML estimates [Laird (1978)], and a likelihood-ratio test is used to compare the model fit against a null model with a single atom. The p -values presented follow Self and Liang (1987), and are used as a way to show the evidence for the fitted model, rather than to formally control type I error. This is relevant because the test is *post hoc* based on exploratory analysis, so there is an element of multiple testing.

TABLE 2

Number of cases detected and recalled by 18 computer-assisted readers. Three cancer cases from center 2 had a missing reader identifier. Analysis is carried out on recall rate u_i

Center	Cancers	Recalls y_{i+}	Screens n_i	MLE (%) $\hat{u}_i = y_{i+}/n_i$	Concentration ($z_{ii} \times 1,000$)
2	11	57	953	6.0	170
2	11	64	1,080	5.9	170
2	14	59	1,012	5.8	160
2	7	61	1,062	5.7	156
2	9	69	1,257	5.5	156
2	9	49	921	5.3	143
1	16	113	2,408	4.7	257
2	8	46	993	4.6	168
2	5	46	1,037	4.4	183
1	12	87	2,150	4.0	322
2	5	36	1,037	3.5	172
1	11	76	2,266	3.4	249
3	9	61	2,045	3.0	171
1	17	79	2,713	2.9	180
3	7	27	953	2.8	141
3	25	84	3,089	2.7	188
3	9	48	1,835	2.6	183
3	10	35	1,390	2.5	192
2 (Unk.)	3	3	3	—	—
OVERALL	198	1,097	28,204	3.9	—

5.4. *Results.* For the first reader, the EM-algorithm fit has just two atoms at (0.0066, 0.0855) with respective masses (0.891, 0.109) and log-likelihood $-1,170.151$. This compares against a null model with a single point 0.0071 and log-likelihood $-1,184.125$. A likelihood-ratio test to compare the models rejects the hypothesis of no difference, with p -value < 0.001 . The estimation results for $p(u)$ corroborate the exploratory analysis: the first location (0.0071) is for the majority of readers (the mass is 0.891); the second location (0.0855) is for the top 3 readers in Table 1 with much higher detection rates.

The model fit for recall rate by readers using CAD also confirms the exploratory analysis. There are two points at (0.0293, 0.0507) with respective mass (0.449 0.551) and log-likelihood $-4,606.186$. The degenerate fit is 0.0389 and has log-likelihood $-4,637.097$, so a likelihood-ratio p -value < 0.001 .

5.5. *Interpretation.* The unusual group of three readers' detection rates, within the same center, can be explained by job title: they were the only radiographers in that center. However, it is unlikely that radiographers are assigned more cancer cases than radiologists because the outcome is unknown prior to the

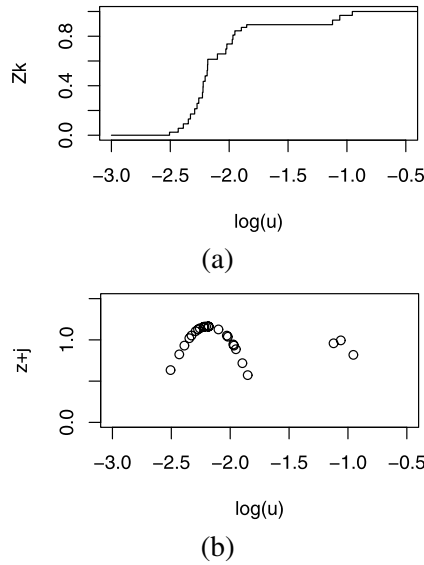


FIG. 1. Exploratory plots for detection rate, first dual reader. On the x-axis are \hat{u}_i on a \log_{10} scale. The y-axis in (a) is Z_k as defined in Section 3.1, on (b) it is z_{+j} , which corresponds to the jump sizes in (a).

screening. It seems more likely that center 2 used a post-event method of deciding who to call the first reader. This is discussed further in the next section.

Single readers with CAD were found overall to have higher recall rates (3.9%) than dual reading (3.4%). Table 2 shows that most of the readers with higher recall rates were in center 2. The z -matrix in Table 3 and the model estimation results point toward a difference that is linked to center 2. That is, the slight overall increase in recall rate of single reading with CAD over dual reading might have been caused by a policy difference, or difference in case-mix at one of the centers rather than errant individual readers.

6. Categorical dual-reader outcomes. The analysis in the previous section focused on binary outcomes. One of the advantages of the similarity matrix for exploratory analysis is that it can be readily applied to any likelihood model $p(\mathbf{y}|\mathbf{u})$. In this section we show an exploratory analysis of dual-reader performance when 6 categorical outcomes are considered and the likelihood of multinomial form.

6.1. *Data.* In this analysis each screenee belongs to a state S_{lm} , where $l = 1, 2$, respectively, denote a decision to recall or not by a reader from the dual-reading regimen; $m = 1$ for cancer present, $m = 2$ for cancer absent and $m = 3$ for cancer unknown. Thus, $P(y_{ik} = S_{lm}) = u_{ilm}$ for each case $k = 1, \dots, n_i$ seen by reader i .

The different states arise because even if a reader does not flag (or does flag) a case for recall, they may (or, respectively, may not) be recalled in the trial. More

TABLE 3

$(z^T \times 1,000)$ -matrix for reader recall rates using CAD. Within center the individuals are ordered ascending by \hat{u}_i . Note that the z -matrix is transposed in all the tables in this article, and so, for example, the diagonal is the largest value down each column, not row

Center	3	3	3	3	3	1	1	1	1	2	2	2	2	2	2	2	2	2
3	192	176	146	117	73	80	13			31								
3	187	183	176	130	102	115	27			45	1							
3	172	176	188	138	132	150	50	1		62	1	1						
3	148	156	174	141	158	175	87	2		84	3	1						
3	111	117	128	136	171	176	149	7		115	7	3						
1	129	136	152	140	168	180	118	4		100	5	2						
1	37	35	24	93	109	77	249	72	1	169	33	18	1					
1	2	1		19	7	1	57	322	75	109	150	111	25	7	5	4	2	3
1				2			2	112	257	26	169	168	97	67	46	41	31	33
2	24	21	11	76	80	47	238	117	2	172	49	27	2					
2				5	1		8	216	214	51	183	161	64	34	22	19	13	15
2				3			2	135	255	31	174	168	89	58	39	35	26	28
2								7	97	3	78	104	143	151	130	124	116	114
2									3	55	2	56	80	139	156	147	143	140
2									1	19	1	31	50	122	145	156	159	164
2										12		25	42	114	137	155	160	168
2										8		19	34	104	126	152	159	170
2										6		16	30	99	119	148	157	170

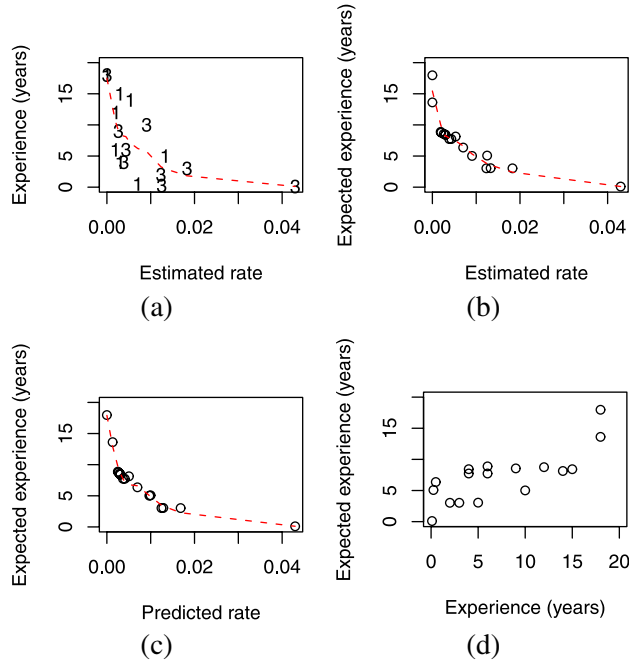


FIG. 2. Exploratory plots for recall-but-overruled rate vs. reader experience (years), based on data from Supplementary Table 2 (S_{13} vs. the rest). The data show some evidence that dual readers with less experience are more likely to be overruled in centers 1 and 3. Readers from center 2 are excluded from the plots because that center did not record when a reader flagged a case for recall that was not recalled (all $S_{13} = 0$). Plot (a) shows experience against the original estimates \hat{u} , with center number as the symbol. Plot (b) uses expected experience on the y-axis, following the approach in Section 3.5. The plots are presented with experience on the y-axis because they show a quantity for the expected experience given u . Plot (c) replaces the original estimate \hat{u} by a prediction from equation (3). Each dashed line (–) is a loess smoother fit. Plot (d) shows how expected experience relates to the original data.

The ordering of individuals by their estimate \hat{u}_i appears to relate to experience shown in the second row of the table, and the matrix pattern is inconsistent with a null hypothesis where everyone has the same u_i (Figure 3). The correlation to experience is most clearly displayed in Figures 2(b), (c).

6.3. Interpretation. The readers in each center worked independently, and made their recall decisions on their own. However, in center 2 the arbitration process involved discussion between several readers, once a disagreement was found between the first and second reader. This might be why readers in center 2 were recorded as first or second reader after the outcomes had been observed, and why the data (Supplementary Table 2) show that when a reader in center 2 flagged a case for recall, the case was always recalled regardless of the other reader. In any case, it is clear that, as originally recorded, it is difficult to compare readers from

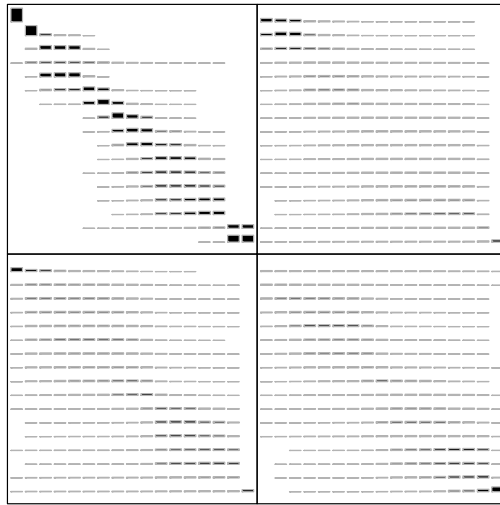


FIG. 3. Graphical testing of the z -matrix printed out in Supplementary Table 4. The top-left graphic shows the z -matrix (not transposed as in Supplementary Table 4) where each cell is represented by a rectangle with area proportional to z_{ij} . The rows are therefore histograms with the same total area for each row. The other three graphics are simulated z -matrices using the overall \hat{u} , obtained by pooling all the data. The same number of screens (n_i) were simulated for each reader i as in the data, and the matrices were ordered descending by simulated \hat{u}_i , for consistency with Supplementary Table 4. This graphical test suggests that there is some evidence to reject a null hypothesis that all readers have the same recall-but-overruled rate.

center 2 with the others in this analysis, and so it is reasonable to leave them out of Figure 2.

The statistical structure shown by the z -matrix exploration and in Figure 2, where the less-experienced readers tended to be overruled more often, fits with a training effect. It is common practice in dual reading to pair experienced readers with less experienced ones. Thus, the increased rate of overruled recall flags (by 3 different readers: the other, generally more experienced dual reader, an arbitrator and the independent reader with CAD) might be linked with less experienced readers being more cautious in their recall decision. Overall, dual reading mitigates this by pairing inexperienced readers with experienced ones who are able to overrule unnecessary recalls. It is unclear whether single reading with CAD would similarly mitigate this because, although the average experience of readers using CAD in CADET II was similar to dual reading, the minimum experience was 4 years (compare Figure 2). Thus, in any implementation of screening based on a single reader with CAD, it might be worth monitoring recall rates for readers with less than 4 years experience.

7. Dual reading vs. CAD false recall. So far we have considered analysis of the two screening regimens separately. Further modeling may be used to look at

them together. We end by investigating the difference in recall rate between single readers with CAD (3.9%) and dual reading (3.4%). To show the technique from a different angle, we proceed as if we did not know about the z -matrix, and first fit a statistical model to the data. Then, the z -matrix will be used to help provide more understanding of what the model has found.

7.1. *Data.* Let $y_{ik} = 1$ if CAD reader i recalls case $k = 1, \dots, n_i$ where no cancer is detected on recall but dual reading does not, and $y_{ik} = 0$ if CAD reader i does not recall the case where no cancer is detected on recall but dual reading does. Note that the comparison to be made is between the cases where single readers with CAD or dual readers flag for recall in error (but not both of them). The data from the trial are shown in Table 7: if $\hat{u}_i < 0.5$, then the CAD reader did better than dual readers, and if $\hat{u}_i > 0.5$, then they did worse.

7.2. *Model.* Consider a model

$$\text{logit}\{P(y_{ik} = 1 | \mathbf{x}_i, v_i; \boldsymbol{\beta}, \sigma^2)\} = \mathbf{x}_{ik}\boldsymbol{\beta}' + v_i,$$

where $\boldsymbol{\beta} = (\beta_0, \beta_1, \beta_2)$ are parameters and $\mathbf{x}_i = (x_{i1}, x_{i2}, x_{i3})$ are covariates; v_i is a random effect taken (for convenience) to be from a Normal distribution with

TABLE 7
Number of noncancers recalled by CAD reader (y_{i+}) when dual readers did not recall, for all cases recalled in error by either CAD readers or dual readers (but not both)

Center	Experience	y_{i+}	n_i	\hat{u}_i
1	4	21	43	0.488
1	6	20	59	0.339
1	12	29	50	0.580
1	14	17	32	0.531
1	15	13	28	0.464
2	4	38	65	0.585
2	4	27	42	0.643
2	5	29	45	0.644
2	5	28	44	0.636
2	6	18	35	0.514
2	7	26	43	0.605
2	8	29	42	0.690
2	17	34	42	0.810
2	22	38	62	0.613
3	4	35	92	0.380
3	6	46	96	0.479
3	9	61	103	0.592
3	18	45	88	0.511

mean 0 and variance σ^2 ; and $\text{logit}(\cdot)$ denotes the logistic function. The covariates are a constant ($x_{i1} = 1$), a factor for center 2 ($x_{i2} = 1$ for center 2, 0 otherwise) and a factor for reader experience (x_{i3}), whose form is explored below. Thus, the baseline is for centers 1 and 3 and readers with the reference reader experience. Other covariates [about the screen: first ever screen (incident) or not (prevalent), age, a score from the CAD algorithm predicting the likelihood of cancer; and about the reader: training (radiographer, radiologist, other)] were explored but did not significantly improve the model fit.

Maximum-likelihood estimation (the routine `xtlogit` in the computer software STATA that uses Gauss–Hermite quadrature for the likelihood) is used to find odds ratios and Wald 95% confidence bounds on the effects. The first definition of reader experience is a binary variable $x_{i3} = 1$ when reader i has more than six years experience, 0 otherwise. This definition was chosen because it roughly balances the readers by center, as seen in Table 7. The estimated odds ratios for center 2 and reader experience effects are, respectively, $1.54^{2.01}_{2.61}$ and $1.23^{1.59}_{2.06}$, where we use the useful notation from Louis and Zeger (2009) to present the point estimate surrounded by a 95% confidence interval. Using this definition of experience seems to account for most between-reader variation because $\ln(\hat{\sigma}^2) = -13.6_{(43.0)}$ [again following Louis and Zeger (2009) to put the standard error as a subscript]. Indeed, identical odds ratios are found from a straight logistic regression without v_i . Other definitions of reader experience suggest that a linear relationship is not a good one: if years of experience are used, then the odds ratio estimate is $1.00^{1.02}_{1.05}$, and the random-effect term becomes more important with $\ln(\hat{\sigma}^2) = 0.15_{(0.01)}$. Another possibility is to use $\log(\text{experience})$, which resulted in an estimated reader experience odds ratio of $1.04^{1.33}_{1.70}$.

The model fits provide some evidence that, perhaps surprisingly, the less experienced readers were less likely to recall in error with CAD than the experienced ones. This is different to the trend seen in Astley et al. (2006), although that was a retrospective study. Taken together with the results in Section 6.3, this might be interesting because it suggests that CAD might help the less experienced readers (<7 years) avoid unnecessary recall decisions. However, given that $n = 18$, one might be interested in understanding more about the data's structure, especially given the change in effect size depending on reader experience definition. We will proceed to further investigate using the z -matrix and some of the plots previously used.

7.3. z -matrix analysis. The z -matrix is shown in Supplementary Table 5. The data driving the experience effect from the model are that two readers with 6 and 4 years experience have relatively low \hat{u}_i , with their z_{ij} close to the other's z_{ji} , and they are relatively concentrated; and one reader with 17 years experience has the highest \hat{u}_i , which is also more concentrated than those in between. A center structure can also be observed: center 2 against the others. The experience pattern is also seen in Figure 4, where the three readers are clear in plots (b) and (c). How-

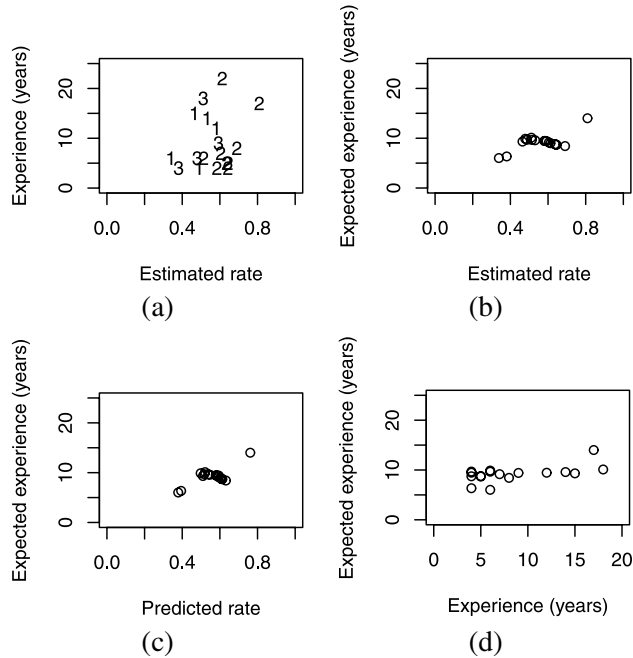


FIG. 4. Exploratory plots for single reader with CAD recall-in-error rate (relative to double reading) vs. reader experience (years). Plot (a) shows experience against the original estimates \hat{u} , with center number as the symbol. Plot (b) uses expected experience on the y-axis, following the approach in Section 3.5. Plot (c) replaces the original estimate \hat{u} by a prediction from equation (3). Plot (d) shows how expected experience relates to the original data.

ever, some caution in interpreting the reader experience correlation is required: differences are seen between the null and observed z -matrices in Supplementary Figure 2, but the pattern of two low \hat{u}_i and a single high \hat{u}_i might be due to chance. The plot casts doubt on whether the pattern is real, or whether it was (mis)fortune that led to the reader experience effect. A z -matrix examination therefore showed that the correlation between reader experience and u_i was driven by 3/18 readers with behaviors in opposite directions, but also showed that it is quite a weak finding.

7.4. *Other techniques.* The model fit may be explored in other ways. We end by using prediction to show that the center 2 effect is a more robust finding. If a noncancer case is not recalled by the single reader with CAD, then, using centers 1 and 3, we fit a logistic-regression model for the probability of recall by dual reading with covariates for incidence/prevalence (first or subsequent screen) and whether the case was arbitrated. A prediction from this model is that 156 such cases could be expected at center 2. This compares against an observed number of 130, so the dual readers did slightly better than might be expected. A similar

logistic-regression model was fitted to centers 1 and 3 for recall by the single reader with CAD, given the case was not a cancer and was not recalled by dual reading. A covariate for incidence/prevalence status was used together with a continuous variable correlated to the probability of cancer according to the computer tool. This model predicted a total of 140 such cases, but 267 were observed.

8. Application of the exploratory approach to other data. The z -matrix applies quite generally to the two-stage statistical setup described in Section 2. A similar data structure is found in other applications, such as the effect of physical tasks of patients, blood glucose levels and rat body weights that are in Crowder and Hand (1990); as well as many others including sport where individuals have repeated attempts to, for example, hit a ball in cricket, or score a goal in football; or in the workforce when productivity is measured by number of items processed by the worker. Thus, the technique might be used for growth curves, point processes or any other data structure where it is possible to write down a likelihood function for the individual.

One aim is to use the data to find structure among the units that would be seen again in future samples. A common approach to this problem is to fit a two-stage model, which, as seen in the above data analysis, might produce similar findings to the z -matrix approach. However, some strengths of the z -matrix as an exploratory technique, relative to use of full statistical models, include the following:

- As seen in Section 2.2, z_{ij} is a comparative measure that has a direct interpretation in terms of how close individual j 's parameter fit is to individual i 's data. Although other approaches can be used to estimate $p(\mathbf{u}_i|\mathbf{y})$, they lose the direct comparative aspect that arises in the z -approach from restricting the \mathbf{u} support to only contain $\hat{\mathbf{U}}_n = (\hat{\mathbf{u}}_1, \dots, \hat{\mathbf{u}}_n)$. For example, when using NPML in Section 5 an equivalent " z_{ij} " would have $j = 1, 2$ because there are two support points.
- Plots such as Figure 1 show that the z -matrix can be used to provide an indication of how many distinct groups there might be; NPML simply gives the most likely number. For exploratory analysis both are useful.
- The measure can be interpreted in a similar manner for different $p(y|\mathbf{u})$ likelihoods, and the information from \mathbf{u}_i vectors is shown in the same two-dimensional way for any dimension of \mathbf{u}_i . That is, the approach standardizes comparisons between the \mathbf{u}_i vectors for different types of response variables.
- The approach is quite general and can be easily applied to different $p(y|\mathbf{u})$ likelihoods. Although with a binomial likelihood many other approaches are feasible using statistical software, this will not always be the case. For example, the z -approach was used for prediction when the likelihood function was of a self-exciting point process form in Brentnall, Crowder and Hand (2008).
- For prediction the approach provides a simple approximate route to BLUP's (best linear unbiased predictors), or posterior means, through equation (3). Some

evidence of the benefit of predictions formed in this way using real data, compared with parametric empirical Bayes predictions, is found in [Brettnall, Crowder and Hand \(2010\)](#).

- Finally, while computationally-intensive methods may be justified for statistical modeling, it seems much less attractive to have to wait for exploratory analysis to run. Once the point estimates have been obtained, the method requires $O(n^2)$ computations for equation (1). This makes it most appealing for small to moderate n .

9. Conclusion. In this work we developed a method of exploratory analysis for applications in which repeated measurements have been recorded on a group of individuals. The aim of the approach is to draw attention to groups of similar behaviors, outliers and trends in the data. It does so by helping to quantify prediction uncertainty between individual point estimates through a “similarity” measure. This z -matrix used can be viewed as a discrete approximation to an empirical Bayes posterior distribution. The approach was motivated by an analysis of reader performance in CADET II. We showed its application to binary and multinomial response variables, and illustrated some identified properties of the measure using the data. One avenue for future research is to extend the approach to explicitly account for more than two levels in the hierarchical data structure. Such an extension would be useful for cancer screening since readers are sampled from screening centers.

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SUPPLEMENTARY MATERIAL

Supplement to “A method for exploratory repeated-measures analysis applied to a breast-cancer screening study” (DOI: [10.1214/11-AOAS481SUPP](https://doi.org/10.1214/11-AOAS481SUPP); .zip). Some additional tables and charts to accompany this paper.

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