National Health and Nutrition Examination Survey:

Technical Documentation for the 1999-2004 Dual Energy X-Ray Absorptiometry (DXA) Multiple Imputation Data files

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Analysts are strongly encouraged to read all of the following documentation. Use of the multiply imputed data files will provide complete DXA data for all participants and more accurate standard errors of estimates.

1. Overview of Multiple Imputation

Imputation, which refers to filling in plausible values for missing data, is a popular approach to handling nonresponse on items in a survey for several reasons. First, imputation adjusts for observed differences between nonrespondents and respondents. Such an adjustment is generally not made by complete-case analysis, also known as listwise deletion, which refers to omitting cases with incomplete data from the analysis. Second, imputation results in a completed data file, so that the data can be analyzed using standard software packages without discarding any observed or measured values. Third, when a data file is being produced for analysis by the public, imputation allows the data producer to incorporate specialized knowledge about the reasons for missing data in the imputation procedure. Moreover, the nonresponse problem is addressed in the same way for all users, so that analyses will be consistent across users. Finally, imputation can be more effective than reweighting in using the statistical relationships among survey variables to produce accurate predictions of the missing data values, leading to more efficient estimates.

Single imputation, which refers to imputing just once for each missing value, does not reflect the uncertainty stemming from the fact that the imputed values are plausible replacements for the missing values but are not the true values themselves. As a result, analyses of singly imputed data that treat the imputed values as if they were measured values tend to produce estimated standard errors that are too small, confidence intervals that are too narrow, and significance tests that reject the null hypothesis too often when it is true. For example, large-sample results reported by Rubin and Schenker (**1986**) suggest that when the rate of missing information is 20% to 30%, nominal 95% confidence intervals computed from singly imputed data have actual coverage rates between 85% and 90%. Moreover, the performance of single imputation can be even worse when inferences are desired for a multi-dimensional quantity. Large-sample results reported by Li, Raghunathan, and Rubin (**1991**) demonstrate that for testing hypotheses about multi-dimensional quantities, the actual rejection rate under the null hypothesis increases as the number of components being tested increases, and the actual rate can be much larger than the nominal rate.

Multiple imputation allows the uncertainty due to imputation to be reflected in the analysis (Rubin, **1978, 1987**). With multiple imputation, $M > 1$ plausible sets of replacements are generated for the missing values, thereby generating M completed data files. The M sets of imputations for the missing values are ideally independent draws from the predictive distribution of the missing values conditional on the observed values. Each of the M completed data files is analyzed separately using the method that would be applied if the data were complete, and the variation in results among the M versions provides a measure of missing-data uncertainty in addition to the usual variation due to sampling. The M sets of results may be formally combined to provide standard errors and confidence levels that incorporate the missing-data uncertainty. Details of how to analyze multiply imputed data are provided in **Section 4.** For public-use data, M is not usually larger than 5 (to limit computational burden for analysts), which is the number of data files imputed for the application described herein.

At the National Center for Health Statistics, multiple imputation has been applied previously to data from the Third National Health and Nutrition Examination Survey (NHANES III: 1988-1994) (National Center for Health Statistics, **2001**), the National Health Interview Survey (Schenker et al., **2006**), and the State and Local Area Integrated Telephone Survey (Pedlow, Luke, and Blumberg, **2007**).

2. Overview of NHANES DXA Data

Dual-energy x-ray absorptiometry (DXA) has long been accepted as the primary method for measuring bone mineral content and bone mineral density because of its high precision, accuracy, and low radiation exposure (Njeh *et al*., **1990**; Wahner *et al*., **1994**; WHO, **1994**; Genant *et al*., **1996**) More recently, whole body DXA also has become one of the most widely accepted methods of measuring body composition due to its speed, ease of use, and strong correlation with criterion methods of assessing body composition (Lohman and Chen, **2005**; Thomas *et al*., **2005**).

The assessment of body composition by DXA has taken on added importance as the prevalence of overweight and obesity in the U.S. over the past 40 years has steadily increased among both adults and children (Flegal *et al*., **2002,** Ogden *et al*., **2002**). In 2003-04, 66.3% of adults 20 years of age and older were overweight or obese and 32.2% were obese (Ogden *et al*., **2006**). Among children 2-19 years of age, 33.6% in 2003-04 were at risk for overweight or overweight and 17.1% were overweight (Ogden *et al*., **2006**). Although body mass index (BMI), calculated as weight in kilograms over height in meters squared, has been commonly used as the standard measure of obesity in the U.S. and other countries (WHO, **1995**), there are recognized limitations to the use of BMI in assessing obesity in a population. The relationship of body fat to BMI varies with age, gender, ethnicity, and physical conditioning (Baumgartner *et al*., **1995**; Gallagher *et al*., **1996**; Deurenberg *et al*., **1998**). Because DXA assesses the proportions of lean mass and fat mass in the body, it is a more accurate measure of percent body fat and obesity than is BMI. In 1999, to provide information on soft tissue composition as well as bone content, the National Health and Nutrition Examination Survey (NHANES) implemented whole body DXA scans of survey participants age 8 years and older. Although DXA scans of the proximal femur had been successfully administered in the NHANES in 1988-94 to assess bone density in adults age 20 years and over in the U.S. population (Looker *et al*., **1998**), these scans were not included in the 1999-2004 protocol.

2.1 DXA Examination

In each NHANES survey year, a nationally representative sample of the U.S. civilian non-institutionalized population is selected using a complex, stratified, multistage probability sampling design. Approximately 5,300 individuals of all ages are interviewed in their homes yearly; of these, approximately 5,000 complete the health examination component of the survey. The 1999-2004 NHANES includes an oversampling of non-Hispanic blacks, Mexican Americans, low-income whites, adolescents 12-19 years of age, and persons 60 years of age and over to provide more reliable estimates for these groups. Although a nationally representative sample of the U.S. is selected each survey year, the NHANES data are released as public use data in two-year cycles to provide adequate sample sizes for subgroup analyses.

DXA scans were administered to eligible survey participants 8 years of age and older in the NHANES mobile examination centers (MECs). Females of ages 12-59 years and menstruating 8-

11 year olds were permitted to take the DXA examination only if a pregnancy test taken at the time of the exam was negative. Females also were excluded from the examination if they said they were pregnant at the time of the exam, even if the pregnancy test was negative. Individuals were excluded from the DXA examination who reported taking tests with radiographic contrast material in the past 72 hours, participated in nuclear medicine studies in the past 3 days, or had a self-reported weight (> 300 pounds) or height (> 6’5”) over the DXA table limit. All other participants were asked to have a DXA scan taken.

The whole body DXA scans were acquired using a Hologic QDR 4500A fan-beam densitometer (Hologic, Inc., Bedford, Massachusetts) following the manufacturer’s acquisition procedures. Hologic DOS software version 8.26:a3* was used to acquire all scans; scanning was done in the fast mode. Participants wore disposable paper gowns and were asked to remove all objects that would interfere with obtaining an analyzable scan image, such as jewelry, watches, hair ornaments, glasses, keys, and wallets. The DXA examination protocol is documented in the January 2004 Body Composition Procedures Manual on the NHANES website http://www.cdc.gov/nchs/nhanes.htm.

The scan for each survey participant was reviewed and analyzed by the University of California, San Francisco (UCSF), Department of Radiology using standard radiologic techniques and study-specific protocols developed for the NHANES. Hologic Discovery software, version 12.1, was used to analyze the scans. Soft tissue measures: fat mass (gm), lean mass including bone mineral content (gm), lean mass excluding bone mineral content (gm), and percent (%) body fat and bone measures: bone mineral content (BMC) (gm), bone area (cm^2), and bone mineral density (BMD) (gm/cm^2) were obtained for the head, arms, legs, and trunk. Bone measures also were obtained for the pelvis, ribs, thoracic spine, and lumbar spine. Invalidity codes were applied by the UCSF to the entire scan or to body regions that could not be analyzed accurately. Data were coded as invalid as a result of jewelry and other objects not removed by participants; the presence of non-removable objects such as prostheses, pacemakers, implants, casts, etc.; excessive x-ray “noise” due to obesity (applied to the trunk region only); arm/leg overlap; body parts out of the DXA table scan area; positioning problems (head, arms/hands or feet turned); and other reasons, which included participant motion, missing limbs, and unknown artifacts. Such invalid data were set to missing in the data file. If data for any region were missing, total body values such as total mass and total %

body fat were coded as missing also since regional data were summed to equal total values. Additional information on the DXA data collection and quality control review procedures, adjustments made to the DXA data, and the structure of the DXA release data files can be found in the DXA Data Documentation on the NHANES website.

Of the 21,230 eligible DXA participants aged 8 years and over who participated in the MEC examinations in 1999-2004, scans with 100% non-missing data were obtained from 16,973 or 80.0%. (For this calculation, pregnant women were not counted as eligible participants.)

2.2 Missing DXA Data

The percentages of survey participants in 1999-2004 with data missing for one or more regions are provided in Table 1 by gender-age group and in Table 2 by BMI category. The percentages increase with increasing age and BMI. Because DXA data missingness is related to age, BMI, weight and height (due to the weight and height exclusions mentioned in **Section 2.1**), and possibly other characteristics, participants with missing data cannot be treated as a random subset of the original sample. Otherwise, analytic results may be biased toward participants with the least amount of missing data.

To resolve the problem of potential biases due to missing DXA data, multiple imputation of the missing data was performed for the survey years 1999-2004. Five completed data files containing both the non-missing and imputed DXA data values were created to allow the assessment of variability due to imputation. For the missing data, each of the 5 data files contains a different set of imputed values, whereas for the non-missing data, the values are identical across the 5 files (since no imputation was carried out for them). The files include DXA total body values, subtotal values (excludes head values), and regional values for fat mass, % body fat, lean mass including bone mineral content, lean mass excluding bone mineral content, BMC, bone area, and BMD; variables indicating the DXA values that were imputed; and variables indicating the reason for invalid regional values. In addition, the common sequence identification number (SEQN) for each participant is provided for purposes of merging the multiply imputed DXA data with other NHANES data. DXA data are not provided for pregnant women and participants with amputations other than fingers or toes. The DXA data have been released in two-year cycles: 1999-2000, 2001-

2002, and 2003-2004. For computational convenience, the five completed data files have been concatenated into a single file for each release cycle.

3. Procedure for Multiply Imputing the NHANES DXA Data

The type of imputation procedure used for the NHANES DXA data is described in **Section 3.1**. This is followed by discussions of some further details of the models used (**Section 3.2**) and evaluations of the models and imputations (**Section 3.3**). Although the discussions of the model development and evaluations are presented sequentially, they were actually performed in an iterative fashion, because a chosen model leads to a specific set of evaluation results, which then suggests modifications to the model, and so on.

3.1 Sequential Regression Multivariate Imputation

The multiple imputations for the NHANES DXA data were created using sequential regression multivariate imputation (SRMI) (Raghunathan *et al*., **2001**), as implemented by the module **IMPUTE** in IVEware (Raghunathan *et al.***, 2002**), a SAS-callable software package for imputation and variance estimation developed by the Survey Methodology Program at the University of Michigan's Institute for Social Research. IVEware is available at the website http://www.isr.umich.edu/src/smp/ive.

A brief description of SRMI is as follows; see Raghunathan *et al*. (**2001**) for further details. Let X denote the fully-observed variables, and let $Y_1, Y_2, ..., Y_k$ denote k variables with missing values, ordered by the amount of missingness, from least to most. The imputation process for $Y_1, Y_2, ..., Y_k$ proceeds in c iterations. In the first iteration: the regression of Y_1 on X is fitted to the cases with Y_1 observed, and the missing values of Y_1 are imputed (randomly from an approximate predictive distribution based on the fitted regression); then the regression of Y_2 on X and Y_1 (including the imputed values of Y_1) is fitted to the cases with Y_2 observed, and the missing values of Y_2 are imputed; then the regression of Y_3 on X, Y_1, and Y_2 is fitted to the cases with Y_3 observed, and the missing values of Y_3 are imputed; and so on, until the regression of Y_k on $X, Y_1, Y_2, ..., Y_{k-1}$ is fitted to the cases with Y_k observed, and the missing values of Y_k are imputed.

In iterations 2 through c, the imputation process carried out in iteration 1 is repeated, except that now, in each regression, all variables except for the variable to be imputed are used as predictors (with their most recent imputed values included). Thus: the regression of Y_1 on $X, Y_2, Y_3, ..., Y_k$ is fitted to the cases with Y_1 observed, and the missing values of Y_1 are re-imputed; then the regression of Y_2 on $X, Y_1, Y_3, ..., Y_k$ is fitted to the cases with Y_2 observed, and the missing values of Y_2 are re-imputed; and so on. After c iterations, the final imputations of the missing values in $Y_1, Y_2, ..., Y_k$ are used.

For each regression in the SRMI procedure, IVEware allows the use of a normal linear regression model if the outcome variable is continuous, a logistic regression model if the outcome variable is binary, a multinomial logit model if the outcome variable is categorical with more than two categories, a Poisson regression model if the outcome variable is a count, and a two-stage model if the outcome variable is semi-continuous. In addition, IVEware allows bounds to be placed on the variables being imputed, by drawing the imputed values from truncated predictive distributions; and it allows for restrictions to be placed on one variable based on the value of another variable, as might be needed to account for skip patterns in a survey. The features of IVEware were particularly helpful in the context of multiply imputing NHANES DXA data, because missing data on both continuous and categorical (non-DXA) variables were handled during the imputation process (see **Section 3.2.2**), and bounds were placed on the imputed values for the DXA variables (see **Section 3.2.4**).

By including every variable other than the variable being imputed as predictors in each regression model, and by cycling through the various regression models, SRMI builds in relationships among the variables included in the imputation procedure. This was especially important in the context of the NHANES DXA data, because the DXA variables are highly interrelated.

Because SRMI requires only the specification of individual regression models for each of the Y-variables, it does not necessarily imply a joint model for all of the Y-variables conditional on X. (See Raghunathan *et al.*, **2001** and Van Buuren *et al.*, **2006** for further discussion of this point.) However, the flexibility of the procedure regarding various types of variables as well as placing bounds on the variables being imputed allowed it to handle complicating factors in the NHANES

DXA imputation project that would have been very difficult to handle using a method based on a full joint model. Moreover, had the variables all been continuous, and had no bounds been placed on the imputations, the SRMI-based imputation procedure would actually have been equivalent to imputation based on a multivariate normal model.

The idea of imputing variables sequentially using regression models dates back at least to Kennickell (**1991**), who used such an algorithm for multiply imputing missing values for the Survey of Consumer Finances of the Federal Reserve Board. Another software package for multiple imputation based on this idea is MICE (multiple imputation by chained equations) (Van Buuren and Oudshoorn, **1999**), which has a stand-alone version as well as versions for R and S-Plus (see http://www.multiple-imputation.com). In addition, the idea has been implemented in a module for Stata; see Roylston (**2005**).

3.2 Further Details of the Procedure

3.2.1 Imputation by age-gender groups

The DXA data were categorized by 10 gender-age groups for the imputation procedure: males 8-11 years, males 12-19 years, males 20-39 years, males 40-59 year, males 60+ years, females 8-11 years, females 12-19 years, females 20-39 years, females 40-59 years, and females 60+ years. The SRMI procedure was implemented separately within each of the groups. Ten iterations of the procedure were used to create one completed dataset. To create multiple imputations (i.e., 5 completed data files), the procedure was repeated independently 5 times. After imputation, the data for the gender-age groups were concatenated.

3.2.2 Variable selection

When multiple imputations are being created, it is beneficial to include a large number of predictors in the imputation model, especially variables that are considered predictive of the items being imputed and variables that will be used in subsequent analyses of the multiply imputed data (Meng, **1994**; Rubin, **1996**; Little and Raghunathan, **1997**). In the context of a survey with complex sample design, the predictors should also include variables related to the design. Based on these considerations, a large number of variables were included in the imputation models for the NHANES DXA data in addition to the DXA variables themselves, including demographic, socioeconomic, and geographic variables, body measurements, indicators of health, variables on diet and use of medications, blood test results, and variables related to the design of the NHANES sample. Complete lists of the DXA and non-DXA variables in the models are given in Tables 3 and 4, respectively. In addition to the missingness on the DXA variables, some of the non-DXA variables had missing values as well. The missing values for the non-DXA variables were imputed as part of the SRMI procedure, but these imputed values were not included in the release of the multiply imputed DXA data.

If related non-DXA variables were found to be nearly linearly dependent, so that the stability of the SRMI procedure was affected, only one of the variables was chosen for inclusion in the model. Collinearity was judged not to be a problem for BMI, weight, height, waist circumference, and waist circumference/height, and all were included in the model. Body mass index was included as both a continuous variable and as a categorical variable since both are used in the analysis of DXA data. Although not released publicly to protect the confidentiality of survey participants, the variables METRO and REGION were included in the model to account for clustering in the complex sample design. A categorical variable (SDDSRVYR) for the survey cycles (1999-2000, 2001-2002, 2003-2004) was included to account for possible changes over time.

If the cells for a categorical variable were sparse, the value of the variable in prediction was evaluated. If sparse data resulted in failure of the algorithm to converge and did not aid in prediction, the variable was dropped from the model. Moreover, some categorical variables that were considered important predictors were included with their categories collapsed to handle sparse data (e.g., general health condition, alcohol consumption, and BMI). Particular attention was paid to variables that not only had sparse cells, but also considerable missing data.

3.2.3 Transformations of the DXA variables

The linear regression models for the DXA variables in the SRMI procedure assume normal distributions for the error terms in the regression equations. To make this assumption more tenable, transformations were used for the DXA variables in the imputation procedure. After multiple imputations were created on the transformed scale, the imputed values for the DXA variables were back-transformed to their original scales.

Several alternative approaches to transformation of the DXA variables were explored, including no transformation, logarithmic transformation, and an iterative Box-Cox power transformation method (Box and Cox, **1964**). When modeling was performed using the untransformed DXA variables, the imputation procedure tended to produce physiologically implausible minimum values. When the logarithmic transformation was used for all of the DXA variables, the imputation procedure appeared to over-predict values at the upper ends of the distributions. After additional exploration of alternatives for transformation of the DXA data, the iterative Box-Cox method was selected.

The iterative Box-Cox algorithm started with initial estimates of 1 for the exponents of the power transformations for all of the DXA variables. The algorithm then iteratively cycled through the variables one by one, updating their estimated transformations. Within each iteration, the cycling and updating proceeded as follows. First, the DXA variables were randomly ordered in a sequence. Then, for each variable in the sequence, the linear regression model that would be used to impute missing values of that variable in the SRMI procedure was fitted to the complete cases, with the transformations of all of the other variables fixed at their most recent estimates, and the method of Box and Cox (**1964**) was used to obtain a new estimate of the optimal transformation for the variable in question. The power transformation for that variable was then updated to the new estimate, and the algorithm moved on to the next variable in the sequence, and so on, until all of the transformations were updated. The iterations continued until the set of estimated transformations converged. The iterative Box-Cox algorithm was implemented separately within each of the 10 gender-age groups used for imputation, and the exponents for the power transformations of the DXA variables determined by the algorithm ranged from -0.50 to 2.50.

3.2.4 Setting lower bounds

Even after the transformations of the DXA variables in the imputation model were determined, evaluations of the imputations indicated occasional instances of imputed values that were implausibly low. This issue was resolved by placing lower bounds on the imputed values, as allowed by IVEware (see **Section 3.1**). Within each of the gender-age groups used for imputation, the lower bound for each DXA variable (before transformation) was set at the minimum of the non-missing values divided by $\sqrt{2}$. The minimum observed value divided by $\sqrt{2}$ is also used with the NHANES laboratory data to calculate “fill” values below the level of detection (LOD).

3.3 Evaluating the Imputation Procedure

Evaluations of the imputation procedure were carried out in terms of both the regression models for the DXA variables and the imputed values themselves.

3.3.1 Evaluating the regression models

Plots of the residuals from fitting the regression models used to impute the DXA variables in the SRMI procedure to the complete cases were examined, with emphasis on plots of the residuals versus the fitted values and normal probability plots. In general, the plots indicated good fits of the regression models, little evidence of heteroscedasticity (i.e., non-constant error variances), and nearly normal error distributions. However, plots of the residuals versus the fitted values for some of the head measurement variables displayed “fan shapes,” indicating possible heteroscedasticity. The estimated Box-Cox transformations for these variables (see **Section 3.2.3**) tended to be quite strong as well. Re-fitting the regression models with untransformed or logarithm-transformed head variables did not improve the fanning in the plots, so the decision was made to continue using the estimated transformations. It was also thought that, while heteroscedasticity could result in implausibly low imputed values, the lower bounds described in **Section 3.2.4** would counteract this effect.

Influential observations in the regression models were identified from plots of the residuals and from review of the numerical diagnotic DFFITS (Belsley *et al.*, **1980**). Sensitivity of the imputations to removal of the influential observations was examined by re-implementing the imputation procedure with the influential observations removed. If lower bounds were not imposed on the imputations (see **Section 3.2.4**), removal of the influential observations occasionally decreased the prevalence of implausibly low values for some variables but increased the prevalence for other variables. Removal of the influential observations also occasionally lowered what were considered to be reasonably high imputed values for still other variables. For most variables, however, removal of the influential observations made little difference in the imputation of the DXA variables. Therefore, the influential observations were retained in the imputation procedure, with the setting of lower bounds resolving the issue of implausibly low imputed values, as discussed earlier (**Section 3.2.4**).

3.3.2 Evaluating the imputed values

To assess whether the imputed DXA values might have disproportionately high survey weights and thus be overly influential, the distributions of the survey weights for the non-missing and imputed values were compared. No systematic relations were found between the survey weights and the occurrence of missing values.

The imputed values were examined in several different ways, by gender-age group, to assess whether they appeared reasonable. For example, total DXA mass, calculated as the sum of the imputed DXA regions, should be highly correlated with measured body weight from the NHANES physical examination, if the imputation is accurate. This was found to be the case for all 10 gender-age groups, based on review of plots of total DXA mass versus measured body weight, with separate plotting symbols used for participants with no missing DXA data and participants with varying amounts of imputed data; see, for example, Figure 1.

Plots of DXA total fat or truncal fat versus variables such as measured BMI, body weight, waist circumference, and waist circumference divided by height were created; see, for example, Figures 2 and 3. The plots showed that the relations involving the imputed DXA values were similar to those involving the non-missing DXA values. The plots also reflected the fact that imputed values for participants with body weight greater than 300 pounds (who were not scanned) and imputed truncal fat values for participants with missing data due to obesity “noise” were extrapolated beyond the observed values, as would be expected.

Plots of DXA values for left limbs and ribs versus right limbs and ribs were also examined; see, for example, Figure 4. Again, the relations involving the imputed data values were similar to those involving the non-missing data values. Moreover, the association between left and right limb values was generally strong for both imputed and non-missing data. However, the association between values for the left and right ribs tended to be weak for both the imputed and the non-missing data, and users should take note of this finding.

As a final example of comparing imputed and non-missing DXA values, numerical summaries were compared; see, for example, Figure 5, which illustrates the comparison for the left arm area (DXDLAA). Such comparisons tended to produce plausible results, especially in light of the fact that participants with missing DXA values were known to often have different characteristics from participants with non-missing values. For example, large maximum imputed values were found to belong to participants with high observed BMIs and were judged to be reasonable. Similarly, a few very small imputed values seen across all five data files were found to belong to participants with low observed BMIs and also were judged to be reasonable.

Since multiple imputation of a variable is supposed to reflect uncertainty due to missing data, some variability among the 5 imputed values for a participant is to be expected. For some participants, however, imputed values for DXA variables were found to vary extremely (from very low values to very high values) among the 5 imputations. Reviews of the data for such participants showed that the values of all of their DXA variables, as well as their measured height and weight (important predictor variables in the imputation models) were missing and therefore had been imputed. Because of these special circumstances and the extreme variability of the imputed values, the DXA data for these participants have been placed in separate files (see the DXA Data File Documentation on the NHANES website). Analysts should be aware of the highly variable nature of these imputed DXA data when considering the use of these separate files.

4. Analyzing Multiply Imputed Data

4.1 General Procedures

Analyzing a multiply imputed dataset is similar to analyzing a conventional dataset with no missing values. Most statistical analysis procedures that would be appropriate for other NHANES data will be appropriate for use with the multiply imputed DXA data. The only major difference is that any estimation procedure must be carried out 5 times, once for each version of the completed data.

Because of the complex survey design used in NHANES, traditional methods of statistical analysis based on the assumption of a simple random sample may not be reliable. Sample weights are needed to produce correct estimates of population quantities. Other aspects of the sample design (e.g. PSU pairings) should be taken into account to obtain correct standard errors and significance levels for hypothesis tests. Use of computer software for data from complex samples, such as SUDAAN, STATA, or IVEware is strongly recommended. Appropriate methods for the analysis of NHANES data are described in the NHANES Analytic and Reporting Guidelines on the NHANES website http://www.cdc.gov/nchs/nhanes.htm.

Users of the NHANES multiply imputed DXA data files should, for the most part, follow the guidelines given for analysis of the other NHANES public-use files. To merge the multiply imputed DXA data with data from other NHANES 1999-2004 public-use files, the common sequence identification number variable (SEQN) should be used.

4.2 Combining Multiple Estimates and Standard Errors

When producing statistical estimates from the multiply imputed DXA data files, the same estimation procedure should be applied to each of the 5 versions of the completed data. The 5 sets of results may then be combined to produce a single statistical summary that formally incorporates uncertainty due to missing data into standard errors, significance levels, etc. In this section, methods for combining the multiple sets of results are described for the common case in which a scalar (one-dimensional) quantity is being estimated; see Rubin and Schenker (**1986**), Rubin (**1987**), and Barnard and Rubin (1999) for further details and derivations. (Multiple-imputation methods for significance tests involving multi-dimensional quantities are discussed in Rubin, **1987**, Li, Meng, Raghunthan, and Rubin, **1991**, Li, Raghunathan, and Rubin, **1991**, and Meng and Rubin, **1992**.)

Suppose that one is interested in producing an estimate and confidence interval for a population quantity *Q*, which may be a prevalence rate, mean, median, regression coefficient, etc. One must first calculate an estimate and standard error for *Q* from each of the *M* completed datasets, using methods that would be statistically appropriate if the data had no missing values. As mentioned in Section **4.1**, because the 1999-2004 NHANES employed a complex sample design, one should use methods appropriate for complex samples. Let $\hat{Q}_1, \hat{Q}_2, ..., \hat{Q}_M$ denote the *M* estimates of *Q*, and let $\hat{V}_1, \hat{V}_2, ..., \hat{V}_M$ denote the associated variance estimates (squared standard errors) from the analyses of the *M* completed datasets. The combined estimate of *Q* is simply the mean of the *M* individual estimates, $\bar{Q} = \sum_{l=1}^{M} \hat{Q}_l / M$. The combined standard error for this estimate is based on the following two quantities:

- The within-imputation variance, which is the mean of the *M* individual variance estimates, that is, $W = \sum_{l=1}^{M} \hat{V}_l / M$.
- The between-imputation variance, which is the sample variance of the *M* individual estimates of *Q*, that is, $B = \sum_{l=1}^{M} (\hat{Q}_l - \overline{Q})^2 /(M-1)$.

The total variance combines the within- and between-imputation variances as follows: $T = W + \frac{M+1}{M} B$. The square root of this total variance, $\sqrt{T}$, is the combined standard error associated with the combined estimate $\overline{Q}$.

In many cases, an acceptable 95% confidence interval for *Q* can be formed based on an approximate normal distribution: $\overline{Q} \pm 1.96\sqrt{T}$ (where 1.96 is the 97.5th percentile of the standard normal distribution). A more accurate approximation, derived by Rubin and Schenker (**1986**), replaces the multiplier 1.96 with the 97.5th percentile of Student's *t*-distribution with degrees of freedom given by $\nu_{RS} = (M-1)\left[1 + \left(\frac{M}{M+1}\right)\left(\frac{W}{B}\right)\right]^2$.

The Rubin/Schenker approximation is based on the assumption that if the data were complete, the analysis of the dataset would be based on a normal distribution or a *t*-distribution with large degrees of freedom. Barnard and Rubin (**1999**) relaxed this assumption to allow for the possibility of small complete-data degrees of freedom, and derived the following degrees of freedom to replace the Rubin/Schenker formula in the multiple-imputation analysis: $\nu_{BR} = \left(\frac{1}{\nu_{RS}} + \frac{1}{k}\right)^{-1}$, where $k = \frac{d(d+1)W}{(d+3)T}$ and *d* denotes the complete-data degrees of freedom. (Note that *d* also represents the degrees of freedom for the analysis of each of the *M* completed datasets.)

Once the estimates $\hat{Q}_1, \hat{Q}_2, ..., \hat{Q}_M$ and $\hat{V}_1, \hat{V}_2, ..., \hat{V}_M$ have been obtained by analyzing each of the *M* completed datasets, it is relatively straightforward to implement the combining rules outlined in this section by using a spreadsheet program, a macro, a specially written program, or even just a calculator. However, the increasing availability of software packages that analyze the completed datasets and implement the combining rules is helping to facilitate multiple-imputation analyses. For example, the SAS-callable package IVEware that was used to create the NHANES DXA multiple imputations (see **Section 3.1**) has three modules for performing various multiple-imputation analyses incorporating complex sample designs. SAS-callable SUDAAN performs such analyses as well, and two examples of its use are given in **Section 4.4**.

4.3 Combining Data across NHANES Survey Cycles

The DXA data files are being released to correspond to the original NHANES data release cycle. One data file is released for each cycle: 1999-2000, 2001-2002, and 2003-2004. Each of these data files contains 5 completed datasets organized as 5 records per survey participant. If a data item was missing, then the imputed values are used and these data items will not be the same across the 5 records per person. Examples of how to use each data cycle, with 5 records per person, are shown in section 4.4 below.

It should be noted that combining data from more than one two-year data cycle is recommended to increase the sample size and to produce statistically reliable estimates. If more than one data cycle is to be combined to create a 4 year or six year data file, then the multiply imputed data files for each cycle can simply be concatenated. That is, a data file for 1999-2004 can be formed by simply concatenating the three individual files for 1999-2000, 2001-2002, and 2003-2004. The resulting data file will still have 5 records per person and analysis as described in section 4.2 can proceed. One important analytic aspect of such combined data files is that the sample weights will need to be adjusted if annualized estimates are required. General information on the statistical analysis of combined 4 or 6 year data files, including the adjustment of sample weights, are described in the NHANES Analytic and Reporting Guidelines on the NHANES website http://www.cdc.gov/nchs/nhanes.htm

4.4 Analytic Examples Using SAS-Callable SUDAAN

SAS-callable SUDAAN is a versatile software package for analyzing data from complex surveys. This section provides code for two examples for analysis of the NHANES multiply imputed DXA data using SUDAAN Version 9.1, which includes a built-in option for analyzing multiply imputed data. The code in the examples has to be modified for a user’s particular analysis.

The 5 datasets can be identified in SUDAAN Version 9.1 by naming the datasets with consecutive numbers at the end of the name, for example DS1. Setting the system variable MI_COUNT via the option MI_COUNT=5 indicates the number of datasets to be analyzed. When encountering this option, SUDAAN will automatically perform the multiple-imputation analysis. Each dataset must be sorted by the "NEST" variables. Example 1 contains SUDAAN code for PROC DESCRIPT and the output from this code . For Example 2, a regression model is fitted using PROC REGRESS. The output from this program also is provided.

```
************************************
* EXAMPLE PROGRAM 1: PROC DESCRIPT *
************************************;

options pagesize=67 nodate pageno=1;

** Change Depending On Where Datasets Are Stored **;
libname nhanes4a 'c:\nhanes\nhanes 1999-2000';
libname nhanes4b 'c:\nhanes\nhanes 2001-2002';
libname nhanes4c 'c:\nhanes\nhanes 2003-2004';

proc format;
  value genfmt
    1='Male'
      2='Female';
  value bmifmt
    1='< 25.0'
      2='25.0-29.9'
      3='30.0-34.9'
    4='35.0+';

data demo;
  set nhanes4a.demo(keep=seqn riagendr ridageyr ridreth1 sddsrvyr sdmvstra
sdmvpsu wtmec4yr)
      nhanes4b.demo_b(keep=seqn riagendr ridageyr ridreth1 sddsrvyr sdmvstra
sdmvpsu wtmec4yr)
      nhanes4c.demo_c(keep=seqn riagendr ridageyr ridreth1 sddsrvyr sdmvstra
sdmvpsu wtmec2yr);

  ** Create MEC Weight Variable For Six Years **;

  if (1 <= sddsrvyr <= 2) then MECWeight = wtmec4yr * 2/3;


data bmx;
  set nhanes4a.bmx(keep=seqn bmxbmi)
      nhanes4b.bmx_b(keep=seqn bmxbmi)
      nhanes4c.bmx_c(keep=seqn bmxbmi);

data dxa;
  set nhanes4a.dxx(keep=seqn _mult_ dxdtrpf)
      nhanes4b.dxx_b(keep=seqn _mult_ dxdtrpf)
      nhanes4c.dxx_c(keep=seqn _mult_ dxdtrpf);
```

```
data ds1 ds2 ds3 ds4 ds5;
  merge demo bmx dxa;
  by seqn;
  select(_mult_);
    when(1) output ds1;
    when(2) output ds2;
    when(3) output ds3;
    when(4) output ds4;

      otherwise;
  end;

%macro Sort;
%do i = 1 %to 5;
  proc sort data=ds&i;
    by sdmvstra sdmvpsu;
  run;
%end;
%mend Sort;
%Sort;

proc descript data=ds1 mi_count=5 design=wr;
  nest sdmvstra sdmvpsu;
 weight MECWeight;

  ** Select If 20+ **;

  subpopn ridageyr >= 20;
  subgroup riagendr bmxbmi;
  recode bmxbmi=(0 25 30 35);
  levels 2 4;
  var dxdtrpf;
  table riagendr*bmxbmi;
  print nsum mean semean lowmean upmean/style=nchs;
rformat riagendr genfmt.;
rformat bmxbmi bmifmt.;
rtitle "NHANES 1999-2004";
rtitle "Mean Percent Trunk Fat by Gender and BMI Group";


******************************************************
* SUDAAN OUTPUT FOR EXAMPLE PROGRAM 1: PROC DESCRIPT *
******************************************************;
```

```
Processing data for set 1 of imputed variables:

Number of observations read    :  22133    Weighted count :243432885
Observations in subpopulation  :  14213    Weighted count:200707729
Denominator degrees of freedom :     44

.
.
.
```

```
Processing data for set 5 of imputed variables:

Number of observations read    :  22133    Weighted count :243432885
Observations in subpopulation  :  14213    Weighted count:200707729
Denominator degrees of freedom :     44


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Page  : 1
Time: 14:32:08                                    The DESCRIPT Procedure
Table : 1

Variance Estimation Method: Taylor Series (WR) Using Multiply Imputed Data
For Subpopulation: RIDAGEYR >= 20
NHANES 1999-2004
Mean Percent Trunk Fat by Gender and BMI Group
Results for Summary Over All Imputations
by: Variable, Gender - Adjudicated., Body Mass Index (kg/m**2).

for: Variable = Trunk Percent Fat.

-----------------------------------------------------------------------------------
Gender -
  Adjudicated.
   Body Mass Index     Sample                               Lower 95%    Upper 95%
     (kg/m**2)         Size             Mean      SE Mean   Limit Mean   Limit Mean
-----------------------------------------------------------------------------------
Total
   Total                  12926        33.79         0.14        33.51        34.08
   < 25.0                  4173        26.87         0.17        26.53        27.21
   25.0-29.9               4643        33.83         0.17        33.48        34.17
   30.0-34.9               2470        39.09         0.18        38.72        39.46
   35.0+                   1640        45.25         0.18        44.89        45.62
Male
   Total                   6477        29.17         0.12        28.93        29.42
   < 25.0                  2015        22.29         0.17        21.96        22.63
   25.0-29.9               2674        29.59         0.14        29.31        29.88
   30.0-34.9               1210        34.44         0.17        34.10        34.78
   35.0+                    578        39.60         0.19        39.20        39.99
Female
   Total                   6449        38.20         0.20        37.81        38.60
   < 25.0                  2158        30.41         0.23        29.94        30.89
   25.0-29.9               1969        39.57         0.14        39.28        39.86
   30.0-34.9               1260        43.89         0.11        43.67        44.12
   35.0+                   1062        48.48         0.18        48.12        48.84
-----------------------------------------------------------------------------------
```

```
***********************************
* EXAMPLE PROGRAM 2: PROC REGRESS *
***********************************;

options pagesize=67 nodate pageno=1;

** Change Depending On Where Datasets Are Stored **;

libname nhanes4a 'c:\nhanes\nhanes 1999-2000';
libname nhanes4b 'c:\nhanes\nhanes 2001-2002';
libname nhanes4c 'c:\nhanes\nhanes 2003-2004';
```

```
proc format;
  value genfmt
    1='Male'
      2='Female';
  value bmifmt
    1='< 25.0'
      2='25.0-29.9'
      3='30.0-34.9'
    4='35.0+';

data demo;
  set nhanes4a.demo(keep=seqn riagendr ridageyr ridreth1 sddsrvyr sdmvstra
sdmvpsu wtmec4yr)
      nhanes4b.demo_b(keep=seqn riagendr ridageyr ridreth1 sddsrvyr sdmvstra
sdmvpsu wtmec4yr)
      nhanes4c.demo_c(keep=seqn riagendr ridageyr ridreth1 sddsrvyr sdmvstra
sdmvpsu wtmec2yr);

  ** Create MEC Weight Variable For Six Years **;

  if (1 <= sddsrvyr <= 2) then MECWeight = wtmec4yr * 2/3;


data bmx;
  set nhanes4a.bmx(keep=seqn bmxbmi)
      nhanes4b.bmx_b(keep=seqn bmxbmi)
      nhanes4c.bmx_c(keep=seqn bmxbmi);

data dxa;
  set nhanes4a.dxx(keep=seqn _mult_ dxdtrpf)
      nhanes4b.dxx_b(keep=seqn _mult_ dxdtrpf)
      nhanes4c.dxx_c(keep=seqn _mult_ dxdtrpf);

data ds1 ds2 ds3 ds4 ds5;
  merge demo bmx dxa;
  by seqn;
  select(_mult_);
    when(1) output ds1;
    when(2) output ds2;
    when(3) output ds3;
    when(4) output ds4;
    when(5) output ds5;
      otherwise;
  end;

%macro Sort;
%do i = 1 %to 5;
  proc sort data=ds&i;
    by sdmvstra sdmvpsu;
  run;
%end;
%mend Sort;
%Sort;

proc regress data=ds1 mi_count=5 design=wr;
  nest sdmvstra sdmvpsu;
  weight MECWeight;
```

```
** Select Males 20+ **;

  subpopn ridageyr >= 20 and riagendr = 1;
  class ridreth1;
  reflevel ridreth1 = 3;
  model bmxbmi = ridreth1 dxdtrpf;
rtitle "NHANES 1999-2004 - Males";
rtitle "Predicting BMI from Percent Trunk Fat & Race/Ethnicity";

proc regress data=ds1 mi_count=5 design=wr;
  nest sdmvstra sdmvpsu;
  weight MECWeight;

** Select Females 20+ **;

  subpopn ridageyr >= 20 and riagendr = 2;
  class ridreth1;
  reflevel ridreth1 = 3;
  model bmxbmi = ridreth1 dxdtrpf;
rtitle "NHANES 1999-2004 - Females";
rtitle "Predicting BMI from Percent Trunk Fat & Race/Ethnicity";
run;


**************************************************************
* SUDAAN OUTPUT FOR EXAMPLE PROGRAM 2 -- MALES: PROC REGRESS *
**************************************************************;
```

```
Processing data for set 1 of imputed variables:

Processing data for set 2 of imputed variables:

Processing data for set 3 of imputed variables:

Processing data for set 4 of imputed variables:

Processing data for set 5 of imputed variables:


Processing data for set 1 of imputed variables:

Number of observations read       :  22133    Weighted count:243432885
Observations in subpopulation     :   6735    Weighted count: 95989894
Observations used in the analysis :   6477    Weighted count: 93285096
Denominator degrees of freedom    :     44


Maximum number of estimable parameters for the model is  6

File DS1 contains   87 Clusters
  87 clusters were used to fit the model
Maximum cluster size is 122 records
Minimum cluster size is  38 records

Weighted mean response is 27.934690


Multiple R-Square for the dependent variable BMXBMI: 0.582144
```

```
.
.
.

Processing data for set 5 of imputed variables:

Number of observations read       :  22133    Weighted count:243432885
Observations in subpopulation     :   6735    Weighted count: 95989894
Observations used in the analysis :   6477    Weighted count: 93285096
Denominator degrees of freedom    :     44


Maximum number of estimable parameters for the model is  6

File DS5 contains   87 Clusters
  87 clusters were used to fit the model
Maximum cluster size is 122 records
Minimum cluster size is  38 records

Weighted mean response is 27.934690

Multiple R-Square for the dependent variable BMXBMI: 0.589335

Overall degrees of freedom (Rubin): 38.92


Date: 02-12-2008                                Research Triangle Institute
Page  : 2
Time: 14:32:10                                     The REGRESS Procedure
Table : 1

Variance Estimation Method: Taylor Series (WR) Using Multiply Imputed Data
SE Method: Robust (Binder, 1983)
Working Correlations: Independent
Link Function: Identity
Response variable BMXBMI: Body Mass Index (kg/m**2)
For Subpopulation: RIDAGEYR >= 20 AND RIAGENDR = 1
NHANES 1999-2004 - Males
Predicting BMI from Percent Trunk Fat & Race/Ethnicity
Results for Summary Over All Imputations
by: Independent Variables and Effects.

---------------------------------------------------------------------------------------------------------
Independent                                                                             P-value
  Variables and        Beta                      Lower 95%    Upper 95%                 T-Test     DDF
  Effects              Coeff.          SE Beta   Limit Beta   Limit Beta   T-Test B=0   B=0        Beta
---------------------------------------------------------------------------------------------------------
Intercept                   11.16         0.34        10.48        11.84        33.25     0.0000   41.299
Race/Ethnicity -
  Recode
  1                         -0.10         0.15        -0.39         0.20        -0.66     0.5158   38.925
  2                          0.11         0.28        -0.45         0.67         0.40     0.6907   40.721
  3                          0.00         0.00         0.00         0.00          .         .       44.000
  4                          1.99         0.17         1.65         2.33        11.73     0.0000   42.062
  5                         -0.90         0.39        -1.69        -0.10        -2.28     0.0281   41.327
Trunk Percent Fat            0.57         0.01         0.55         0.59        47.59     0.0000   41.309
---------------------------------------------------------------------------------------------------------
```

```
Date: 02-12-2008                                Research Triangle Institute
Page  : 3
Time: 14:32:10                                     The REGRESS Procedure
Table : 1

Variance Estimation Method: Taylor Series (WR) Using Multiply Imputed Data
SE Method: Robust (Binder, 1983)
Working Correlations: Independent
Link Function: Identity
Response variable BMXBMI: Body Mass Index (kg/m**2)
For Subpopulation: RIDAGEYR >= 20 AND RIAGENDR = 1
NHANES 1999-2004 - Males
Predicting BMI from Percent Trunk Fat & Race/Ethnicity
Results for Summary Over All Imputations
by: Contrast.

-------------------------------------------------------

Contrast               Degrees
                       of                       P-value
                       Freedom        Wald F   Wald F
-------------------------------------------------------
OVERALL MODEL                 6     28244.49     0.0000
MODEL MINUS
  INTERCEPT                   5       473.72     0.0000
INTERCEPT                     .            .        .
RIDRETH1                      4        66.03     0.0000
DXDTRPF                       1      2265.27     0.0000
-------------------------------------------------------
```

```
*****************************************************************
* SUDAAN OUTPUT FOR EXAMPLE PROGRAM 2 – FEMALES: PROC REGRESS *
*****************************************************************;
```

```
Processing data for set 1 of imputed variables:

Processing data for set 2 of imputed variables:

Processing data for set 3 of imputed variables:

Processing data for set 4 of imputed variables:

Processing data for set 5 of imputed variables:


Processing data for set 1 of imputed variables:

Number of observations read       :  22133    Weighted count:243432885
Observations in subpopulation     :   7478    Weighted count:104717834
Observations used in the analysis :   6449    Weighted count: 97673612
Denominator degrees of freedom    :     44

.
.
.

Processing data for set 5 of imputed variables:

Number of observations read       :  22133    Weighted count:243432885
Observations in subpopulation     :   7478    Weighted count:104717834
Observations used in the analysis :   6449    Weighted count: 97673612
Denominator degrees of freedom    :     44


Maximum number of estimable parameters for the model is  6

File DS5 contains   87 Clusters
  87 clusters were used to fit the model
Maximum cluster size is 118 records
Minimum cluster size is  34 records

Weighted mean response is 28.206126

Multiple R-Square for the dependent variable BMXBMI: 0.660758

Overall degrees of freedom (Rubin): 29.20



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Page  : 2
Time: 14:32:12                                     The REGRESS Procedure
Table : 1

Variance Estimation Method: Taylor Series (WR) Using Multiply Imputed Data
SE Method: Robust (Binder, 1983)
Working Correlations: Independent
Link Function: Identity
Response variable BMXBMI: Body Mass Index (kg/m**2)
For Subpopulation: RIDAGEYR >= 20 AND RIAGENDR = 2
NHANES 1999-2004 - Females
Predicting BMI from Percent Trunk Fat & Race/Ethnicity
Results for Summary Over All Imputations
by: Independent Variables and Effects.

---------------------------------------------------------------------------------------------------------
Independent                                                                             P-value
  Variables and        Beta                      Lower 95%    Upper 95%                 T-Test     DDF
  Effects              Coeff.          SE Beta   Limit Beta   Limit Beta   T-Test B=0   B=0        Beta
---------------------------------------------------------------------------------------------------------
Intercept                    3.12         0.42         2.26         3.98         7.39     0.0000   29.200
Race/Ethnicity -
  Recode
  1                         -0.28         0.16        -0.62         0.05        -1.74     0.0913   35.475
  2                         -0.45         0.34        -1.13         0.24        -1.32     0.1944   39.921
  3                          0.00         0.00         0.00         0.00          .          .       44.000
  4                          2.46         0.15         2.16         2.77        16.37     0.0000   37.736
  5                         -1.22         0.35        -1.94        -0.50        -3.44     0.0014   37.879
Trunk Percent Fat            0.65         0.01         0.63         0.68        54.31     0.0000   32.460
---------------------------------------------------------------------------------------------------------



Date: 02-12-2008                                Research Triangle Institute
Page  : 3
Time: 14:32:12                                     The REGRESS Procedure
Table : 1

Variance Estimation Method: Taylor Series (WR) Using Multiply Imputed Data
SE Method: Robust (Binder, 1983)
Working Correlations: Independent
```

```
Link Function: Identity
Response variable BMXBMI: Body Mass Index (kg/m**2)
For Subpopulation: RIDAGEYR >= 20 AND RIAGENDR = 2
NHANES 1999-2004 - Females
Predicting BMI from Percent Trunk Fat & Race/Ethnicity
Results for Summary Over All Imputations
by: Contrast.

-------------------------------------------------------

Contrast               Degrees
                       of                      P-value
                       Freedom        Wald F   Wald F
-------------------------------------------------------
OVERALL MODEL                 6     22254.65     0.0000
MODEL MINUS
  INTERCEPT                   5      1002.94     0.0000
INTERCEPT                     .          .        .
RIDRETH1                      4       129.41     0.0000
DXDTRPF                       1      2949.71     0.0000
-------------------------------------------------------
```

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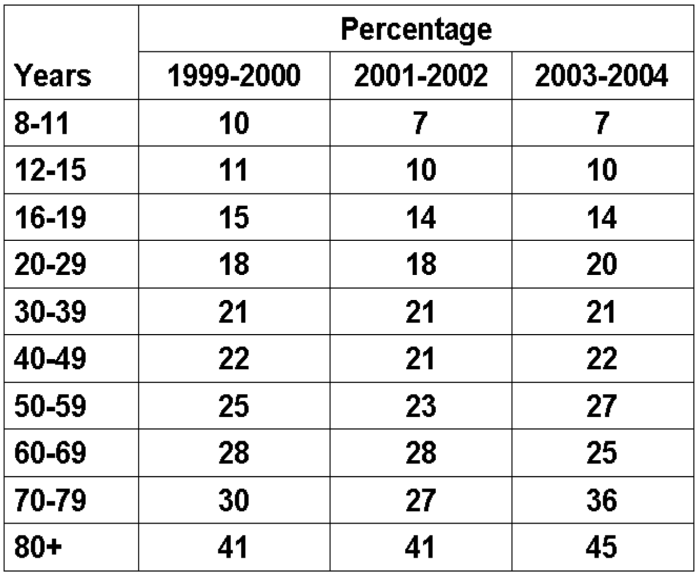
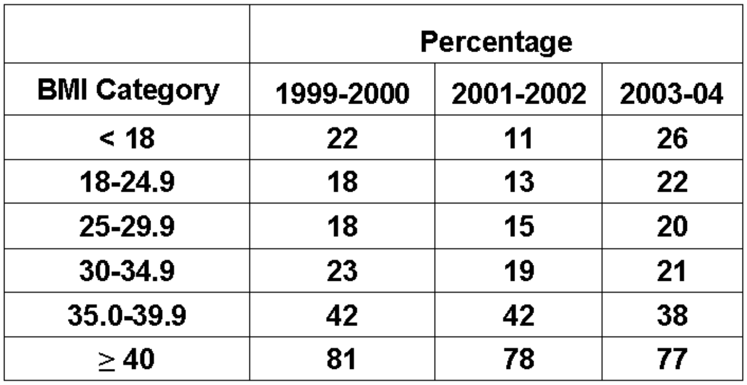
Table 1. Percentages of survey participants in 1999-2004 with data missing for one or more regions by age group.



	Percentage		
Years	1999-2000	2001-2002	2003-2004
8-11	10	7	7
12-15	11	10	10
16-19	15	14	14
20-29	18	18	20
30-39	21	21	21
40-49	22	21	22
50-59	25	23	27
60-69	28	28	25
70-79	30	27	36
80+	41	41	45

Table 2. Percentages of survey participants in 1999-2004 with data missing for one or more regions by body mass index (BMI) category.



	Percentage		
BMI Category	1999-2000	2001-2002	2003-04
< 18	22	11	26
18-24.9	18	13	22
25-29.9	18	15	20
30-34.9	23	19	21
35.0-39.9	42	42	38
≥ 40	81	78	77

Table 3. DXA variables included in the imputation model.

Name of Original Variable	Description
DXDLAA	Left Arm Area (cm^2)
DXDLABMC	Left Arm BMC (g)
DXDLAFAT	Left Arm Fat (g)
DXDLALER	Left Arm Lean excl BMC (g)
DXDRAA	Right Arm Area (cm^2)
DXDRABMC	Right Arm BMC (g)
DXDRAFAT	Right Arm Fat (g)
DXDRALER	Right Arm Lean excl BMC (g)
DXDTRFAT	Truncal fat (g)
XDTRLER	Trunk Lean excl BMC (g)
DXDLLA	Left Leg Area (cm^2)
DXDLLBMC	Left Leg BMC (g)
DXDLLFAT	Left Leg Fat (g)
DXDLLLER	Left Leg Lean excl BMC (g)
DXDRLA	Right Leg Area (cm^2)
DXDRLBMC	Right Leg BMC (g)
DXDRLFAT	Right Leg Fat (g)
DXDRLLER	Right Leg Lean excl BMC (g)
DXDHEA	Head Area (cm^2)
DXDHEBMC	Head Bone Mineral Content (g)
DXDHEFAT	Head Fat (g)
DXDHELER	Head Lean excl BMC (g)
DXDLRA	Left Ribs Area (cm^2)
DXDLRBMC	Left Ribs BMC (g)
DXDRRA	Right Ribs Area (cm^2)
DXDRRBMC	Right Ribs BMC (g)
DXDTSA	Thoracic Spine Area (cm^2)
DXDTSBMC	Thoracic Spine BMC (g)
DXDLSA	Lumbar Spine Area (cm^2)
DXDLSBMC	Lumbar Spine BMC (g)
DXDPEA	Pelvis Area (cm^2)
DXDPEBMC	Pelvis BMC (g)

Table 4. Non-DXA variables included in the imputation model.

Name of Original Variable	**Analytic Variable Name**	**Description**	**Age Range**
RIDRETH1	NEWRACE	Race/Ethnicity 1=Mexican American 2=Non-Hispanic White 3=Non-Hispanic Black 4=Other (includes other Hispanic and multiracial)	8+
RIAAGEYR	RIAAGEYR	Age at Screening	8+ (Although age is top-coded at 85+years in the release data files, continuous age was used for those 80+ years.)
INDFMINC	INCOME	Annual CPS Family Income 1=<$20,000 2=>=$20,000	8+
DMD140, DMDEDUC	DMDEDUC	Education- Recode 1= < High School 2=High School diploma (includes GED) 3= > High School	20+
SDASTAND (represents location of mobile examination center)	METRO	Indicates if sample person lives in a metropolitan area 1=Metro 2=Non-Metro area	8+
SDASTAND (represents location of mobile examination center)	REGION	Indicates region of the country where sample person lives 1=Northeast 2=Midwest 3=South 4=West	8+
WTMEC4YR	WTMEC4YR	Full Sample 4 Year MEC Exam Weight (includes only those with MEC EXAM Weight > 0)	8+
SDDSRVYR	SDDSRVYR	Data Release Number 1=1999-2000 2=2001-2002 3=2003-2004	8+
BPXDAR	BPXDAR	Average Diastolic Blood Pressure	8+
BPXSAR	BPXSAR	Average Systolic Blood Pressure	8+
BPQ050a, BPQ010, BPQ020, BPQ040a	BPMED	Now taking prescribed medicine for blood pressure	16+

		1=yes 2=no	
BMXWT	BMXWT	Weight (kg)	8+
BMXARMC	BMXARMC	Arm Circumference (cm)	8+
BMXSUB	BMXSUB	Subscapular Skinfold (mm)	8+
BMXTRI	BMXTRI	Triceps Skinfold (mm)	8+
BMXWAIST	BMXWAIST	Waist Circumference (cm)	8+
BMXHT	BMXHT	Height (cm)	8+
BMXWAIST_BMXHT	BMXWAIST_BMXHT	Waist Circumference (cm)/Height (cm)	8+
BMXBMI	BMXBMI	Body Mass Index (kg/m**2)	8+
BMXBMI	OBESEIND	3 BMI categories 1=Under or normal weight <25 2=Overweight 25-<30 3=Obese >=30	20+
DIQ010	DRDIAB[#]	Doctor told you have diabetes 1=yes 2=no (DIQ010=2 or 3)	8+
HUQ010	HEALTHSTAT	General Health Condition 1=excellent/very good 2=good 3=fair/poor	8+
LBXTC	LBXTC	Total Cholesterol (mg/dL)	8+
LBDHDL	LBDHDL	HDL Cholesterol (mg/dL)	8+
LBXSTR***	LBXSTR	**Natural Log** Trigylcerides (mg/dL) –nonfasting	12+
BPQ100D, BPQ060, BPQ080, BPQ090d	CHOLMED	Now taking prescribed medicine for cholesterol 1=yes 2=no	20+
PAD200, PAD320	PHYSICALACTIVITY	Moderate or Vigorous Activity past 30 days 1=yes 2=no	12+
SMQ620, SMD630, SMQ640, SMQ020, SMQ040	SMOKER	Smoking Status 1=Never 2=Former 3=Current	12+
OSQ030aa to OSQ030cf, OSQ010a, OSQ010b, OSQ010c	FRACTURE	Experienced a fracture 1=yes 2=no	20+
MCQ250e, MCQ260ea, MCQ260eb	FAMOSTEO	Family History of Osteoporosis 1=yes 2=no	20+
RHQ420, RHQ440, RHQ510, RHQ520	BCEVER	Ever take birth control 1=yes 2=no	Females 12+
RHQ030, RHQ040, RHQ310, RHQ050, RHQ060, RHQ340,	NEWMENO	Menopause Status 1=Premenopausal 2=Menopause Transition	Females 12+

RHQ290		3=Surgical/ Medical Amenorrhea 4=Natural Menopause	
RHQ554, RHQ570, RHQ580, RHQ596, RHQ540	ANYEST	Ever take non-birth control estrogen 1=yes 2=no	Females 20+
ALCDRNKYR	DRNKYR_CAT	Categories for average alcohol consumption per year 0=none 1=Less than once a week 2=Less than once a day 3=Once a day or more	20+
Nhcode in (01900, 51500, 50900, 09400)	OSTEORX	Osteoporosis Treatments: alendronate, risedronate, raloxifene, calcitonin 1=yes 0=no	8+
fdacode =1374	ANTICONV	Anticonvulsants 1=yes 0=no	8+
Nhcode in (16400 17500 25300 31000 39600 39700 48600 49000 58100 58300 36100 56300 36200 38700 50100 56300 92400)	PRESMEDS	Prescription Meds: Cortisone, Thyroid, levothyroxine, liotrix, methimazole, propylthiouracil 1=yes 0=no	8+
DSD010, DSDANTA	ANTACID	Antacids (of those who answered yes/no to dietary supplement) 1=took antacid past month 2=did not take antacid past month	8+
DSD010	DSD0101	Any dietary supplements taken? 1=yes 2=no	8+
DBD196	DBD196_NEW	Past 30 day milk consumption recode 1=Never/Rarely less than once a week 2=Sometimes/Often/Varies	8+
DRXTCALC, DRXTPROT, DRDTSODI, DRXTPOTA, DRXTVC, DRXTZINC, DRXTMAGN, DRXTCOPP, DRXTIRON, DRXTCAFF	DRXTCALC, DRXTPROT, DRDTSODI, DRXTPOTA, DRXTVC, DRXTZINC, DRXTMAGN, DRXTCOPP, DRXTIRON, DRXTCAFF DRXTTFAT	Diet: Calcium, protein, sodium, potassium, vitamin C, zinc, magnesium, copper, iron, caffeine, total fat	8+

Figure 1

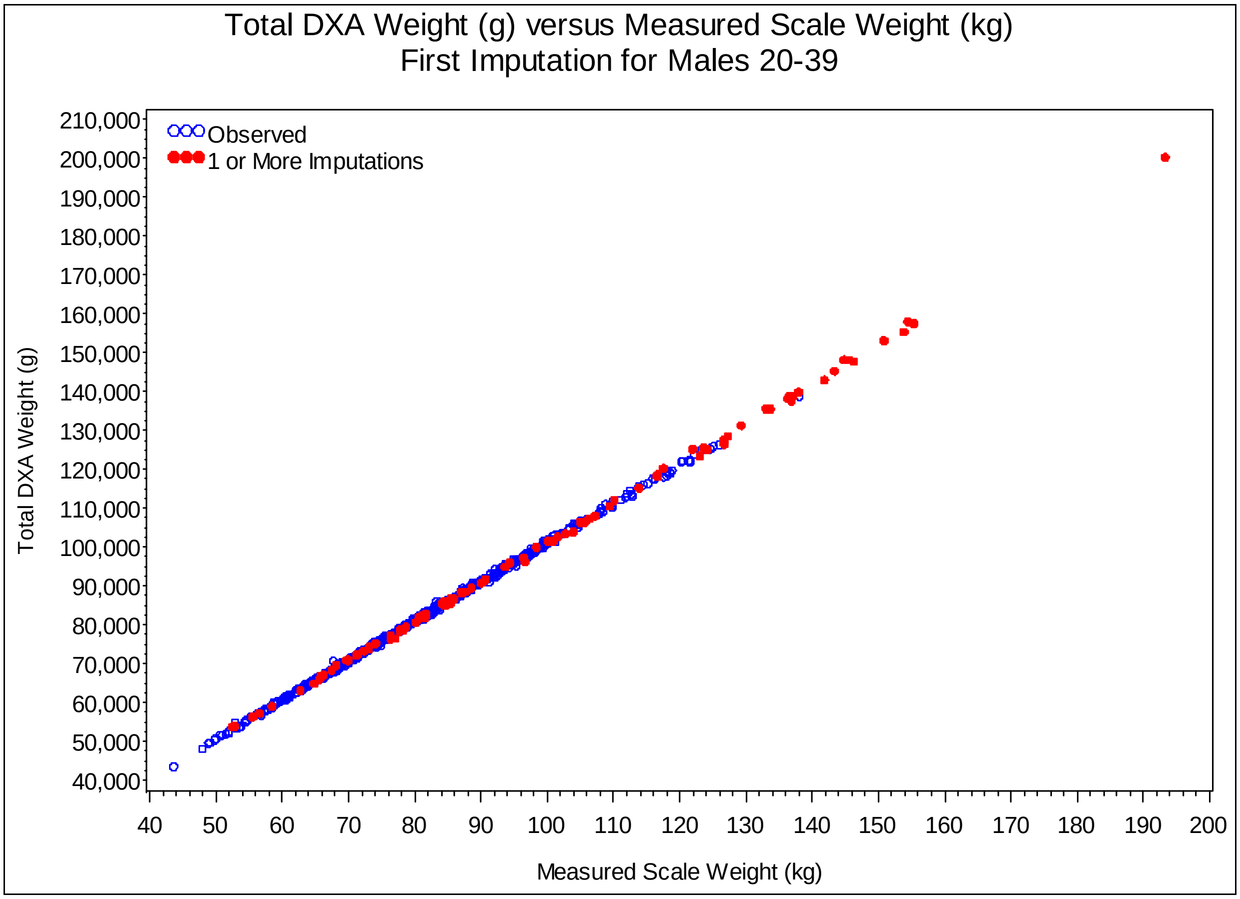

Total DXA Weight (g) versus Measured Scale Weight (kg)
First Imputation for Males 20-39
○○○ Observed
●●● 1 or More Imputations
Total DXA Weight (g)
210,000
200,000
190,000
180,000
170,000
160,000
150,000
140,000
130,000
120,000
110,000
100,000
90,000
80,000
70,000
60,000
50,000
40,000
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
Measured Scale Weight (kg)

Figure 2

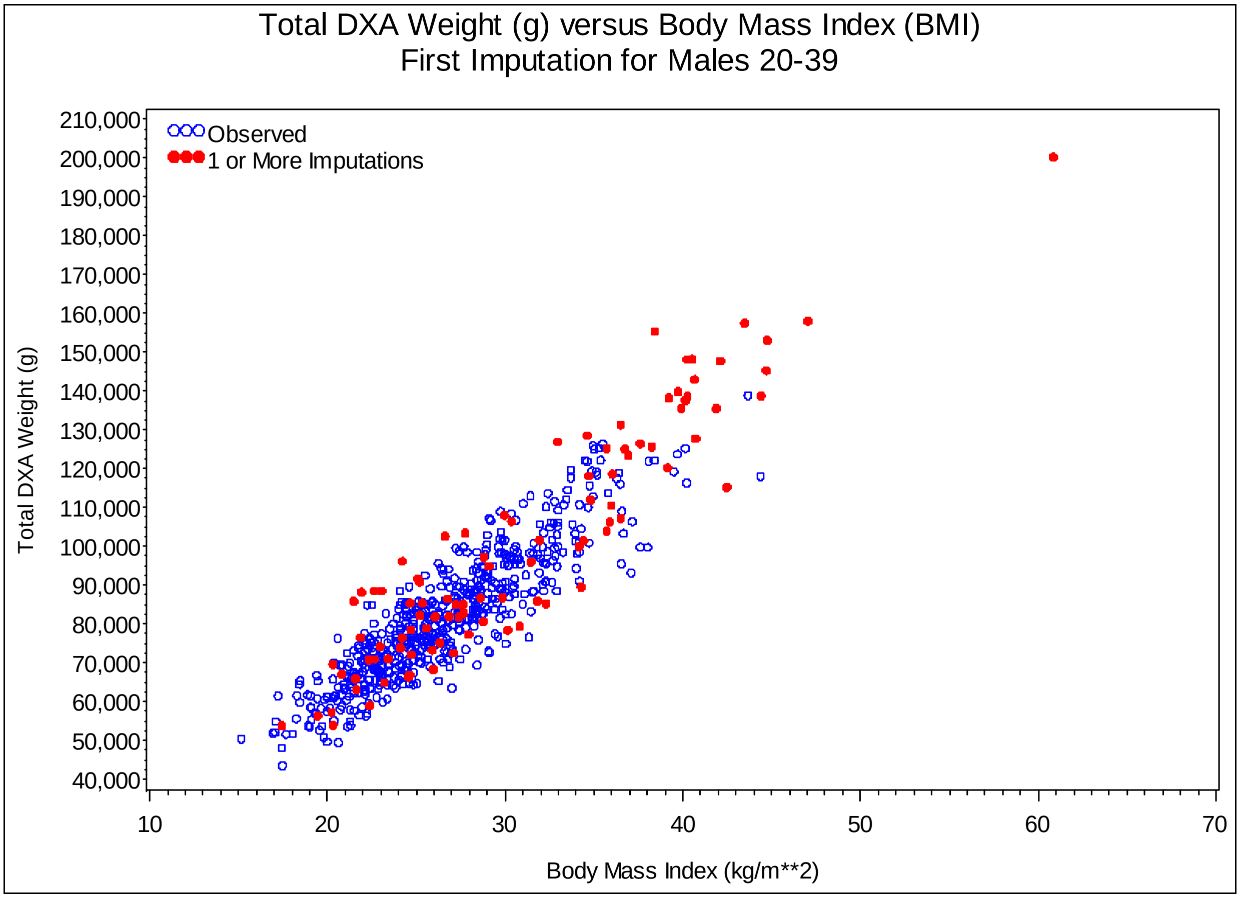

Total DXA Weight (g) versus Body Mass Index (BMI)
First Imputation for Males 20-39
○○○ Observed
●●● 1 or More Imputations
Total DXA Weight (g)
210,000
200,000
190,000
180,000
170,000
160,000
150,000
140,000
130,000
120,000
110,000
100,000
90,000
80,000
70,000
60,000
50,000
40,000
10
20
30
40
50
60
70
Body Mass Index (kg/m**2)

Figure 3

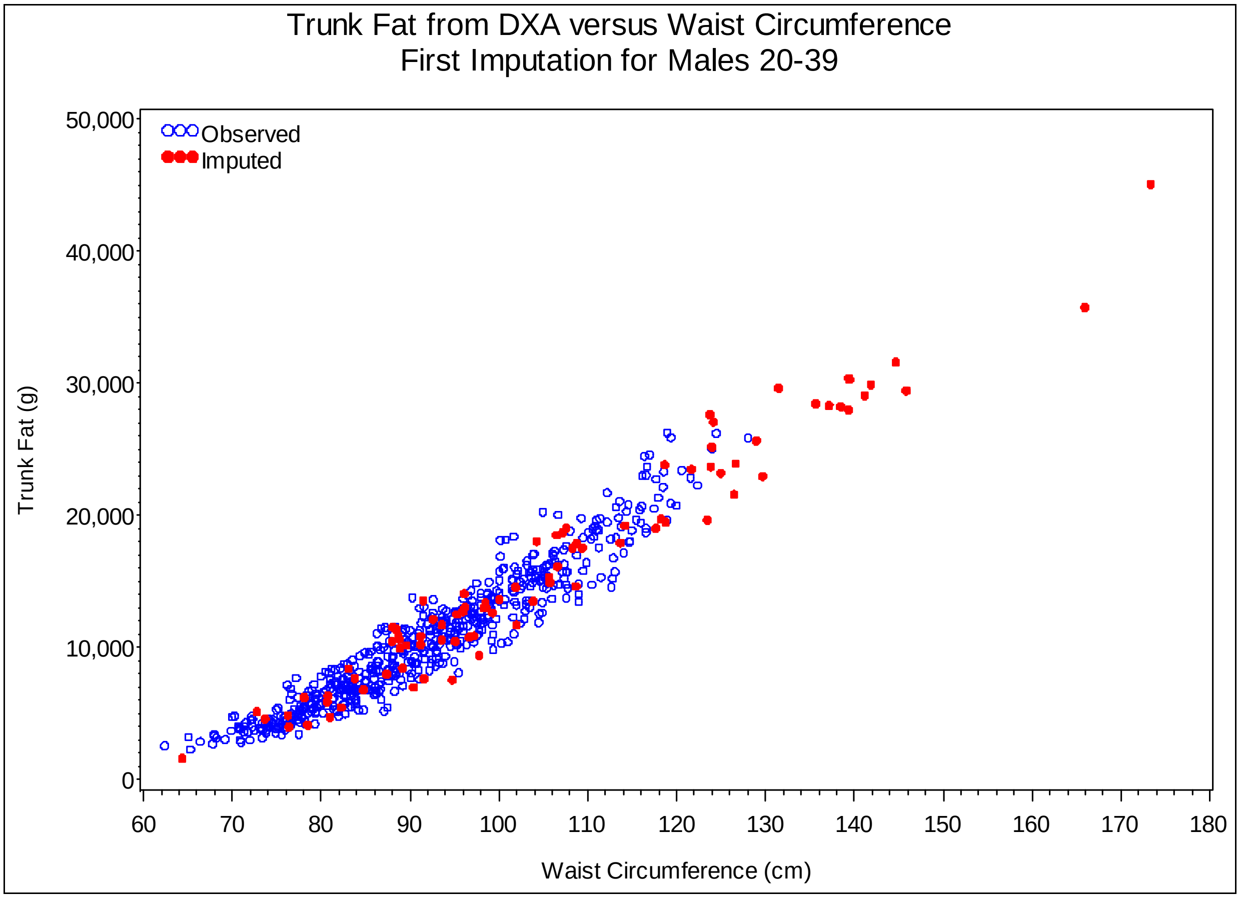

Trunk Fat from DXA versus Waist Circumference
First Imputation for Males 20-39
Observed
Imputed
Trunk Fat (g)
50,000
40,000
30,000
20,000
10,000
0
60
70
80
90
100
110
120
130
140
150
160
170
180
Waist Circumference (cm)

Figure 4

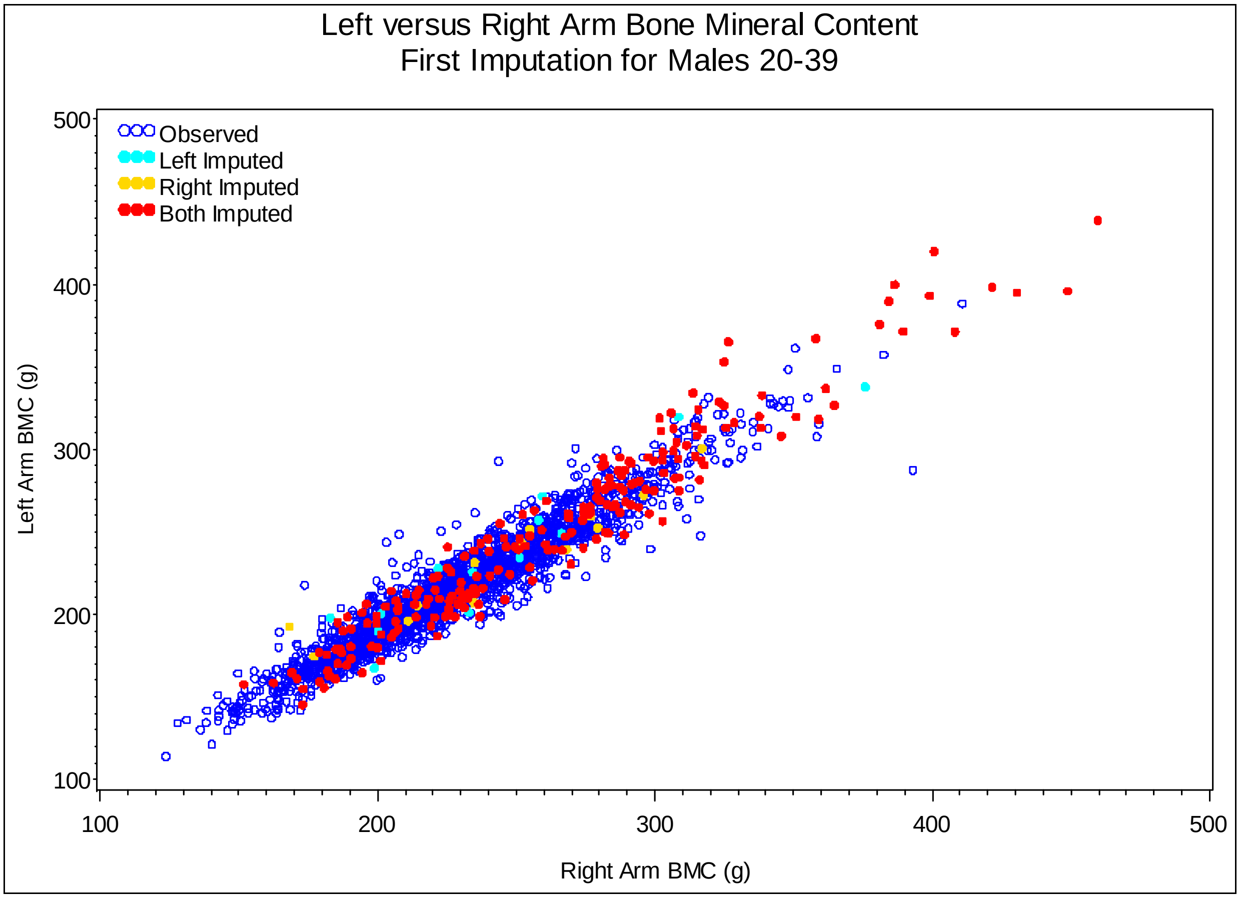
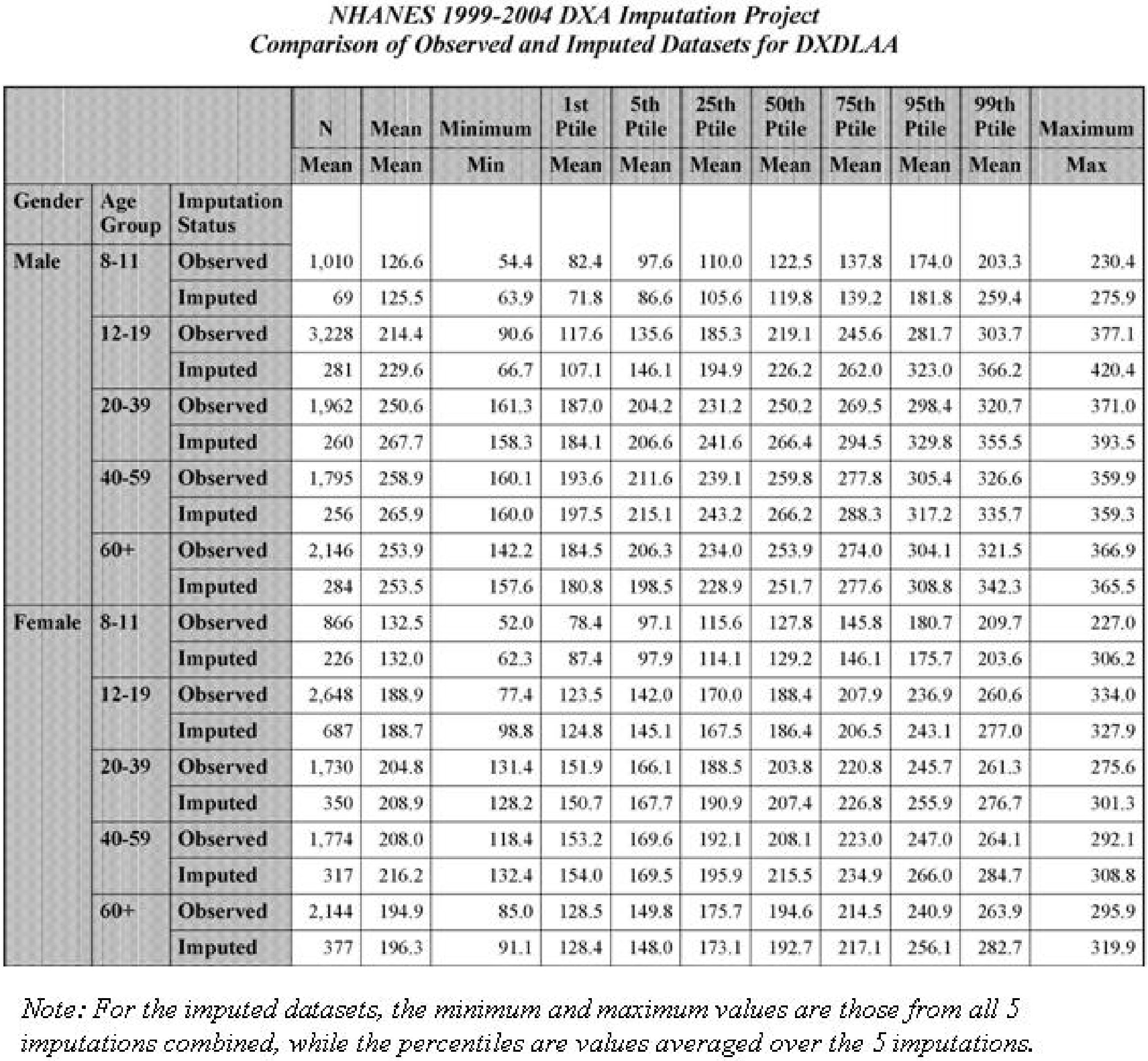

Left versus Right Arm Bone Mineral Content
First Imputation for Males 20-39
Observed
Left Imputed
Right Imputed
Both Imputed
Left Arm BMC (g)
100
200
300
400
500
Right Arm BMC (g)
100
200
300
400
500

Figure 5



NHANES 1999-2004 DXA Imputation Project
Comparison of Observed and Imputed Datasets for DXDLAA

			N	Mean	Minimum	1st Ptile	5th Ptile	25th Ptile	50th Ptile	75th Ptile	95th Ptile	99th Ptile	Maximum
			Mean	Mean	Min	Mean	Mean	Mean	Mean	Mean	Mean	Mean	Max
Gender	Age Group	Imputation Status											
Male	8-11	Observed	1,010	126.6	54.4	82.4	97.6	110.0	122.5	137.8	174.0	203.3	230.4
		Imputed	69	125.5	63.9	71.8	86.6	105.6	119.8	139.2	181.8	259.4	275.9
	12-19	Observed	3,228	214.4	90.6	117.6	135.6	185.3	219.1	245.6	281.7	303.7	377.1
		Imputed	281	229.6	66.7	107.1	146.1	194.9	226.2	262.0	323.0	366.2	420.4
	20-39	Observed	1,962	250.6	161.3	187.0	204.2	231.2	250.2	269.5	298.4	320.7	371.0
		Imputed	260	267.7	158.3	184.1	206.6	241.6	266.4	294.5	329.8	355.5	393.5
	40-59	Observed	1,795	258.9	160.1	193.6	211.6	239.1	259.8	277.8	305.4	326.6	359.9
		Imputed	256	265.9	160.0	197.5	215.1	243.2	266.2	288.3	317.2	335.7	359.3
	60+	Observed	2,146	253.9	142.2	184.5	206.3	234.0	253.9	274.0	304.1	321.5	366.9
		Imputed	284	253.5	157.6	180.8	198.5	228.9	251.7	277.6	308.8	342.3	365.5
Female	8-11	Observed	866	132.5	52.0	78.4	97.1	115.6	127.8	145.8	180.7	209.7	227.0
		Imputed	226	132.0	62.3	87.4	97.9	114.1	129.2	146.1	175.7	203.6	306.2
	12-19	Observed	2,648	188.9	77.4	123.5	142.0	170.0	188.4	207.9	236.9	260.6	334.0
		Imputed	687	188.7	98.8	124.8	145.1	167.5	186.4	206.5	243.1	277.0	327.9
	20-39	Observed	1,730	204.8	131.4	151.9	166.1	188.5	203.8	220.8	245.7	261.3	275.6
		Imputed	350	208.9	128.2	150.7	167.7	190.9	207.4	226.8	255.9	276.7	301.3
	40-59	Observed	1,774	208.0	118.4	153.2	169.6	192.1	208.1	223.0	247.0	264.1	292.1
		Imputed	317	216.2	132.4	154.0	169.5	195.9	215.5	234.9	266.0	284.7	308.8
	60+	Observed	2,144	194.9	85.0	128.5	149.8	175.7	194.6	214.5	240.9	263.9	295.9
		Imputed	377	196.3	91.1	128.4	148.0	173.1	192.7	217.1	256.1	282.7	319.9

Note: For the imputed datasets, the minimum and maximum values are those from all 5 imputations combined, while the percentiles are values averaged over the 5 imputations.