

## University of Pennsylvania UPenn Biostatistics Working Papers

*Year* 2007

Paper 15

## Analysis of multi-level correlated data in the framework of generalized estimating equations via xtmultcorr procedures in Stata and qls functions in Matlab

Justine Shults\*

Sarah J. Ratcliffe<sup>†</sup>

\*University of Pennsylvania School of Medicine, jshults@cceb.med.upenn.edu

<sup>†</sup>University of Pennsylvania Perelman School of Medicine, sratclif@mail.med.upenn.edu This working paper is hosted by The Berkeley Electronic Press (bepress) and may not be commercially reproduced without the permission of the copyright holder.

http://biostats.bepress.com/upennbiostat/art15

Copyright ©2007 by the authors.

#### Analysis of multi-level correlated data in the framework of generalized estimating equations via xtmultcorr procedures in Stata and qls functions in Matlab Justine Shults

and

#### Sarah J. Ratcliffe

Department of Biostatistics and Epidemiology Center for Clinical Epidemiology and Biostatistics University of Pennsylvania School of Medicine 6th Floor Blockley Hall, 423 Guardian Drive Philadelphia, Pennsylvania, 19104-6021, USA Homepage: http://www.cceb.upenn.edu/faculty/?id=167 E-mail: jshults@cceb.med.upenn.edu

**Abstract.** Many studies yield data with multiple sources of correlation. For example, in a study of repeated measurements collected on each eye of spouses, three sources of correlation may be present, due to the fact that measurements within the same family will be more similar if they are measured on the same eye (left versus right), within the same person (husband versus wife), or at the same measurement occasion. This article reviews an algorithm for analysis of data with two or more sources of correlation (Shults, Whitt, Kumanyika, 2004) that can be implemented using quasi-least squares, an approach in the framework of generalized estimating equations. It then describes and demonstrates implementation of this algorithm with xtmultcorr procedures in Stata and the qls functions in Matlab. The Stata and Matlab procedures are available on the website for the Longitudinal Analysis for Diverse Populations project:

http://www.cceb.upenn.edu/~sratclif/QLSproject.html.

**Keywords:** Cholesky decomposition; correlated data; generalized estimating equations; multi-level data; multivariate data; quasi-least squares

## 1 Introduction

We consider the usual set-up for generalized estimating equations (GEE, Liang and Zeger, 1986), for which measurements are collected on multiple subjects, or clusters. Measurements from different clusters are assumed to be independent, but measurements from within the same cluster are assumed to be correlated.

The typical GEE analysis involves one source of correlation, where a source of correlation is defined as a factor that impacts the similarity (and therefore the correlation) of measurements. For example, in a longitudinal study that measures the weight of unrelated subjects, the timing of measurements will represent the one source of correlation because measurements within a subject that are collected more closely together in time should be more similar (and



therefore more highly correlated) than if they are measured farther apart in time, e.g. weights at baseline and two months post-baseline should be more highly correlated than weights collected at baseline and 12 months post-baseline.

This article considers data with multiple sources of correlation, which are sometimes referred to as multi-level data or multivariate longitudinal data. For example, suppose the longitudinal study described above was modified to measure weights on siblings over time. In this situation, we might expect an additional source of correlation in the data, due to anticipated similarity between siblings. Or, consider a study in which grip strength is measured on both hands of elderly twins at baseline and at one month post baseline. This study might be expected to yield data with three sources of correlation, because we anticipate that two measurements within a sibling pair will be more similar if they are measured on the same twin (older versus younger), on the same hand (left versus right), or at the same measurement occasion (baseline or one month post baseline). Many other examples of multi-level correlated data are described in Goldstein (1995).

The usual goal of a GEE analysis is to explore the relationship between the expected value of the outcome variable and covariates measured on each of the subjects, while adjusting for the correlation within the measurements on each cluster. Although the regression parameter is often the primary parameter of interest, the estimated correlations can often yield interesting information. For example, if the intra-hand correlations of grip strength in the intervention to improve strength in elderly subjects are negative, this might suggest that subjects are focusing their efforts on one hand to the detriment of the other. Or, if the intra-twin correlations of birth weight are negative in an intervention to improve birth weight in twins born to high risk mothers, this might suggest that improvement in birth weight for one twin is occurring at the expense of the other.

Although many studies yield data with multiple sources of correlation, GEE is typically implemented for data with one source of correlation, with relatively simple correlation structures used to describe the pattern of association amongst the repeated measurements on each subject (or cluster). In this manuscript we review an algorithm for analysis of data with multiple sources of correlation (Shults et al., 2004) in the framework of GEE. We then demonstrate implementation of this algorithm with the the user-written xtmultcorr and qls programs in Stata and Matlab, respectively.

We note that the majority of our descriptions in this manuscript are for data with three sources of correlation; however, all results can easily be generalized for data with two or more than three sources of correlation.

## 2 Methods

#### 2.1 Notation

The usual notation for a typical GEE analysis (Shults, Ratcliffe, Leonard, 2006) with one source of correlation is readily modified for data with multiple sources.

COBRA A BEPRESS REPOSITORY Collection of Biostatistics Research Archive

For example, consider a study in which repeated measurements are collected on independent subjects at baseline, and then at three and six months postbaseline. In this study we might anticipate that there is one source of correlation, due to the timing of measurements;  $y_{ij}$  and  $x'_{ij}$  might then represent the measurement of the outcome variable and vector of associated covariates that are collected on subject *i* at time *j*. Note that this notation for data with one source of correlation involves two subscripts, *i* that denotes the subject (or cluster) and *j* that denotes the value of the first (and only) source of correlation. To extend our notation to a study with three sources of correlation, we simply expand the number of subscripts to four, so that  $y_{ij_1j_2j_3}$  and  $x'_{ij_1j_2j_3}$  represents the value of the outcome variable and associated  $p \times 1$  vector of covariates that are collected on subject (or cluster) *i* when the values of the first, second, and third source of correlation are  $j_1$ ,  $j_2$  and  $j_3$ , respectively.

Next, it will be helpful to refer to  $Y_i[a, b, c]$  as the vector of outcomes of measurements  $y_{ij_aj_bj_c}$  on subject *i* that has been sorted first according to  $j_a$ , and then  $j_b$ , and then  $j_c$ . Our approach for analysis of multi-level data is appropriate for data that are balanced overall, so that  $j_c = 1, 2, \ldots, n_c$  in  $Y_i[a, b, c]$  for all *i* and (a, b, c) in the class of all permutations of (1, 2, 3). For example, in a longitudinal study of visual acuity measured on both eyes of spouses at baseline and six months post-baseline, the study will be balanced overall if there are no missing observations; in this case, we might let spouse, eye, and time represent the first, second, and third sources of correlation, with  $j_1 = 1, 2$  (1 for wife, 2 for husband),  $j_2 = 1, 2$  (1 for left eye, 2 for right eye), and  $j_3 = 1, 2, 3$  (number of measurement occasion) within husband/wife cluster *i*.

Our manuscript provides programs in Stata and Matlab for data that are balanced overall. We note that our programs check for balance and return an error message if the data are not balanced. We also note that extensions to our programs are underway for data that are not balanced overall, but that are balanced within clusters.

Note that GEE is usually applied for analyses that involve a relatively large number of small clusters (or subjects), with 30 often used as an informal lower bound for the number of clusters that are required to yield valid results. In multi-level analyses the cluster sizes can be larger than in the typical analysis, that might involve 3 or 4 measurements per cluster. For example, in the study of visual acuity described above, if the data are totally balanced, the cluster sizes will be  $n_1 \times n_2 \times n_3 = 2 \times 2 \times 3 = 12$ . We suspect that the correlations may play a more prominent role in multi-level studies because they typically yield data with larger cluster sizes, and hence provide more information with which to estimate the pattern of association in the data.

# 2.2 Specification of a working correlation structure for analysis of multi-level data in the framework of GEE

GEE analyses specify a generalized linear model to describe the relationship between the outcome and covariates measured on each subject: The expected value and variance of measurement  $y_{ij_1j_2j_3}$  on subject (or cluster) *i* are assumed

COBRA A BEPRESS REPOSITORY Collection of Biostatistics Research Archive

to equal  $E(y_{ij_1j_2j_3}) = g^{-1}(x'_{ij_1j_2j_3}\beta) = u_{ij_1j_2j_3}$  and  $Var(y_{ij_1j_2j_3}) = \phi h(u_{ij_1j_2j_3})$ , respectively, where  $\phi$  is a known or unknown scale parameter. We also let  $U_i(\beta)$  represent the  $w_i \times 1$  vector of expected values  $u_{ij_1j_2j_3}$  on subject i, where  $w_i = n_1 \times n_2 \times n_3$ .

The intra-cluster correlation of measurements is then accounted for in the analysis by specifying a patterned correlation matrix  $R_i$  to describe the pattern of association of measurements within cluster i, for i = 1, 2, ..., m. Some popular structures for data with one source of correlation include the following:

- 1. The Equicorrelated (Exchangeable): This assumes equality of correlations within each cluster, so that  $R_i[j,k] = \alpha$ . For  $n \times n$  structure  $R_i$ ,  $R_i$  will be positive definite for  $\alpha$  in (-1/(n-1), 1).
- 2. The first-order autoregressive AR(1): This assumes correlations will be smaller for measurements that are farther apart in terms of measurement occasion, so that  $R_i[j,k] = \alpha^{j-k}$  for  $\alpha$  in (-1,1).
- 3. The tri-diagonal correlation structure: This structure has ones on the diagonal and  $\alpha$  on the off-diagonal, so that  $R_i[j,k] = \alpha$  for |j-k| = 1and is zero otherwise. If  $R_i$  is  $n \times n$ , it will be positive definite for  $\alpha$  in  $(-1/c_m, 1/c_m)$ , where  $c_m = 2 \sin \left(\frac{\pi [n-1]}{2[n+1]}\right)$ . This interval is approximately (-1/2, 1/2) for large n and contains (-1/2, 1/2) for all n.

We will use the structures just described to construct a biologically plausible correlation structure for data with multiple sources of correlation: (As noted earlier, we will describe all results for data with three sources of correlation, but the results can be readily generalized for two or > 3 sources.)

To construct a biologically plausible structure for data with multiple sources of correlation:

- 1. First, within each cluster (or subject) identify one source of correlation as the first source, another source as the second, and another as the third.
- 2. For each source of correlation, choose the correlation structure that would be appropriate if the source under consideration was the only source of correlation in the data. Let  $R_a$  be the correlation structure for source a; a = 1, 2, 3.
- 3. When done, construct the correlation structure for the vector of measurements  $Y_i[1,2,3]$  as the Kronecker product of  $R_1$ ,  $R_2$ , and  $R_3$ , i.e.  $Corr(Y_i[1,2,3]) = R_1 \bigotimes R_2 \bigotimes R_3$ . The covariance matrix of  $Y_i[1,2,3]$  is then given by  $Cov(Y_i[1,2,3]) = \phi A_i^{1/2} R_1 \bigotimes R_2 \bigotimes R_3 A_i^{1/2}$ , where  $A_i = diag(h(u_{i111}), \ldots, h(u_{in_1n_2n_3}))$ ; it is also easily shown that  $Corr(Y_i[a, b, c]) = \phi A_i^{1/2} R_a \bigotimes R_b \bigotimes R_c A_i^{1/2}$ , where (a, b, c) is any permutation of (1, 2, 3).

For example, consider the study of visual acuity described above for data that are balanced overall. To specify a correlation structure for the first source



of correlation (spouse), we imagine that the only source of correlation is due to spouse, e.g. we have a study in which only one measurement was collected on one eye of each spouse; in this situation a reasonable structure for  $R_1$  is  $2 \times 2$  structure

$$R_1 = \left(\begin{array}{cc} 1 & \alpha_1 \\ \alpha_1 & 1 \end{array}\right).$$

Similarly, a reasonable structure for the second source of correlation (eye) is given by

$$R_2 = \left(\begin{array}{cc} 1 & \alpha_2 \\ \alpha_2 & 1 \end{array}\right).$$

For the third source of correlation, we might specify an AR(1) correlation structure:

$$R_3 = \begin{pmatrix} 1 & \alpha_3 & \alpha_3^2 \\ \alpha_3 & 1 & \alpha_3 \\ \alpha_3^2 & \alpha_3 & 1 \end{pmatrix}$$

The correlation structure for  $Y_i[1,2,3]$  is then constructed as  $R_1(\alpha_1) \bigotimes R_2(\alpha_2) \bigotimes R_3(\alpha_3)$ .

This Kronecker product structure has been discussed and implemented by several authors, including Galecki (1994) and Naik and Rao (2001), Roy and Khattree (2005) and Lu and Zimmerman (2005) developed tests for this structure for multivariate repeated measures data that are normally distributed. It is a popular structure for analysis of multi-level correlated data because it forces the correlation between measurements to be smaller when they have more disagreement with respect to the sources of correlation in the data, which is often biologically plausible.

For example, if  $Corr(Y_i[1,2,3]) = R_1 \bigotimes R_2 \bigotimes R_3$ , then using the definition of Kronecker product,  $Corr(y_{ij_1j_2j_3}, y_{ik_1k_2k_3}) = R_1[j_1, k_1] \times R_2[j_2, k_2] \times R_3[j_3, k_3]$ . If we apply this to our visual acuity example, then we see that the correlation between measurements collected on the same spouse and same eye (left versus right) at visits one and two is  $\alpha_3$ . However, if the measurements are collected on the same spouse, but on different eyes, at visits one and two, then the correlation is  $\alpha_2 \times \alpha_3$ . Finally, if the measurements within families were collected on different spouses and different eyes at visits one and two, then the correlation would be  $\alpha_1 \times \alpha_2 \times \alpha_3$ . Therefore, if the parameters are all positive, we see that the correlation between measurements will be smaller as their degree of disagreement with respect to the sources of correlation in the data decreases.

Shults and Morrow (2002) and Chaganty and Naik (2002) implemented the Kronecker product structure for data with two sources of correlation. Shults, Whitt, and Kumanyika (2004) proposed a general algorithm that allows for data with 2 or more sources of correlation; this is the approach we use in this manuscript.

COBRA A BEPRESS REPOSITORY Collection of Biostatistics Research Archive

#### 2.3 Overview of algorithm for implementation of the Kronecker Product Structure

The xtmultcorr and qls procedures implement the Kronecker product correlation structure using quasi-least squares (Chaganty and Shults, 1999), an approach in the framework of GEE that allows for easier implementation of some correlation structures, including the Kronecker product structure.

To summarize briefly, QLS is a two-stage approach that in stage one alternates between updating the estimate of the regression parameter  $\beta$  by solving the GEE estimating equation for  $\beta$  (Liang and Zeger, 1986) and updating the estimate of the correlation parameter  $\alpha$  by solving the QLS stage one estimating equation for  $\alpha$ . (The QLS stage one estimate of  $\alpha$  (Chaganty, 1997) has the drawback of being inconsistent, even when the working correlation structure is correctly specified.) After convergence in stage one, the (consistent) stage two estimate of  $\alpha$  is obtained solving the QLS stage two estimating equation for  $\alpha$ . The final QLS estimate of  $\beta$  is then obtained by again solving the GEE estimating equation for  $\beta$  evaluated at the stage two estimate of  $\alpha$ . For more details of the QLS approach and its implementation for data with one source of correlation in Stata, see Shults et al. (2006) and Sun et al. (2006). For information on implementation of QLS in Matlab, see Ratcliffe and Shults (2006).

Programs for the stage one and stage two QLS estimating equations for  $\alpha$  for a particular correlation structure require subject id, the variable indicating timing of measurements, and the vector of Pearson residuals as arguments. The Pearson residuals, defined for data with one source of correlation, are defined for subject *i* as  $Z_i(\beta) = (z_{i1}, z_{i2}, \ldots, z_{in_i})'$  for  $z_{ij} = (y_{ij} - u_{ij})/h(u_{ij})$ . The covariance matrix of the vector of Pearson residuals, for data with one source of correlation, is easily shown to be equal to  $\phi R_i$ , so that the covariance matrix for the vector of Pearson residuals that is obtained by stacking the vectors for all subjects,  $Z = (Z_1', Z_2', \ldots, Z_m')'$ , is given by  $I(m \times m) \bigotimes R_i$ , the kronecker product of an  $m \times m$  identity matrix and  $R_i$ .

The stage one QLS algorithm for implementation of the Kronecker product correlation structure that is appropriate for data with > 2 sources of correlation is based on the observation that if we pre-multiply the vector of Pearson residuals  $Z_i[a, b, c]$  by the kronecker product of the square root of the inverse of  $R_a$  and the square root of the inverse of  $R_b$  and an  $n_c \times n_c$  identity matrix, then we obtain the usual correlation structure for data with one source of correlation. In particular,  $Corr\left(R_a^{-1/2} \otimes R_b^{-1/2} \otimes R_c^{-1/2}\right) Z_i[a, b, c]$  $= \left(R_a^{-1/2} \otimes R_b^{-1/2} \otimes I(n_c \times n_c)\right) \phi\left(R_a \otimes R_b \otimes R_c\right) \left(R_a^{-1/2} \otimes R_b^{-1/2} \otimes I(n_c \times n_c)\right)$  $= \phi I(n, n_i \times n_i) \otimes R$  To undate the correlation parameters in stage one

 $= \phi I(n_a n_b \times n_a n_b) \bigotimes R_c$ . To update the correlation parameters in stage one, we were therefore able to utilize an approach that alternated between sorting, pre-multiplying, and using programs written earlier for data with one source of correlation, applied to the vector of pre-multiplied Pearson residuals.

To obtain estimates in stage two, Shults et al. (2004) proved that each correlation parameter can be updated separately, e.g. the stage two estimate of  $\alpha_2$  is only a function of the stage one estimate of this parameter.

COBRA A BEPRESS REPOSITORY Collection of Biostatistics Research Archive

#### 2.3.1 Algorithm for Estimation of the Correlation and Regression Parameters for Data with Multiple Sources of Correlation

The xtqls and qlsr procedures implements the following algorithm for estimation of  $\beta$  and of  $\alpha_j$  (j = 1,2,3): (Please see Shults et al. (2004) for more details and justification of this approach.)

- 1. Let  $\hat{\alpha}_j = 0$  represent initial estimates of  $\alpha_j$ , for j = 1, 2, 3. Let  $old_j = \hat{\alpha}_j$  for j = 1, 2, 3.
- 2. Obtain a starting value for  $\hat{\beta}$  by assuming  $\alpha_j = 0$  and then obtaining a solution to the GEE estimating equation for  $\beta$  at  $\alpha_j = 0$  for j = 1, 2, and 3. (Note that this is equivalent to using linear regression, logistic regression, or Poisson regression to obtain a starting value for  $\hat{\beta}$ , for an outcome variable that is continuous, binary, or that represents counts, respectively.)
- 3. For (a, b, c) = (1, 2, 3), (3, 1, 2), and (2, 3, 1), do the following: Sort on i,  $j_a, j_b$ , and then  $j_c$  and create a new id variable id[a, b, c] that takes values  $1, 2, \ldots$  and that takes a different value for each distinct value of  $(i, j_a, j_b)$ . These new identification variables will be used when updating the  $\alpha_j$  in stage one of QLS.
- Alternate between the following steps till convergence in the estimates of β:
  - (a) Obtain updated values of the Pearson residuals  $z_{ij_1j_2j_3}$  at the current estimate of  $\beta$ .
  - (b) Update the estimate of the correlation parameters by alternating between the following steps until  $\Delta_j \approx 0$  for j = 1, 2, 3:
    - i. Implement the stage one updating step (given below) for (a, b, c) = (1, 2, 3):
    - ii. Implement the stage one updating step for (a, b, c) = (3, 1, 2).
    - iii. Implement the stage one updating step for (a, b, c) = (2, 3, 1).

Stage one updating step: First, sort the data with respect to i, then  $j_a$ ,  $j_b$ , and  $j_c$ . Next, pre-multiply the vectors of Pearson residuals  $Z_i[a, b, c]$  within each subject i by  $R_a^{-1/2} \bigotimes R_b^{-1/2} \bigotimes I(n_c \times n_c)$ ; call the vector of pre-multiplied residuals  $Z_i^*[a, b, c]$ . Solve the QLS stage one estimating equation for  $\alpha_c$ , under the assumption that the working correlation structure is  $R_c(\alpha_c)$ . (Note that the programs to solve this equation will require the following as arguments:  $Z_i^*[a, b, c]$  (pre-multiplied Pearson residuals), id[a, b, c] (identification variable), and  $j_c$  (representing the timings for each cluster indicated by different values of id[a, b, c]). After obtaining an updated estimate of  $\alpha_c$ , update the estimate



of  $R_i^{-1/2}(\alpha_c)$  and then obtain  $\Delta_c$ , the difference between the updated estimate of  $\alpha_c$  and the previous estimate  $old_c$ . Next, let  $old_c$  equal the updated estimate of  $\alpha_c$ .

- (c) Construct the estimated working correlation structure  $W(\hat{\alpha}_1, \hat{\alpha}_2, \hat{\alpha}_3) = R_1(\hat{\alpha}_1) \bigotimes R_2(\hat{\alpha}_2) \bigotimes R_3(\hat{\alpha}_3)$  that corresponds to the updated estimates of  $\alpha_j$  (j = 1, 2, 3).
- (d) Update the estimate of β by solving the GEE estimating equation (for β) with a correlation structure that is treated as fixed and equal to W(â<sub>1</sub>, â<sub>2</sub>, â<sub>3</sub>).
- 5. After convergence in stage one of QLS, update the estimate of  $\alpha_j$  (j = 1, 2, 3) by solving the stage two estimating equation for each parameter. Note that for each parameter this only involves specification of the working structure and the vector of timings for each cluster.
- 6. Construct the estimated working correlation structure  $W(\hat{\alpha}_1, \hat{\alpha}_2, \hat{\alpha}_3) = R_1(\hat{\alpha}_1) \bigotimes R_2(\hat{\alpha}_2) \bigotimes R_3(\hat{\alpha}_3)$  that corresponds to the stage two estimates of  $\alpha_j$  (j = 1, 2, 3).
- 7. Update the estimate of  $\beta$  by solving the GEE estimating equation (for  $\beta$ ) with a correlation structure that is treated as fixed and equal to  $W(\hat{\alpha}_1, \hat{\alpha}_2, \hat{\alpha}_3)$ .

The xtmultcorr Stata procedures implement the xtgee procedure to solve the GEE estimating equation for  $\beta$  in steps 4(d) and 7 of the algorithm. This exploits the fact that the xtgee procedure allows for solution of the GEE estimating equation at a current estimate of the correlation structure that is treated as fixed and known. An important consequence is that all the usual post regression commands in Stata are available after implementation of xtqls.

The Matlab programs implement an approach for updating the estimate of  $\beta$  that is based on the inverse of the Cholesky decomposition of the working correlation structure; this approach is described in Shults (1996) and Shults and Chaganty (1998).

## 3 The xtmultcorr commands in Stata 9.0

#### 3.1 Syntax

The xtmultcorr commands have the following syntax which is similar to the syntax for the xtgee procedure, expect that the command requires specification of additional variables for each source of correlation and options to indicate the correlation structure that will be implemented for each source of correlation

For data with 2 sources of correlation, the xtmultcorr2 procedure is used.

xtmultcorr2 depvar [indepvars], options

8

Collection of Biostatistics Research Archive where *depvar* is the dependent variable; *indepvars* are the covariates; and *options* are the required options that are described below, in the following section.

For data with 3 or 4 sources of correlation, the xtmultcorr3 and xtmultcorr4 procedures are used, respectively. The syntax will be the same as for xtmultcorr2, but the options will differ, as described in the following section.

#### 3.2 Description

The xtmultcorr2, xtmultcorr3, and xtmultcorr4 commands provide QLS estimates of the regression and correlation parameters for data with 2, 3, and 4 sources of correlation, respectively. This is done by implementation of a Kronecker product correlation structure of 2, 3, or 4 correlation structures (for 2,3, or 4 sources of correlation, respectively), each of which would be appropriate for data with one source of correlation. The correlation structures can be chosen from among the equicorrelated, AR(1), Markov, and tri-diagonal correlation structures.

#### 3.3 Options

The options for xtmultcorr2 (all required) are as follows:

- 1. i(var1) where var1 is the ID variable for subjects, or clusters
- 2. 11(var2) where var2 is the variable that indicates the value of source one of correlation
- 3.  $12(var\beta)$  where  $var\beta$  is the variable that indicates the value of source two of correlation
- 4. c1(*corr1*) where *corr1* is the correlation structure for source one of correlation
- 5. c2(corr2) where corr2 is the correlation structure for source two of correlation. The following correlation structures can be implemented in the xtmultcorr programs:
  - (a) AR 1 (AR(1))
  - (b) sta 1 (tridiagonal)
  - (c) exc (equicorrelated)
- 6. f(*family*) where *family* is the distribution of depvar. The following families can be implemented in the xtmultcorr programs:
  - (a) gau (Gaussian)
  - (b) bin (Bernoulli/binomial)
  - (c) poi (Poisson)

- 7. vce(*vcetype*) where *vcetype* indicates the type of covariance structure for estimation of  $\hat{\beta}$ . The following covariance structures can be implemented in the xtmultcorr programs:
  - (a) model (model based covariance structure)
  - (b) robust (sandwich type robust sandwich covariance matrix)
  - (c) jack (obtains jack-knife standard errors)
  - (d) boot (obtains boot-strapped standard errors)

The options for xtmultcorr3 (all required) are as follows:

- 1. i(var1) where var1 is the ID variable for subjects, or clusters
- 2. 11(var2) where var2 is the variable that indicates the value of source one of correlation
- 3.  $l2(var\beta)$  where  $var\beta$  is the variable that indicates the value of source two of correlation
- 4.  $13(var_4)$  where  $var_4$  is the variable that indicates the value of source three of correlation
- 5. c1(*corr1*) where *corr1* is the correlation structure for source one of correlation
- 6. c2(*corr2*) where *corr2* is the correlation structure for source two of correlation.
- 7. c3(corr3) where corr3 is the correlation structure for source three of correlation.
- 8. f(family) where family is the distribution of depvar.
- 9. vce(*vcetype*) where *vcetype* indicates the type of covariance structure for estimation of  $\hat{\beta}$ .

The *options* for xtmultcorr4 (all required) are as follows:

- 1. i(var1) where var1 is the ID variable for subjects, or clusters
- 2. 11(var2) where var2 is the variable that indicates the value of source one of correlation
- 3. 12(*var3*) where *var3* is the variable that indicates the value of source two of correlation
- 4. 13(var4) where var4 is the variable that indicates the value of source three of correlation



- 5. 14(var5) where var5 is the variable that indicates the value of source four of correlation
- 6. c1(corr1) where corr1 is the correlation structure for source one of correlation
- 7. c2(*corr2*) where *corr2* is the correlation structure for source two of correlation.
- 8. c3(corr3) where corr3 is the correlation structure for source three of correlation.
- 9. c4(*corr4*) where *corr4* is the correlation structure for source four of correlation.
- 10. f(family) where family is the distribution of depvar.
- 11. vce(*vcetype*) where *vcetype* indicates the type of covariance structure for estimation of  $\hat{\beta}$ .

#### 3.4 Relationship to the xtgee procedure

The xtmultcorr procedure implements the xtgee procedure and has important similarities to the xtgee procedure that are the same as the similarities between xtqls and xtgee; please see section 3.4 of Shults, Ratcliffe, Leonard (2006) for more details.

#### 3.5 Saved Results

The saved results for the xtmultcorr programs are the same as those for the xtgee procedure in Stata. For example, typing xtcorr after implementing xtmultcorr2 in an analysis will display the estimated correlation matrix.

## 4 Examples in Stata

Here we demonstrate implementation of the xtmultcorr commands in Stata.

#### 4.1 Data and variables

We will use the data set

example\_multlevel.dta

that is available on http://www.cceb.upenn.edu/~sratclif/QLSproject.html. This is a data set that is based on Table 3.7 (p. 65) of Davis (2002). The data are from a study (Weissfeld and Kshirsagar, 1992) in which three methods of suctioning an endotracheal tube were applied in random order to 25 patients in an intensive care unit. The outcome variable was oxygen saturation, that was measured on each patient at baseline, first suctioning pass, second suctioning pass, third suctioning pass, and five minutes after suctioning.

Let's open the data set in Stata and describe the variables:



```
. use example_multlevel, clear
. de Contains data from example_multlevel.dta
 obs:
      375
vars:
            6
                                 30 Nov 2006 09:06
size:
        19,500 (98.1% of memory free)
_____
                                          _____
> ---
         storage display
                        value
variable name type format
                         label variable label
> --
          double %10.0g
id
                                 subject id
         double %10.0g
time
                                measurement occasion
type
         double %10.0g
                               method of suctioning
o2
          double %10.0g
                               oxygen saturation
          double %10.0g
family
                                artificial family variable
          double %10.0g
                                1 if o2>96; 0 otherwise
high
Sorted by: id type time
  Let's next check the number of subjects:
. summ id
  Variable | Obs Mean Std. Dev.
                                      Min
                                               Max
  _____+____
       id |
             375 13.68 7.603405
                                        1
                                                 26
. qui tab id
. di _result(2) 25
  There are 25 subjects.
  Next, let's tabulate time and type of measurement:
. tab type
 method of |
            Freq. Percent
suctioning |
                            Cum.
            ------
      1 |
             125 33.33
                             33.33
      2
              125
                     33.33
                             66.67
                  33.33
                           100.00
             125
      3 |
    Total |
               375 100.00
                      12
```

```
. tab time
```

measurement occasion	   Freq.	Percent	Cum.
1	75	20.00	20.00
2	75	20.00	40.00
3	75	20.00	60.00
4	75	20.00	80.00
5	75	20.00	100.00
Total	375	100.00	

It appears that type and time are balanced overall, although this will be checked in our programs. Next, let's summarize family:

summ	famil	y
		~

Variable	Obs	Mean	Std. Dev.	Min	Max
family	375	6.76	3.619023	1	13

The variable family is an artificial grouping (not in the original data set) that was created to demonstrate analysis of data with 3 sources of correlation. There are 12 families of size two and one family (that contains the subject with id = 26) of size one.

For the examples we consider here, we will regress oxygen saturation score (o2) on time. We consider a simple regression model for the mean because our goal is to demonstrate our xtmultcorr programs. We will demonstrate implementation of the robust sandwich-based covariance matrix and also of the model based covariance matrix. In addition, we will consider a binary outcome, high, that takes value one if  $o_2 > 96$  and takes value zero otherwise.

#### 4.2 Adjustment for two sources of correlation

First, we will account for two sources of correlation. In this analysis the measurements will be clustered by subject and type and time will be identified as the first and second source of correlation. (However, note that the ordering of type and time could have been reversed.) We specify the equicorrelated structure for source one (type) and the AR(1) structure for source two (time). We also specify the model based covariance matrix for estimation of the covariance matrix of  $\beta$ :

```
. xtmultcorr2 o2 time, i(id) l1(type) l2(time) c1(exc) c2(AR 1)
f(gau) vce(model)
```

Estimated correlation associated with level one: symmetric \_\_000003[3,3] c1 c2 c3 r1 1 r2 .14911158 1 r3 .14911158 .14911158 1 Estimated correlation associated with level two: symmetric \_\_000004[5,5] c1 c3 c4 c2 c5 1 r1 r2 .68092105 1 r3 .46365348 .68092105 1 r4 .31571141 .46365348 .68092105 1 r5 .21497455 .31571141 .46365348 .68092105 1 Iteration 1: tolerance = .01781086 Iteration 2: tolerance = 0 GEE population-averaged model Number of obs = 375 Group and time vars: id \_\_00001T Number of groups = 25 Link: identity Obs per group: min = 15 avg = 15. Family: Gaussian Correlation: fixed (specified) max = 15.Wald chi2(1) 0.57 Prob > chi2 Scale parameter: 7.566478 = 0.4493\_\_\_\_\_ o2 | Coef. Std. Err. z P>|z| [95% Conf. Interval] \_\_\_\_\_ \_\_\_\_\_ time | .0856649 .1132207 0.76 0.449 -.1362436 .3075734 \_cons | 95.66081 .4356795 219.57 0.000 94.80689 96.51473

#### 4.3 Adjustment for Three Sources of Correlation

In this analysis we will take the artificial family groupings into account, so that the measurements will be clustered according to family. Our data are not balanced with respect to family because we have 25 families of size two and one family (for id = 26) of size one. Because our programs assume the data are balanced overall, we will first drop subject with id = 26, in order to have 24 equally sized families:

. drop if id==26

COBRA A BEPRESS REPOSITORY Collection of Biostatistics Research Archive

Next, let's demonstrate analysis of the binary outcome, with a robust sandwich based covariance matrix for estimation of the covariance matrix of the regression parameter:

```
. xtmultcorr3 high time, i(family) l1(id) l2(type) l3(time) c1(exc)
c2(exc) c3(AR 1) f(bin 1) vce(robust)
```

Data are not balanced within subjects with respect to sources of correlation.

The variable *id* must take value  $1, 2, ..., n_1$  for each subject *i*, *after sorting* on type and time. We therefore need to create a new identification variable that can be used in the xtmultcorr3 program:

```
. sort family id
.qui by family id: gen id2=1 if _n==1
.qui by family: replace id2 = sum(id2)
. xtmultcorr3 high time, i(family) 11(id2) 12(type) 13(time) c1(exc)
c2(exc) c3(AR 1) f(bin 1) vce(robust)
Estimated correlation associated with level one:
symmetric __000003[2,2]
           c1
                      c2
            1
r1
   .04860953
                       1
r2
Estimated correlation associated with level two:
symmetric __000004[3,3]
          c1
                               c3
                    c2
r1
           1
r2
   .1518791
                     1
r3
   .1518791
             .1518791
                                1
Estimated correlation associated with level three:
symmetric __000005[5,5]
          c1
                      c2
                                 c3
                                             c4
                                                        c5
            1
r1
    .64306572
r2
                       1
r3
    .41353352 .64306572 1
r4
    .26592923
               .41353352
                          .64306572
                                              1
r5
    .17100997 .26592923 .41353352 .64306572
                                                        1
                                15
```

Collection of Biostatistics Research Archive

```
Iteration 1: tolerance = .00844386

Iteration 2: tolerance = .00004461

Iteration 3: tolerance = 7.387e-09

GEE population-averaged model Number of obs =

Group and time vars: family __00001U Number of groups =

Link: logit Obs per group: min = 30

Family: binomial avg = 30
```

Family:binomialavg = 30Correlation:fixed (specified)max = 30Wald-chi2(1)=0.31Scale parameter:1Prob > chi2=0.5759

(Std. Err. adjusted for clustering on family )

= 360

= 12

high	Coef.	Semi-robust Std. Err.	z	P> z	[95% Conf.	Interval]
time	.0308239	.0551098	0.56	0.576	0771892	.1388371
_cons	3893841	.3379246	-1.15	0.249	-1.051704	.2729359

As we might expect (based on the fact that the family grouping was artificial) the estimated correlation associated with family was very small, with  $\hat{\alpha}_1 = .04860953$ .

We also note that because the xtmultcorr programs make use of the xtgee program in Stata, all the usual post-regression estimation commands are available after analysis. For example, if we use the xtcorr command in Stata we can print the estimated correlation matrix that is the Kronecker product of the estimated working structures for each source of correlation. Below, the first 5 lines of the correlation matrix are displayed:

#### . xtcorr

#### Estimated within-family correlation matrix R:

	c1:	c1:	c1:	c1:	c1	.: c	2:	c2:	c2:
	c1	c2	c3	c4	c5	5 c	:1	c2	c3
r1:r1	1.0000								
r1:r2	0.6431	1.0000							
r1:r3	0.4135	0.6431	1.0000						
r1:r4	0.2659	0.4135	0.6431	1.0000					
r1:r5	0.1710	0.2659	0.4135 0	0.6431	1.0000				

16

Collection of Biostatistics Research Archive

## 5 Using Matlab

The above analyses can also be performed in Matlab using the qls functions. Here we present a brief outline of the commands and results. Further information can be obtained using the help function, and in the user guide available online.

#### 5.1 Syntax

The qls function has the following syntax:

[bhat, alpha, results] = qls(id, y, t, X, Family, CorrStruct, varnames, tol, maxit)

where id is the unique subject/cluster identification variable, y is the dependent variable, t is the variable(s) indicating the sources of correlation, and X are the covariates. The remaining parameters are optional and are used to specify the assumed distribution of the data (Family, default=Gaussian), assumed correlation structure for each source of correlation (CorrStruct, default=AR(1)), variable names for X used in result displays (varnames), and convergence tolerance (tol) and maximum number of iterations (maxit) used in the qls algorithm. When multiple sources of correlation need to be accounted for, then the qls2 (for 2 sources of correlation) and qls3 (3 sources) functions should be used. These functions have the same syntax as the qls function, except t and CorrStruct have multiple inputs.

The qls functions return three result variables; bhat contains the estimated covariate parameters, alpha contains the estimated correlation parameters, and results contains the final results displayed (estimates, standard errors, p-values, 95% confidence intervals) using both the model based and sandwich type robust covariance matrices.

#### 5.2 Example for Two Sources of Correlation

Here we present the same results that were presented in the previous section, but in Matlab. We will use the

```
example_multlevel
```

data set.



type	375x1	3000	double array
varnames	1x2	144	cell array

```
Grand total is 3014 elements using 24144 bytes >>
```

To account for the two sources of correlation (type and time), we use the qls2 function.

```
>> [betah,alphah,results] = qls2(id,o2,[type time],X,'n',{'3','1'},varnames);
Normal distribution family assumed
Initial estimate of beta=[0.0666667
                                          95.65331
AR(1) Correlation structure assumed for Level 2
Equicorrelated structure assumed for Level 1
Stage 1 estimate of alpha1 = 0.072642
Stage 1 estimate of alpha2 = 0.39318
Stage 1 estimate of beta = [0.0780062]
                                            95.6481]
Stage 2 estimate of alpha1 = 0.14899
Stage 2 estimate of alpha2 = 0.68107
Stage 2 estimate of beta = [0.0856684
                                            95.6608]
Estimated correlation associated with level one:
    1.0000
              0.1490
                        0.1490
    0.1490
              1.0000
                        0.1490
    0.1490
              0.1490
                        1.0000
Estimated correlation associated with level two:
    1.0000
             0.6811 0.4639
                                  0.3159
                                             0.2152
              1.0000
    0.6811
                        0.6811
                                   0.4639
                                             0.3159
    0.4639
              0.6811
                        1.0000
                                   0.6811
                                             0.4639
    0.3159
              0.4639
                        0.6811
                                   1.0000
                                             0.6811
    0.2152
              0.3159
                        0.4639
                                   0.6811
                                             1.0000
QLS estimate of scale parameter = 7.5627
Estimates based on ROBUST covariance matrix
        ,,
                     ,,
                                   ,,
                                                                 ,,
                                                                       '95% CI'
'Variable'
            'Beta'
                          'Std.Error'
                                         'z value'
                                                       'p-value'
                                                                     'low lim'
                                                                                 'up lim'
'time'
            [ 0.0857]
                         [
                             0.0348]
                                         [ 2.4644]
                                                       [ 0.0137]
                                                                     [ 0.0175]
                                                                                 [ 0.1538]
'constant' [95.6608]
                         [
                             0.3636]
                                         [263.1137]
                                                              0]
                                                                     [94.9482]
                                                                                 [96.3734]
                                                       Γ
Estimates based on MODEL based covariance matrix
                                                   ,,
                     ,,
                                     ,,
                                                                 ,,
                                                                       '95% CI'
        ,,
                                18
```

'Variable'	'Beta'	'St	d.Error'	'z	value'	'p-≀	/alue'	'low	/ lim/	'up	lim'
'time'	[ 0.0857]	[	0.1132]	Γ	0.7570]	[ 0.	.4490]	[-0.	1361]	[ 0	.3075]
'constant'	[95.6608]	Γ	0.4355]	[2	19.6483]	Γ	0]	[94.	8072]	[96	.5144]

>>

#### 5.3 Example for Three Sources of Correlation

First we need to drop subject with id = 26, and create the id2 variable to ensure balanced data.

```
>> id = id(1:360,1);
>> type = type(1:360,1);
>> time = time(1:360,1);
>> o2 = o2(1:360,1);
>> family = family(1:360,1);
>> high = high(1:360,1);
>> X = [time ones(360,1)];
>> id2 = kron(ones(12,1),[ones(15,1); 2*ones(15,1)]);
```

Next, we can analyze the binary outcome high, with family as the clustering variable and subject, type and time as our three sources of correlation:

```
>>[betah,alphah,results]=qls3(family,high,[id2 type time],X,'b',{'3','3','1'},varnames);
Bernoulli distribution family assumed
Initial estimate of beta = [0.039611
                                         -0.3873]
AR(1) Correlation structure assumed for Level 3
Equicorrelated structure assumed for Level 1
Equicorrelated structure assumed for Level 2
Stage 1 estimate of alpha1 = 0.024319
Stage 1 estimate of alpha2 = 0.074032
Stage 1 estimate of alpha3 = 0.36418
Stage 1 estimate of beta = [0.034523]
                                        -0.38469]
Stage 2 estimate of alpha1 = 0.048609
Stage 2 estimate of alpha2 = 0.15188
Stage 2 estimate of alpha3 = 0.64307
Stage 2 estimate of beta = [0.030824]
                                        -0.38938]
Estimated correlation associated with level one:
    1.0000
              0.0486
    0.0486 1.0000
Estimated correlation associated with level two:
    1.0000
              0.1519
                        0.1519
    0.1519
              1.0000
                        0.1519
                                19
```

#### 0.1519 0.1519 1.0000

Estimated	correlation	associated	with level	three:
1.0000	0.6431	0.4135	0.2659	0.1710
0.6431	1.0000	0.6431	0.4135	0.2659
0.4135	0.6431	1.0000	0.6431	0.4135
0.2659	0.4135	0.6431	1.0000	0.6431
0.1710	0.2659	0.4135	0.6431	1.0000

QLS estimate of scale parameter = 1

Estimates based on ROBUST covariance matrix

, ,	, ,		, ,	,,	, ,	'95% CI'	,
'Variable'	'Beta'	'S	td.Error'	'z value'	'p-value'	'low lim'	'up lim'
'time'	[ 0.0308]	[	0.0527]	[ 0.5849]	[ 0.5586]	[-0.0725]	[0.1341]
'constant'	[-0.3894]	[	0.3231]	[-1.2053]	[ 0.2281]	[-1.0226]	[0.2438]
Estimates ba	ased on MODEL ,,	base	d covariar ,,	nce matrix ,,	,,	'95% CI'	,
'Variable'	'Beta'	'Std	.Error'	'z value'	'p-value'	'low lim'	'up lim'
'time'	[ 0.0308]	[	0.0895]	[ 0.3445]	[ 0.7304]	[-0.1445]	[0.2062]
'constant'	[-0.3894]	Γ	0.3383]	[-1.1510]	[ 0.2497]	[-1.0524]	[0.2737]

>>

### 6 Discussion

In this paper we have implemented quasi-least squares for analysis of data with multiple sources of correlation with the user-written xtmultcorr procedures in Stata and the qls procedures in Matlab.

It is important to note that our programs assume that the data are balanced overall, and they check that this condition is satisfied. However, we are currently working on extensions that will be appropriate for data that are not balanced overall, but that are balanced within subjects (e.g. if two measurements are collected on both eyes of variable sized families).

## 7 Acknowledgments

Work on this manuscript was supported by the NIH funded grant R01CA096885 "Longitudinal Analysis for Diverse Populations". The authors also note the that this manuscript, excluding the description of the Matlab procedures, is under review at the Stata Journal.



## References

- Chaganty, N. R. 1997. An alternative approach to the analysis of longitudinal data via generalized estimating equations. 1997 *Journal of Statistical Planning and Inference* 63: 39-54.
- Chaganty, N.R. and Shults, J. 1999. On eliminating the asymptotic bias in the quasi-least squares estimate of the correlation parameter. *Journal of Statistical Planning and Inference* 76: 127-144.
- Chaganty, N.R. and Naik, D. (2002). Analysis of multivariate longitudinal data using quasi-least squares. Journal of Statistical Planning and Inference 103: 421-436.
- Davis, C.S. 2002. *Statistical Methods for the Analysis of Repeated Measurements*. Springer-Verlag New York, Inc.
- Galecki, A.T. 1994. General class of covariance structures for two or more repeated factors in longitudinal data analysis. *Communications in Statistics-Theory and Methods* 23: 3105-3120.
- Goldstein H. 1995. *Multilevel statistical models. 2nd ed.* London: Edward Arnold.
- Liang, K.-Y. and Zeger, S. L. 1986. Longitudinal data analysis using generalized linear models. *Biometrika* 73: 13-22.
- Lu, N. and Zimmerman, D.L. 2005. The likelihood ratio test for a seperable covariance matrix. *Statistics & Probability Letters* 73: 449-457.
- Naik, D.N. and Rao, S.S. 2001. Analysis of multivariate repeated measures data with a Kronecker product structured covariance matrix, *Journal of Applied Statistics* 28: 91105.
- Ratcliffe, S. & Shults, J. 2006. *GEEQBOX: A Matlab toolbox for generalized* estimating equations and quasi-least squares. (Under review).
- Roy, A. and Khattree, R. 2005. Testing the hypothesis of a Kroneckar product covariance matrix in multivariate repeated measures data. SAS Users Group International, Proceedings of the Statistics and Data Analysis Section. Paper 199-30, 1-11.
- Shults, J. 1996. The analysis of unbalanced and unequally spaced longitudinal data using quasi-least squares. Ph.D. Thesis, Department of Mathematics and Statistics, Old Dominion University: Norfolk, Virginia.
- Shults, J. and Chaganty, N.R. 1998. Analysis of serially correlated data using quasi-least squares. *Biometrics* 54: 1622-1630.
- Shults, J. and Morrow, A. 2002. Use of Quasi-Least Squares to Adjust for Two Levels of Correlation. *Biometrics*, 58: 521530.



- Justine Shults, Sarah J. Ratcliffe, and Mary Leonard. 2006. Improved generalized estimating equation analysis via xtqls for implementation of quasi-least squares in Stata. UPenn Biostatistics Working Papers. Working Paper 13.
- Shults, J., Whitt, M.C. and Kumanyika, S. 2004. Analysis of data with multiple sources of correlation in the framework of generalize estimating equations. *Statistics in Medicine* 23(20): 3209-3226.
- Stata XT manual for Longitudinal/Panel Data. 2005. Stata Press: College Station, Texas.
- Unbi-Sun, W., Shults, J., and Leonard, М., 2006.Use of ased Estimating Equations  $\operatorname{to}$ Estimate Correlation inGen-Equation Analysis Trials. eralized Estimating of Longitudinal http://www.biostatsresearch.com/upennbiostat/papers/art4.
- Weissfeld, L.A. and Kshirsagar, A.M. (1992). A modified growth curve model and its application to clinical studies. *Australian Journal of Statistics* 34: 161-168.

## 8 About the Authors

Justine Shults, Ph.D. and Sarah Ratcliffe, Ph.D. are Assistant Professors of Biostatistics in the Center for Clinical Epidemiology and Biostatistics, Department of Biostatistics and Epidemiology, University of Pennsylvania School of Medicine.

