



Developing Sampling Weights for Statistical Analysis of Parent–Child Pair Data From the National Health Interview Survey

Data Evaluation and Methods Research



**Centers for Disease
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Data Evaluation and Methods Research

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES
Centers for Disease Control and Prevention
National Center for Health Statistics

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Developing Sampling Weights for Statistical Analysis of Parent–Child Pair Data From the National Health Interview Survey

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Abstract

Background

The National Health Interview Survey (NHIS), conducted by the National Center for Health Statistics since 1957, is the principal source of information on the health of the U.S. civilian noninstitutionalized population. NHIS selects one adult (Sample Adult) and, when applicable, one child (Sample Child) randomly within a family (through 2018) or a household (2019 and forward). Sampling weights for the separate analysis of data from Sample Adults and Sample Children are provided annually by the National Center for Health Statistics. A growing interest in analysis of parent–child pair data using NHIS has been observed, which necessitated the development of appropriate analytic weights.

Objective

This report explains how dyad weights were created such that data users can analyze NHIS data from both Sample Children and their mothers or fathers, respectively.

Methods

Using data from the 2019 NHIS, adult–child pair-level sampling weights were developed by combining each pair’s conditional selection probability with their household-level sampling weight. The calculated pair weights were then adjusted for pair-level nonresponse, and large sampling weights were trimmed at the 99th percentile of the derived sampling weights. Examples of analyzing parent–child pair data by means of domain estimation methods (that is, statistical analysis for subpopulations or subgroups) are included in this report.

Conclusions

The National Center for Health Statistics has created dyad or pair weights that can be used for studies using parent–child pairs in NHIS. This method could potentially be adapted to other surveys with similar sampling design and statistical needs.

Keywords: parent–child pair data • pair weights • domain analysis

Introduction

The National Health Interview Survey (NHIS) is a cross-sectional survey conducted annually since 1957 by the National Center for Health Statistics (NCHS). NHIS uses a geographically-clustered design that results in a probability sample of households. Through 2018, all families within a selected household were included in the survey as part of the NHIS family component. Within a family, one adult age 18 or older (Sample Adult) and one child (if any) (Sample Child) were randomly selected, and face-to-face interviews that collected health-related information were conducted with that Sample Adult and with an adult respondent knowledgeable for the health of the Sample Child (typically the parent). Starting in 2019, the NHIS questionnaire was redesigned, and one Sample Adult and

one Sample Child (if any) were randomly selected within a household instead of a family. The probability design of NHIS results in a representative sampling of the U.S. civilian noninstitutionalized population (1,2).

NCHS releases NHIS public-use data at the Sample Adult level (Sample Adult file) and Sample Child level (Sample Child file). To represent the distribution of the U.S. population, sampling weights have been developed for each of these public-use data sets. In recent years, a growing interest in analysis of parent–child pair (or dyadic) data using NHIS Sample Adult and Sample Child data files has been observed. Dyadic relationships are used in social, behavioral, and epidemiological research to study health and health behaviors of dyadic members (3) as members of dyads can influence each other. One of the main objectives of research

using dyadic data is to understand how the characteristics and behaviors of one dyad member may be associated with the other dyad member (4).

The NHIS Sample Adult and Sample Child questionnaires collect detailed information on the health status, healthcare services, and health behaviors of the Sample Adult and Sample Child. As a result, NHIS parent–child pair data are potentially a rich source to study dyadic relationships between mothers or fathers and their children. Because NHIS does not sample a parent–child pair from all possible parent–child pairs within a family or a household, the sampling weights for specific dyads (for example, father–child and mother–child) cannot be developed. However, sampling weights for adult–child pairs more generally can be created. Once adult–child pair sampling weights are created, domain estimation methods (that is, statistical analysis for subpopulations or subgroups) can produce estimates separately for mother–child and father–child pairs because mother–child and father–child pairs are a subset of all adult–child pairs (5–7). To meet the needs of data users, adult–child pair sampling weights were developed in this study for use in the analysis of mother–child and father–child pair data of NHIS, and the weights will be released for public use.

The report describes how weights were created for Sample Adult–Sample Child pairs using the 2019 NHIS and how to use these weights in analyses. Four examples of univariate and multivariate statistical analyses are applied to the NHIS dyadic data.

Deriving Sampling Weights for Sample Adult–Sample Child Pairs in the 2019 NHIS

This report documents how the 2019 NHIS dyad weights were created. All sampled households in the 2019 NHIS had a "base" sampling weight associated with them, which reflects their probability of selection (8). Because not all selected households agreed to participate, NCHS conducted household-level nonresponse adjustment using multilevel regression models that included variables predictive of both survey response and selected key health outcomes (1,8). Building upon the nonresponse-adjusted household sampling weights and given the independent sampling feature of Sample Adults and Sample Children, adult–child pair-level sampling weights can be developed by first deriving each adult–child pair's conditional selection probability and then combining that with their household's sampling weight, as described in the next section.

The weights created using this method are for use in the analysis of NHIS mother–child or father–child pair data separately. These weights can be used when data from a mother (or father separately) are incorporated in a child-

level analysis as an exposure or independent variable, or if a joint mother–child or father–child outcome is used in the analysis. An example of the former would be to examine the association of maternal asthma on child obesity. An example of the latter would be to examine factors associated with both a father and a child having asthma. These weights should not be used to analyze nonparent–child pairs due to either the small sample size (for example, grandmother–child pair) or other pairs that are not representative of any meaningful groups (for example, nonrelative adult–child pair).

Deriving Adult–Child Pair Weights Among Eligible Households in the 2019 NHIS

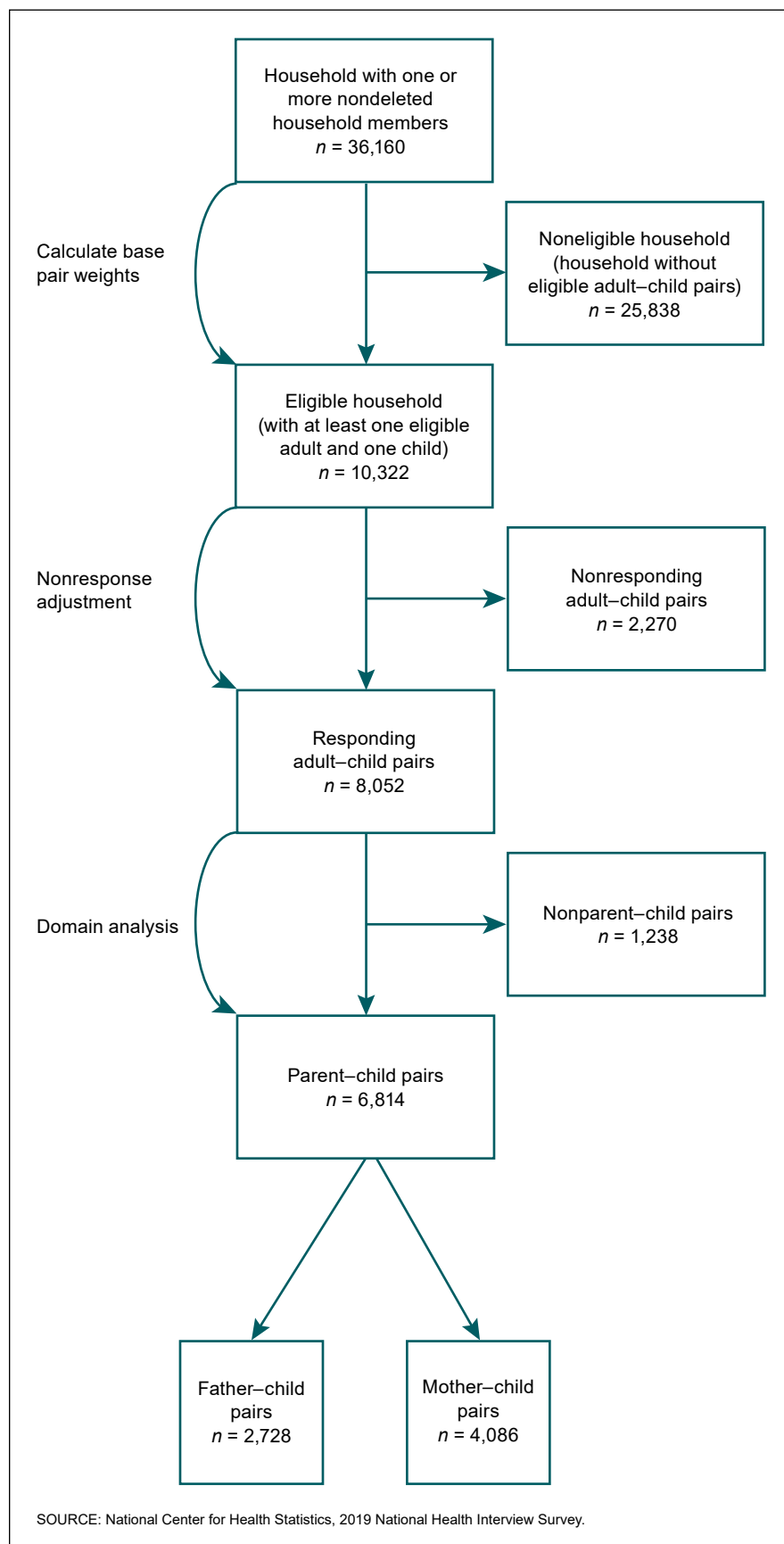
To derive sampling weights for adult–child pairs in the 2019 NHIS, an eligible household was first defined as a household that participated in the 2019 NHIS with an adult–child pair sampled, that is, with both a Sample Adult and a Sample Child (younger than or equal to age 17 years) selected for the Sample Adult and Sample Child interviews, regardless of the pair's responding status. Households without children were excluded from the pair-level analysis, as were households with no eligible adults (for example, all adults who are active-duty Armed Forces personnel). Among the 36,160 responding households in the 2019 NHIS, 10,322 households met the eligibility criteria (Figure), that is, had at least one eligible adult and one child. Among these eligible households, 8,052 households had completed Sample Adult and Sample Child interviews. Among these 8,052 responding Sample Adult–Sample Child pairs, 6,814 (84.6%) were parent–child pairs (2,728 father–child pairs and 4,086 mother–child pairs). The parent–child pairs consist of all degrees of the parent–child relationship (biological, adoptive, or other nonbiological). The variable *SAPARENTSC_A* (Sample Adult relationship to Sample Child), which is available in the Sample Adult public-use data file, can be used to identify parent–child pairs from nonparent–child pairs.

To derive each Sample Adult–Sample Child pair's sampling weight, the adult–child pair's conditional selection probability, that is, each pair's selection probability given their household was in NHIS, was first derived, and then the pair-level selection probability was combined with the household-level sampling weight to derive the sampling weight of each Sample Adult–Sample Child pair.

Let h be a household in the NHIS sample, and let W_h be household h 's sampling weight developed by NCHS. Let $i = 1, 2, \dots, I$ index the eligible adults in household h , where I is the total number of eligible adults, and let $P_{i|h}$ be adult i 's conditional selection probability given h ; for the 2019 NHIS,

$$P_{i|h} = \frac{1}{I}.$$

Figure. Sample size flowchart for pair weights development: National Health Interview Survey, 2019



Let $j = 1, 2, \dots, J$ index the J children in household h , and let $P_{j|h}$ be child j 's conditional selection probability given h ; for the 2019 NHIS,

$$P_{j|h} = \frac{1}{J}.$$

The conditional selection probability for pair k , where $k = (i, j)$, given h is

$$\pi_{k|h} = P_{i|h} \cdot P_{j|h}.$$

Then pair k 's base sampling weight is

$$\begin{aligned} w^k &= W_h / \pi_{k|h} \\ &= W_h / (P_{i|h} \cdot P_{j|h}) \quad (1.1) \\ &= W_h \cdot I \cdot J. \end{aligned}$$

Adult-Child Pair-level Nonresponse Adjustment

Among the 2019 NHIS eligible households ($n = 10,322$), 8,052 adult-child pairs (78.0%) completed both the Sample Adult and Sample Child interviews; the remaining households completed only the Sample Adult interview ($n = 701$, 6.8%), only the Sample Child interview ($n = 1,141$, 11.1%), or neither interview ($n = 428$, 4.1%). To create dyad weights, households who completed both the Sample Adult and Sample Child interviews were retained in the analysis; the remaining households were treated as nonrespondents in terms of pair-level statistical analysis. For the purpose of the creation of adult-child pair weights, nonresponding households were eligible households with a responding adult only [denoted as (RA, NC), where RA denotes a responding adult and NC denotes a nonresponse to the Sample Child interview]; a completed Sample Child interview only [denoted as (NA, RC), where NA denotes a nonresponse to the Sample Adult interview and RC denotes a response to the Sample Child interview]; or neither an adult interview response nor a child interview response (NA, NC). The adult-child pair weights for these households were set to 0, and their sampling weights were redistributed to households with both

adult- and child-completed interviews to the survey (RA, RC). The adjustment factor was defined as:

Adjustment factor (AF) =

$$\frac{\sum_{RA,NC} w^k + \sum_{NA,RC} w^k + \sum_{RA,RC} w^k + \sum_{NA,NC} w^k}{\sum_{RA,RC} w^k} \quad (1.2)$$

where w^k was pair k 's base sampling weight, which was derived using formula (1.1),

$$\sum_{RA,NC} w^k$$

was the summation of adult-child pairs' sampling weights over all households with responding adults only. The remaining terms in (1.2) had similar definitions as those of

$$\sum_{RA,NC} w^k.$$

The nonresponse adjustment shown in (1.2) can be performed across all eligible households. It is appropriate when the nonresponse is not related to any factors, that is, missing completely at random. However, if pair-level nonresponse propensity is different among different groups, then factors related to missingness should be considered for nonresponse adjustment. Consequently, households with responding pairs and households with nonresponding pairs (that is, nonrespondents to the Sample Adult and/or Sample Child interviews) were compared and factors related to nonresponse were identified using chi-squared tests and logistic regression models. The response propensity was calculated from a logistic regression model that included all the selected factors, including household type (one-adult household versus multi-adult household); number of families in a household (one family versus multiple families in the household); metropolitan statistical area status; census region; highest level of education among all household members; Sample Adult's age, sex, and race and ethnicity; urban or rural status; and the median family income within a census block group (results not shown). Twenty adjustment cells were formed based on the equidistant quantiles from the 5th percentile to the 100th percentile of the predicted propensity of response, and the pair-level nonresponse adjustment was conducted within each adjustment cell. The adjustment factor was calculated within each adjustment cell as:

Adjustment factor within cell q (AF_q) =

$$\frac{\sum_{RA,NC} I_k(q)w^k + \sum_{NA,RC} I_k(q)w^k + \sum_{RA,RC} I_k(q)w^k + \sum_{NA,NC} I_k(q)w^k}{\sum_{RA,RC} I_k(q)w^k}, \quad (1.3)$$

where $I_k(q)$ was an indicator variable with $I_k(q) = 1$ if pair k was in cell q , and 0 otherwise, and q was an adjustment cell defined by the propensity of response. The adjusted

sampling weight for the responding adult-child pair data was

$$w_k = w^k \cdot AF_q, \forall k \in q \quad (1.4)$$

where w^k was defined in (1.1), AF_q was defined in (1.3), and w_k was the nonresponse-adjusted pair weight for pair k .

Trimming Extreme Pair-level Sampling Weights

Excessively large sampling weights are related to increased variance estimates for weighted statistical analyses (9–11). To reduce large variation in the final sampling weights, the nonresponse-adjusted pair weights derived from (1.4) were trimmed at the 99th quantile (denoted as w^{99th}) of the nonresponse-adjusted sampling weights, that is, sampling weights w_k greater than w^{99th} were set as w^{99th} . Then the trimmed sampling weights were readjusted by an adjustment factor defined as,

Adjustment factor after trimming (AF_T) =

$$\frac{\sum_{RA,RC} w_k}{\sum_{RA,RC} I(w_k < w^{99th})w_k + \sum_{RA,RC} I(w_k \geq w^{99th})w^{99th}}, \quad (1.5)$$

where $I()$ was an indicator variable that equaled 1 if the event inside the parentheses was true, and 0 otherwise. The final pair-level sampling weight was

$$w_{k,final} = [I_k(w_k < w^{99th}) \cdot w_k + I_k(w_k \geq w^{99th}) \cdot w^{99th}] \cdot AF_T, \quad (1.6)$$

where w_k was the nonresponse-adjusted pair weight for pair k defined in (1.4), AF_T was the adjustment factor after trimming the sampling weights at the 99th percentile, and $w_{k,final}$ was the final pair-level sampling weights derived for pair-level analysis.

Statistical Properties of the Adult-Child Pair Weights in the 2019 NHIS

Table A shows selected statistical measures and quantiles of the 2019 NHIS adult-child pair weights developed from the procedures described above. Among the responding adult-child pairs ($n = 8,052$), the mean of the sampling weights was 16,796 [standard deviation (SD) = 12,826] and the median was 13,682. The range of the sampling weights was from 810 to 75,098. The maximal value of the sampling weight was the same as the 99th percentile due to the trimming procedure on the extreme sampling weights (the adjustment was done for all adult-child pairs, so this result differed for mother-child and father-child pairs). Among the mother-child pairs ($n = 4,086$), the mean of the sampling weights was 14,636 (SD = 11,142) and the median was 12,181; among the father-child pairs ($n = 2,728$), the mean of the sampling weights was 17,318 (SD = 11,974) and the median was 14,632.

Table A. Selected moments and quantiles of the adult–child pair weights among all adult–child pairs, mother–child pairs, and father–child pairs: National Health Interview Survey, 2019

Measure	Moment		
	All adult–child pairs	Mother–child pairs	Father–child pairs
Sample size	8,052	4,086	2,728
Mean	16,796	14,636	17,318
Standard deviation	12,826	11,142	11,974

Percent	Quantiles		
	All adult–child pairs	Mother–child pairs	Father–child pairs
100.00 ¹	75,098	75,098	75,098
99.00	75,098	59,217	63,689
95.00	42,022	35,754	40,486
90.00	32,519	27,744	32,519
75.00	21,241	18,851	22,103
50.00 ²	13,682	12,181	14,632
25.00	7,852	7,004	8,599
10.00	5,396	3,956	6,273
5.00	3,515	3,170	4,044
1.00	2,529	2,263	2,823
0.00 ³	810	976	810

¹Maximal value.

²Median value.

³Minimal value.

SOURCE: National Center for Health Statistics, 2019 National Health Interview Survey.

Producing Estimates for Mother–Child and Father–Child Pairs

Mother–child and father–child pairs are a subset of all adult–child pairs, and domain estimation methods can be used to produce estimates separately for mother–child and father–child pairs using the adult–child pair weights (5–7). To produce estimates for subpopulations using sample survey data, the survey design feature needs to be incorporated for valid design-based variance estimation (12,13). As a result, even if the analysis concentrates on a particular domain, such as the mother–child domain, data from all dyadic pairs are needed for valid variance estimation. Subsetting the data (for example, removing nonmother–child pair data from the mother–child domain analysis) generally underestimates the variances.

Let U represent the population of adult–child pairs among all households with adult(s) and child(ren). To conduct a mother–child or father–child pair-level analysis, U is partitioned into the relevant domains. Let U_1 represent the mother–child pair domain, U_2 represent the father–child pair domain, and U_3 represent the nonparent–child pair domain, and let z be a variable such that

$z_k = 1$ if pair k is a mother–child pair (U_1),

$z_k = 2$ if pair k is a father–child pair (U_2),

$z_k = 3$ if pair k is a nonparent–child pair (U_3).

Let g_k be any pair-level measurement for pair k ; for example, let g_k be the reported health status (NHIS variable *PHSTAT*, 1 = excellent, 2 = very good, 3 = good, 4 = fair, and 5 = poor) of the Sample Adult and the Sample Child in a household, where $g_k = 1$ if both were in good to excellent health; $g_k = 0$ if not. Using the mother–child domain as an example, if data for all mother–child pairs in the population

are available, then the mother–child domain total, the total number of mother–child pairs in the population with both mother and child in good to excellent health is

$$t_{U_1} = \sum_{U_1} g_k = \sum_U g_k I(z_k = 1). \quad (2.1)$$

From the 2019 NHIS Sample Adult and Sample Child data, the estimated total number of mother–child pairs with both mother and child in good to excellent health is

$$\hat{t}_{U_1} = \sum_{k=1}^{n_{s,AC}} w_{k,final} g_k I(z_k = 1), \quad (2.2)$$

where $n_{s,AC}$ is the number of adult–child pairs in the sample with completed Sample Adult and Sample Child interviews, $w_{k,final}$ is pair k 's final sampling weight, and $I()$ is an indicator variable that equals 1 if the event inside the parentheses is true, and 0 otherwise.

Other mother–child or father–child level analyses follow the same procedure, applying domain estimation with the sampling weights of adult–child pairs.

Examples of Statistical Analyses of the 2019 NHIS Pair Data

This section contains four examples of statistical analyses applied to the 2019 NHIS pair data using the adult–child pair weights and domain estimation methods: A univariate statistical analysis on reported health status of mother–child and father–child pairs and three multivariable logistic regression models with pair-level or individual-level reported health status as the outcome variables, respectively. All statistical analyses in this report were conducted using the survey procedures in SAS version 9.4 (14), and the code used to produce the examples is included in Appendix I of this report. Other software packages, such as R, can also be used to analyze the NHIS parent-pair data. For

example, the subset function from the survey package in R can be used with survey functions such as svymean and svyglm for domain estimation of the NHIS parent-pair data (15,16). The complex survey features (strata, primary sampling unit, and adult-child sample weights) were incorporated into the variance estimation for all analyses in this report.

Example 1. Univariate Statistical Analysis of a Joint Outcome Created Between Parent and Child

A composite adult-child pair health status variable (denoted as *HEALTH_COMPOSITE*) was created with two levels, as follows,

HEALTH_COMPOSITE = 1 if both members of a pair were in good to excellent health (defined as *PHSTAT* = 1, 2, 3 for both the Sample Adult and Sample Child);

HEALTH_COMPOSITE = 0 if at least one member of a pair was in poor or fair health (*PHSTAT* = 4, 5 for at least one member).

When domain estimation methods are used, any recodes need to be conducted for the entire adult-child pair file. The weighted percentage of both members in good to excellent health (that is, *HEALTH_COMPOSITE* = 1) was calculated using the SAS

surveyfreq procedure. Multiway tables were used to conduct domain analysis, that is, including the domain variable(s) (for example, variable *z*, with *z* = 1 denoted a mother-child pair, 2 a father-child pair, and 3 otherwise) before the analytical variable(s) (for example, *HEALTH_COMPOSITE*). The sample SAS code is in Appendix I. Percentage and 95% confidence interval (95% CI) estimates for the mother-child and father-child domains are shown in Table B. The percentage estimates meet NCHS data presentation standards for proportions (17). Among the mother-child and father-child pairs, 89.1% [95% CI = (87.7%, 90.5%)] and 90.0% [95% CI = (88.5%, 91.5%)] were in good to excellent health for both members of a pair, respectively.

Example 2. A Logistic Regression Model With the Composite Pair-level Health Status as the Dependent Variable and Selected Covariates as Predictors

This section shows an example of a logistic regression model for mother-child pairs using the pair-level measurement as the dependent variable. In particular, the composite adult-child pair-level health status derived in Example 1 was the dependent variable, and the predictors (NHIS variable name) included census region (*REGION*), 2013 NCHS urban-rural classification (*URBRRL*) (18), adult's age (in years; *AGEP_A*), race and ethnicity (*HISPALLP_R_A*) and education (*EDUC_R_A*), and child's age (in years; *AGEP_C*) and sex (*SEX_C*). The example is for illustration purposes and may not be the optimal model to study the associations of the outcome and the covariates. The model was in the following form:

$$\text{logit}(P(\text{HEALTH_COMPOSITE} = 1)) = \beta_0 + \beta_1 \text{REGION} + \beta_2 \text{URBRRL} + \beta_3 \text{AGEP_A} + \beta_4 \text{HISPALLP_R_A} + \beta_5 \text{EDUC_R_A} + \beta_6 \text{AGEP_C} + \beta_7 \text{SEX_C},$$

where β_0 was the intercept and $\beta_1 - \beta_7$ were each either a scalar [that is, when the covariate was a continuous variable (*AGEP_A*, *AGEP_C*) or a categorical variable with two categories] or a vector (that is, when the covariate was a categorical variable with more than two categories) of coefficients of the covariates. The SAS surveylogistic procedure was used to fit the model, and the domain statement was used for domain analysis for mother-child pairs. The sample SAS code (Example 2) is shown in Appendix I, and the results of the mother-child pairs are in Table C.

Odds ratios (ORs) demonstrated significant associations between mother-child pair-level health status and most 2013 NCHS urban-rural classification categories, as well as mothers' age, race and ethnicity, and education. That is, both members

Table B. Unweighted sample size, weighted frequency, weighted percent distributions with standard errors, and 95% confidence interval estimates of mother-child and father-child pairs' health status using domain estimation in Example 1: National Health Interview Survey, 2019

Domain and adult-child pair's composite health status	Unweighted sample size ¹	Weighted frequency	Percent ²	Standard error	95% confidence interval
Father-Child pairs					
Both in good to excellent health.	2,464	42,524,330	90.0	0.8	(88.5, 91.5)
At least one not in good health.	263	4,716,691	10.0	0.8	(8.5, 11.5)
Mother-Child pairs					
Both in good to excellent health.	3,622	53,204,288	89.1	0.7	(87.7, 90.5)
At least one not in good health.	457	6,520,731	10.9	0.7	(9.5, 12.3)

¹One father-child pair and seven mother-child pairs were excluded from the analyses due to missing data in composite health status.

²Percentage estimates meet the National Center for Health Statistics data presentation standards for proportions.

NOTES: For father-child and mother-child pairs, Both in good to excellent health is defined as health status is excellent, very good, or good for both the Sample Adult and Sample Child; At least one not in good health is defined as health status is fair or poor for at least one member of the Sample Adult-Sample Child pair.

SOURCE: National Center for Health Statistics, 2019 National Health Interview Survey.

Table C. Odds ratio and 95% confidence interval estimates of the logistic regression model in Example 2 predicting adult–child pair-level composite health status given selected characteristics with results for mother–child pairs: National Health Interview Survey, 2019

Characteristic, (variable name), and category	Mother–Child pairs	
	Odds ratio	95% confidence interval
Age of mother (<i>AGEP_A</i>)	0.98	0.96 1.00
Age of child (<i>AGEP_C</i>)	0.97	0.94 1.00
Census region (<i>REGION</i>)		
Northeast	0.70	0.42 1.18
Midwest	0.94	0.58 1.52
South	0.79	0.52 1.18
West	Ref	
2013 NCHS Urban–Rural Classification (<i>URBRRL</i>)		
Large central metropolitan ³	1.44	0.91 2.27
Large fringe metropolitan ⁴	2.25	1.42 3.56
Medium or small metropolitan ⁵	1.57	1.04 2.38
Nonmetropolitan ⁶	Ref	
Sex of child (<i>SEX_C</i>)		
Male	1.08	0.84 1.39
Female	Ref	
Race and ethnicity of mother (<i>HISPALLP_R_A</i>)		
Black, non-Hispanic	Ref	
White, non-Hispanic	1.65	1.14 2.39
Other, non-Hispanic ⁷	1.57	0.88 2.81
Hispanic ⁸	1.11	0.73 1.67
Education of mother (<i>EDUC_R_A</i>)		
High school or less	0.20	0.14 0.30
Some college (including associate's degree)	0.29	0.21 0.42
Bachelor's degree and above	Ref	

... Category not applicable.

¹Rounded to 1.00 from 0.998.

²Rounded to 1.00 from 1.001.

³Counties in metropolitan statistical areas (MSAs) of 1 million or more population that contain the entire population of the largest principal city of the MSA, have their entire population contained in the largest principal city of the MSA, or contain at least 250,000 inhabitants of any principal city of the MSA.

⁴Counties in MSAs of 1 million or more population that did not qualify as large central metropolitan counties.

⁵Counties in MSAs of populations of 250,000 to 999,999 and counties in MSAs of populations less than 250,000.

⁶Counties in micropolitan statistical areas and nonmetropolitan counties that did not qualify as micropolitan.

⁷Includes other non-Hispanic people not shown separately due to smaller groups not being statistically reliable.

⁸People of Hispanic origin may be of any race.

NOTE: Ref is the reference group.

SOURCE: National Center for Health Statistics, 2019 National Health Interview Survey.

of the mother–child pair were more likely to have good to excellent health when the mother was younger [OR = 0.98, 95% CI = (0.96, 1.00)], the mother was White, non-Hispanic [OR = 1.65, 95% CI = (1.14, 2.39)], and the household was in a small, medium, or large fringe metropolitan area [OR = 1.57, 95% CI = (1.04, 2.38), and OR = 2.25, 95% CI = (1.42, 3.56), respectively], whereas both pair members were less likely to have good to excellent health when the mother had some college or a high school degree or less [OR = 0.29, 95% CI = (0.21, 0.42), and OR = 0.20, 95% CI = (0.14, 0.30), respectively].

Example 3. A Repeated Measurement Model With the Individual-level Health Status as the Outcome Variable and Selected Covariates as Predictors

The logistic regression model in Example 2 used a composite dyadic-level health status as the response variable. Using the composite measurement from a dyad as the unit of analysis has a few limitations. First, it only includes dyads in which both members have no missing values for the outcome variable. Second, it studies the associations of the covariates and the composite dyadic-level response, but it does not examine the associations of the covariates and the individual-level response for each member of the dyad.

This section shows an example of a logistic regression with the individual-level measurement as the response variable, that is, data from the Sample Adult and Sample Child were not used to create a composite measurement. Instead, they were included in the analysis as two separate observations for a household (that is, each household had two rows of data, one for the Sample Adult and one for the Sample Child). Let *HEALTH_SELF* be a sample person's health status (Sample Adult or Sample Child), where

HEALTH_SELF = 1 if a sample person was in good to excellent health (*PHSTAT* = 1, 2, 3);

HEALTH_SELF = 0, otherwise (*PHSTAT* = 4, 5).

A logistic regression model was fit with *HEALTH_SELF* as the response variable, and the following predictors: Census region (*REGION*), 2013 NCHS urban–rural classification (*URBRRL*), sample person's age (in years; *AGEP*), race and ethnicity (*HISPALLP_R*), Sample Adult's education (*EDUC_R_A*), and an indicator variable to indicate if a person was an adult or a child [that is, *I(ADULT)* = 1 if the person was an adult, and 0 otherwise]. In addition, to study the association of the health status of a

person (*HEALTH_SELF*) with the health status of the other dyadic member, the health status of the other dyadic member was included as a covariate (denoted as *HEALTH_OTHER*). The overall logistic regression model can be written as:

$$\begin{aligned} \text{logit}(P(\text{HEALTH_SELF} = 1)) \\ = \beta_0 + \beta_1 \text{REGION} \\ + \beta_2 \text{URBRRL} + \beta_3 \text{AGEP} \\ + \beta_4 \text{HISPALLP_R} \\ + \beta_5 \text{EDUC_R_A} \\ + \beta_6 I(\text{ADULT}) \\ + \beta_7 \text{HEALTH_OTHER}. \end{aligned}$$

Because two observations were included for each household, the model was a repeated measurement model. For each household the model was the following,

$$\begin{aligned} \begin{bmatrix} \text{logit}(P(\text{HEALTH_A} = 1)) \\ \text{logit}(P(\text{HEALTH_C} = 1)) \end{bmatrix} \\ = \beta_0 \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \beta_1 \begin{bmatrix} \text{REGION} \\ \text{REGION} \end{bmatrix} \\ + \beta_2 \begin{bmatrix} \text{URBRRL} \\ \text{URBRRL} \end{bmatrix} + \beta_3 \begin{bmatrix} \text{AGEP_A} \\ \text{AGEP_C} \end{bmatrix} \\ + \beta_4 \begin{bmatrix} \text{HISPALLP_R_A} \\ \text{HISPALLP_R_C} \end{bmatrix} \\ + \beta_5 \begin{bmatrix} \text{EDUC_R_A} \\ \text{EDUC_R_A} \end{bmatrix} + \beta_6 \begin{bmatrix} 1 \\ 0 \end{bmatrix} \\ + \beta_7 \begin{bmatrix} \text{HEALTH_C} \\ \text{HEALTH_A} \end{bmatrix}, \end{aligned}$$

where *_A* and *_C* represented the Sample Adult and Sample Child, respectively (for example, *HEALTH_A* was the Sample Adult's health status); β_0 was the intercept, and $\beta_1 - \beta_7$ were each either a scalar [that is, when the covariate was a continuous variable (*AGEP_A*, *AGEP_C*) or a categorical variable with two categories] or a vector (that is, when the covariate was a categorical variable with more than two categories) of coefficients of the covariates. The model was fit using the SAS surveylogistic procedure. The Example 3 SAS code is shown in Appendix I, and the results of the mother-child pair domain analysis are shown in Table D.

Like the results of Example 2, ORs were significant between individual-level health status (*HEALTH_SELF*) and most urban-rural categories, age, race and ethnicity, and mothers' education. In addition, a positive association was also observed between a person's health status and the health status of the other dyadic member [OR = 3.51, 95% CI = (2.04, 6.02)]; and mothers were less likely to report good to excellent health than their children [that is, OR = 0.51, 95% CI = (0.29, 0.91) for the adult indicator variable].

Table D. Odds ratio and 95% confidence interval estimates of the repeated measurement model in Example 3 predicting individual-level health status given selected characteristics with results for mother-child pairs: National Health Interview Survey, 2019

Characteristic, (variable name), and category	Mother-Child pairs		
	Odds ratio	95% confidence interval	
Age (<i>AGEP</i>)	0.97	0.95	0.98
Health status of the other dyadic member (<i>HEALTH_OTHER</i>)			
Excellent, very good, or good	3.51	2.04	6.02
Fair or poor	Ref	...	...
Census region (<i>REGION</i>)			
Northeast	0.75	0.48	1.18
Midwest	0.98	0.65	1.47
South	0.78	0.55	1.12
West	Ref	...	...
2013 NCHS Urban-Rural Classification (<i>URBRRL</i>)			
Large central metropolitan ¹	1.41	0.97	2.07
Large fringe metropolitan ²	2.05	1.38	3.05
Medium or small metropolitan ³	1.53	1.07	2.17
Nonmetropolitan ⁴	Ref	...	...
Race and ethnicity (<i>HISPALLP_R</i>)			
Black, non-Hispanic	Ref	...	...
White, non-Hispanic	1.48	1.06	2.05
Other, non-Hispanic ⁵	1.52	0.92	2.50
Hispanic ⁶	1.09	0.77	1.54
Education of mother (<i>EDUC_R_A</i>)			
High school or less	0.22	0.15	0.31
Some college (including associate's degree)	0.30	0.22	0.43
Bachelor's degree and above	Ref	...	...
Adult indicator (<i>ADULT_ID</i>)			
Mother	0.51	0.29	0.91
Child	Ref	...	...

... Category not applicable.

¹Counties in metropolitan statistical areas (MSAs) of 1 million or more population that contain the entire population of the largest principal city of the MSA, have their entire population contained in the largest principal city of the MSA, or contain at least 250,000 inhabitants of any principal city of the MSA.

²Counties in MSAs of 1 million or more population that did not qualify as large central metropolitan counties.

³Counties in MSAs of populations of 250,000 to 999,999 and counties in MSAs of populations less than 250,000.

⁴Counties in micropolitan statistical areas and nonmetropolitan counties that did not qualify as micropolitan.

⁵Includes other non-Hispanic people not shown separately due to smaller groups not being statistically reliable.

⁶People of Hispanic origin may be of any race.

NOTE: Ref is the reference group.

SOURCE: National Center for Health Statistics, 2019 National Health Interview Survey.

Example 4. A Logistic Regression Model With the Sample Child's Measurement as the Outcome Variable and Selected Maternal Measurements as Predictors

The logistic regression models described in Examples 2 and 3 used measurements from both dyad members as the outcome of interest. The composite dyadic-level measurement was the outcome variable in Example 2, and the individual-level measurements from both dyad members were used as repeated measurements in Example 3. This section uses the measurement from one dyadic member as the outcome variable. In particular, the child's health status was the outcome variable, and the association of the child's health status with the mother's health status was studied. A health status variable of the Sample Child (denoted as *HEALTH_C*) was created, as follows,

HEALTH_C = 1 if the Sample Child was in good to excellent health
(*PHSTAT* = 1, 2, 3);

HEALTH_C = 0 if the Sample Child was in poor or fair health
(*PHSTAT* = 4, 5).

The Sample Adult's health status (denoted as *HEALTH_A*) was defined in the same way. A logistic regression model was fit with *HEALTH_C* as the response variable and following predictors were included in the model: Census region (*REGION*), 2013 NCHS urban–rural classification (*URBRRL*), Sample Child's age (in years; *AGEP_C*), sex (*SEX_C*) and race and ethnicity (*HISPALLP_R_C*), the Sample Adult's education (*EDUC_R_A*), and health status (*HEALTH_A*). The model was

$$\text{logit} \left(P(\text{HEALTH_C} = 1) \right) = \beta_0 + \beta_1 \text{REGION} + \beta_2 \text{URBRRL} + \beta_3 \text{AGEP_C} \\ + \beta_4 \text{HISPALLP_R_C} + \beta_5 \text{SEX_C} + \beta_6 \text{EDUC_R_A} + \beta_7 \text{HEALTH_A},$$

where β_0 was the intercept and $\beta_1 - \beta_7$ were each either a scalar [that is, when the covariate was a continuous variable (*AGEP_C*) or a categorical variable with two categories] or a vector (that is, when the covariate was a categorical variable with more than two categories) of coefficients of the covariates. The model was fit using the SAS surveylogistic procedure. The Example 4 SAS code is shown in Appendix I, and the results of the mother–child pair domain analysis are shown in Table E.

ORs were significant between the child's health status (*HEALTH_C*) and the mother's health status (*HEALTH_A*), the mother's education, and the child's sex. The child was more likely to have good to excellent health [OR = 4.07, 95% CI = (2.31, 7.17)], and less likely if the mother had a high school degree or less [OR = 0.47, 95% CI = (0.25, 0.87)] and if the child was male [OR = 0.46, 95% CI = (0.28, 0.75)].

Discussion

This report provides details of the methodology for creating sampling weights for adult–child pairs in the 2019 NHIS and guidance on how to use and access these weights. This report also provides examples of how mother–child or father–child pair data can be analyzed. The availability of these weights creates new research opportunities with NHIS data, which contain rich information on mother–child or father–child pairs' health status, health behaviors, and healthcare access and use. Dyad weights starting with the 2019 NHIS will be available on the NCHS website. Each year's dyad weights will be in a file that includes a household ID (*HHX*, for linking to Sample Adult and Sample Child data) and the pair weights (*final_pair_weight*). After linking the pair weights to Sample Adult and Sample Child data sets using *HHX*, users can derive mother–child, father–child, and nonparent–child pairs using variables *SAPARENTSC_A* (Sample Adult relationship to Sample Child)

and *SEX_A*. These two variables are available in the Sample Adult public-use data files. The SAS code associated with Example 1 demonstrates how to prepare a file for analysis.

The adult–child pair weights incorporate the sampling probability at each level and are adjusted for nonresponse. However, calibration (that is, raking or poststratification) to external control totals was not used in the creation of these weights. Calibration has been used in sample surveys to adjust for the differences between the sample and the population (19,20). Proper use of additional information for poststratification may yield more efficient estimators if the sample proportions are quite different from the population proportions (21). Unfortunately, no reliable independent estimates for adult–child pairs in the United States exist, so calibration to independent external estimates was not conducted.

The pair weights described in this report are developed for parent–child pair-level statistical analyses. This method is expected to be used for NHIS data files (2019 and forward), and this document will continue to serve as a reference. Households (with children) that completed only the Sample Adult interview ($n = 701$, 6.8%) or completed only the Sample Child interview ($n = 1,141$, 11.0%) are treated as nonresponse among the eligible households in terms of pair-level analyses. The pair weights should not be used if the statistical analyses focus exclusively on all Sample Adults (or all Sample Children); instead, the Sample Adult (or Sample Child) sampling weights developed by NCHS should be used for the corresponding analyses. For example, Sample Child sampling weights should be used for an analysis of a health outcome for children using data from all Sample Children (that is, including those whose families did not complete a Sample Adult interview). Although the Sample Adult (and Sample Child) sampling weights are correlated with the pair weights, pair-level statistical analyses should use the pair-level sampling

Table E. Odds ratio and 95% confidence interval estimates of the logistic regression model in Example 4 predicting the child's health status given selected characteristics with results for mother-child pairs: National Health Interview Survey, 2019

Characteristic, (variable name), and category	Mother-Child pairs		
	Odds ratio	95% confidence interval	
Child's age (<i>AGEP_C</i>)	0.97	0.92	1.01
Census region (<i>REGION</i>)			
Northeast	1.29	0.57	2.89
Midwest	0.69	0.30	1.59
South	0.58	0.32	1.04
West	Ref	...	...
2013 NCHS Urban-Rural Classification (<i>URBRL</i>)			
Large central metropolitan ¹	0.89	0.44	1.81
Large fringe metropolitan ²	1.18	0.56	2.49
Medium or small metropolitan ³	1.02	0.52	1.99
Nonmetropolitan ⁴	Ref	...	...
Child's sex (<i>SEX_C</i>)			
Male	0.46	0.28	0.75
Female	Ref	...	...
Child's race and ethnicity (<i>HISPALLP_R_C</i>)			
Black, non-Hispanic	Ref	...	...
White, non-Hispanic	1.19	0.54	2.64
Other, non-Hispanic ⁵	1.76	0.65	4.79
Hispanic ⁶	0.63	0.29	1.38
Mother's education (<i>EDUC_R_A</i>)			
High school or less	0.47	0.25	0.87
Some college (including associate's degree)	0.62	0.33	1.16
Bachelor's degree and above	Ref	...	...
Mother's health status (<i>HEALTH_A</i>)			
Excellent, very good, or good	4.07	2.31	7.17
Fair or poor	Ref	...	...

... Category not applicable.

¹Counties in metropolitan statistical areas (MSAs) of 1 million or more population that contain the entire population of the largest principal city of the MSA, have their entire population contained in the largest principal city of the MSA, or contain at least 250,000 inhabitants of any principal city of the MSA.

²Counties in MSAs of 1 million or more population that did not qualify as large central metropolitan counties.

³Counties in MSAs of populations of 250,000 to 999,999 and counties in MSAs of populations less than 250,000.

⁴Counties in micropolitan statistical areas and nonmetropolitan counties that did not qualify as micropolitan.

⁵Includes other non-Hispanic people not shown separately due to smaller groups not being statistically reliable.

⁶People of Hispanic origin may be of any race.

NOTE: Ref is the reference group.

SOURCE: National Center for Health Statistics, 2019 National Health Interview Survey.

weights, as they incorporate the sampling probabilities of both the Sample Adult and the Sample Child and are adjusted for pair-level nonresponse. Using Sample Adult weights or Sample Child weights for pair-level statistical analysis may lead to biased results. Appendix II compares mean estimates using the pair weights and the Sample Adult weights under a simplified scenario. Factors found to be related to the differences in the mean estimates using the two sampling weights included the distribution of the outcome of interest, the number of children across households, and the sampling weights of Sample Adults.

Three logistic regression models were applied to the 2019 NHIS dyadic data, which use the dyadic-level or the individual-level measurement as the response variables, respectively. Other statistical models, such as structural equation modeling (22) and multilevel modeling (23,24), may also be applied to the NHIS parent-child data. In practice, different estimation methods can be used for different research goals; and more research is needed to explore how to use the pair data from NHIS (2019 and forward). Design-based variance estimation was used for the repeated measurement model in this report, which incorporates the survey design features (strata, PSU, and sampling weights) for variance estimation and is expected to yield conservative variance estimates. However, it does not reflect the nested data structure of parent-child pairs within a household. To control for the additional parent-child correlation, alternative statistical methods can be used, for example, random or mixed-effect models, which may incorporate the correlation of the Sample Adult and the Sample Child within a household. In addition, resampling methods such as Jackknife and Bootstrap methods may also be used for variance estimation of the dyadic data.

Although traditional household surveys usually focus on the household-level and the individual-level measurements, dyadic data in national household surveys are not uncommon. The National Survey of Drug Use and Health, conducted by the Substance Abuse and Mental Health Services Administration, collects detailed information on tobacco, alcohol, and drug use, as well as mental health-related issues in the United States (25). Zero, one, or two people are selected within a household, and the sampling weights for the selected pairs have been developed. NHIS selects a Sample Adult and a Sample Child (when applicable) independently within a family or a household. Because the sampling weights for the selected pairs are the inverse of the pairs' selection probabilities, the adult-child pair

weights for the 2019 NHIS can be derived, and then domain estimation can be used for inferences on mother–child and father–child pairs. The methods used to produce NHIS pair weights can easily be adapted to other surveys with similar sampling designs in which one or more people within a family have been sampled independently of their specified relationships. Dyadic data in national surveys provide new research opportunities to study the interdependence of social behaviors and health status among members within families or households.

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Appendix I. SAS Code for the Examples in the Report

Example 1 SAS Code

```
libname w "directory of the folder where the pair weights file is saved";

libname public "directory of the folder where the Sample Adult and Sample Child data
is saved";

*****

*Prepare pair weights data          *
*****;

data final_weight;
set    w.final_pair_weight2019;
eligible_familyID=1;
Keep HHX final_pair_weight eligible_familyID;
run;

proc sort data= final_weight;
by HHX ;
run;

*****

*Prepare Sample Adult and Sample Child data*
*****;

data adult;
set public.adult19 ;
format _all_;
HISPALLP_R_A=.;
if HISPALLP_A=1 then HISPALLP_R_A=1;      /*Hispanic*/
else if HISPALLP_A=2 then HISPALLP_R_A=2; /*White, non-Hispanic*/
else if HISPALLP_A=3 then HISPALLP_R_A=3; /*Black, non-Hispanic*/
else HISPALLP_R_A=4;                      /*other, non-Hispanic */
```

```

if 0<=EDUC_A <=4 then EDUC_R_A =1 ;      /* high school or less*/
else if 5<=EDUC_A <=7 then EDUC_R_A =2 ; /* some college*/
else if 8<=EDUC_A <=11 then EDUC_R_A =3 ; /*Bachelors degree or higher*/
else EDUC_R_A =.;

keep

HHX                PSTRAT                PPSU
SAPARENTSC_A       AGEP_A                SEX_A
HISPALLP_R_A       EDUC_R_A              PHSTAT_A
REGION              URBRL;

run;

proc sort data=adult;
by HHX;
run;

data child;
set public.child19 ;
format _all_;
if SEX_C in ( 1 2) then SEX_C=SEX_C; else SEX_C=.;
keep
HHX  AGEP_C  SEX_C  HISPALLP_C  PHSTAT_C;
run;

proc sort data=child;
by HHX;
run;

data all1;
merge final_weight  adult  child;
by HHX ;

if eligible_familyID=1;

```

```

if SAPARENTSC_A=1 then parent_child=1;
else parent_child=0;

if parent_child=1 then do;
    if SEX_A=1 then z= 2;          /*father-child*/
    else if SEX_A=2 then z= 1 ; /*mother-child*/
end;

if parent_child=0 then z= 3;      /*non-parent-child*/

if PHSTAT_A in (7 9 )then PHSTAT_A=.;
if PHSTAT_C in (7 9 )then PHSTAT_C=.;

if PHSTAT_A ^=. and PHSTAT_C ^=. then do;
if PHSTAT_A in (1 2 3 ) and PHSTAT_C in (1 2 3 ) then HEALTH_COMPOSITE ='Both mem-
bers of dyad in at least good health';
else HEALTH_COMPOSITE ='at least one member has fair, poor health';
end;

run;

*****
*Table B: Freq of health status *
*****;

title "Table B. Health status of the pair";
proc surveyfreq data=all1 ;
stratum PSTRAT ;
cluster PPSU ;
weight final_pair_weight;
table z*HEALTH_COMPOSITE/row CL NOCELLPERCENT ;
run;

*****

```

```

*NOTE:
*Definition of the variables:
*z: 1 = mother-child pairs, 2 = father-child pairs, 3=non-parent-child pairs*
*HEALTH_COMPOSITE: composite adult-child pair health status variable.
*final_pair_weight: adult-child pair weight.
*PSTRAT : strata variable.
*PPSU : PSU variable.
*
>Data structure: one row each pair
*****;

```

Example 2 SAS Code

```

*****
*Refer to Example 1 SAS code for Data preparation procedure *
*****;

title "The logistic regression model with the composite pair level health status as
the response variable";

proc surveylogistic data=all1;
stratum PSTRAT ;
cluster PPSU ;
weight final_pair_weight;
class REGION URBRL SEX_C HISPALLP_R_A (ref='3') EDUC_R_A ;
model HEALTH_COMPOSITE = REGION URBRL AGEPA AGEPC SEX_C HISPALLP_R_A
EDUC_R_A ;
domain z;
run;

*****
*Definition of the variables:
*HEALTH_COMPOSITE: composite adult-child pair health status variable.
*REGION: region.
*URBRL: 2013 NCHS Urban-Rural Classification.
*AGEPA: age of Sample Adult.
*AGEPC: age of Sample Child.
*SEX_C: sex of Sample Child.

```

```

*HISPALLP_R_A: race/ethnicity of Sample Adult.
*EDUC_R_A: education of Sample Adult.
*z: 1 = mother-child pairs, 2 = father-child pairs, 3=non-parent-child pairs*
*PSTRAT : strata variable.
*PPSU : PSU variable.
*final_pair_weight: adult-child pair weight.
*
*Data structure: one row each pair
*****;

```

Example 3 SAS Code

```

*****

*Prepare pair weights data
*****;

data final_weight;
set w.final_pair_weight2019;
eligible_familyID=1;
Keep HHX final_pair_weight eligible_familyID;
run;

proc sort data= final_weight;
by HHX ;
run;

*****

*Prepare Sample Adult and Sample Child data*
*****;

data adult;
set public.adult19 ;

format _all_;

if SAPARENTSC_A=1 then parent_child=1;
else parent_child=0;

```

```

if parent_child=1 then do;
    if SEX_A=1 then z= 2;          /*father-child*/
    else if SEX_A=2 then z= 1 ; /*mother-child*/
end;
if parent_child=0 then z= 3;      /*non-parent-child */

AGEP =AGEP_A ;
SEX =SEX_A;

HISPALLP_R=.;
if HISPALLP_A=1 then HISPALLP_R=1;      /*Hispanic*/
else if HISPALLP_A=2 then HISPALLP_R=2; /*White, non-Hispanic*/
else if HISPALLP_A=3 then HISPALLP_R=3; /*Black, non-Hispanic*/
else HISPALLP_R=4;                      /*other, non-Hispanic*/

if 0<=EDUC_A <=4 then EDUC_R_A =1 ;      /* high school or less*/
else if 5<=EDUC_A <=7 then EDUC_R_A =2 ; /* some college*/
else if 8<=EDUC_A <=11 then EDUC_R_A =3 ;/*Bachelors degree or higher*/
else EDUC_R_A =.;

if PHSTAT_A in (7 9 )then PHSTAT_A=.;
else if PHSTAT_A in (1 2 3 ) then HEALTH_SELF =1 ;/*at least good*/
else if PHSTAT_A in (4 5 ) then HEALTH_SELF=0 ; /*fair or poor*/

ADULT_ID=1; /*adult indicator*/

keep

HHX          PSTRAT          PPSU
REGION       URBRL          AGEP
SEX          HISPALLP_R      EDUC_R_A
HEALTH_SELF ADULT_ID        z
;
run;

```



```

proc sort data=adult;
by HHX;
run;

data child;
set public.child19 ;

format _all_;

AGEP =AGEP_C;
if SEX_C in ( 1 2) then SEX=SEX_C; else SEX=.;

HISPALLP_R=.;
if HISPALLP_C=1 then HISPALLP_R=1;          /*Hispanic*/
else if HISPALLP_C=2 then HISPALLP_R=2; /*White, non-Hispanic*/
else if HISPALLP_C=3 then HISPALLP_R=3; /*Black, non-Hispanic*/
else HISPALLP_R=4;                          /*other, non-Hispanic*/

if PHSTAT_C in (7 9 )then PHSTAT_C=.;
else if PHSTAT_C in (1 2 3 ) then HEALTH_SELF=1 /* at least good*/
else if PHSTAT_C in (4 5 ) then HEALTH_SELF=0 ; /* fair or poor */

ADULT_ID=0; /*child indicator*/

keep
HHX AGEP SEX HISPALLP_R HEALTH_SELF ADULT_ID;
run;

proc sort data=child;
by HHX;
run;

data var_for_adult;

```

```

set child;

HEALTH_OTHER=HEALTH_SELF; /*health of the other person (that is, the child)*/
keep HHX HEALTH_OTHER;

run;


data adult1;
merge final_weight adult var_for_adult ;
by HHX ;
if eligible_familyID=1;

run;


data var_for_child;
set adult1;

HEALTH_OTHER= HEALTH_SELF; /*health of the other person(that is, the adult)*/
keep
HHX          PSTRAT          PPSU
final_pair_weight
REGION          URBRL          eligible_familyID
EDUC_R_A      HEALTH_OTHER  z;

run;


data child1;
merge child var_for_child;
by hhx;
if eligible_familyID=1;

run;


data adult_child;
set adult1 child1;

run;


proc sort data=adult_child;
by hhx;

run;

```

```

*****

*Table D: repeated measurement model *
*****;

proc surveylogistic data=adult_child;
strata PSTRAT;
cluster PPSU ;
weight final_pair_weight;
class HISPALLP_R (ref='3') EDUC_R_A REGION URBRL ;
model HEALTH_SELF(descending ) = HEALTH_OTHER AGEP HISPALLP_R EDUC_R_A REGION
URBRL ADULT_ID ;

domain z;

run;

*****

*Definition of the variables: *
*HEALTH_SELF: health status of self. *
*health_other:health status of the other dyadic member *
*REGION: region. *
*URBRL: 2013 NCHS Urban-Rural Classification. *
*AGEP: age of sample person *
*HISPALLP_R: race/ethnicity of sample person. *
*EDUC_R_A: education of Sample Adult. *
*ADULT_ID = 1 if adult and 0 otherwise. *
*z: 1 = mother-child, 2 = father-child,3=non-parent-child pairs*
* *
*Data structure: one row each person, two rows each pair. *
*****;

```

Example 4 SAS Code

```

libname w "directory of the folder where the weights file is saved";

libname public "directory of the folder where the Sample Adult and Sample Child data
is saved";

*****

*Prepare pair weights data *
*****;

```

```

data final_weight;
set w.final_pair_weight2019;
eligible_familyID=1;
Keep HHX final_pair_weight eligible_familyID;
run;

proc sort data= final_weight;
by HHX ;
run;

*****
*Prepare Sample Adult and Sample Child data*
*****;

data adult;
set public.adult19 ;

format _all_;

if SAPARENTSC_A=1 then parent_child=1;
else parent_child=0;

if parent_child=1 then do;
    if SEX_A=1 then z= 2;          /*father-child*/
    else if SEX_A=2 then z= 1 ; /*mother-child*/
end;

if parent_child=0 then z= 3;      /*adult-child*/

if 0<=EDUC_A <=4 then EDUC_R_A =1 ;          /* high school or less*/
else if 5<=EDUC_A <=7 then EDUC_R_A =2 ; /* some college*/
else if 8<=EDUC_A <=11 then EDUC_R_A =3 ;/*Bachelors degree or higher */
else EDUC_R_A =.;

if PHSTAT_A in (7 9 )then HEALTH_A=.;
else if PHSTAT_A in (1 2 3 ) then HEALTH_A =1 ;/*at least good*/

```

```

else if PHSTAT_A in (4 5 ) then HEALTH_A =0 ;    /* fair or poor */

keep

HHX          PSTRAT      PPSU
REGION       URBRL      AGEPA
EDUC_R_A     HEALTH_A    z
;
run;

proc sort data=adult;
by HHX;
run;

data child;
set public.child19 ;
format _all_;

if SEX_C in (1 2) then SEX_C=SEX_C; else SEX_C=.;

HISPALLP_R_C =.;
if HISPALLP_C=1 then HISPALLP_R_C =1;          /*Hispanic*/
else if HISPALLP_C=2 then HISPALLP_R_C =2; /*White, non-Hispanic*/
else if HISPALLP_C=3 then HISPALLP_R_C =3; /*Black, non-Hispanic*/
else HISPALLP_R_C =4;                          /*other, non-Hispanic*/

if PHSTAT_C in (7 9 )then HEALTH_C=.;
else if PHSTAT_C in (1 2 3 ) then HEALTH_C =1 ;/* at least good*/
else if PHSTAT_C in (4 5 ) then HEALTH_C =0 ;    /* fair or poor */
keep HHX AGEPA SEX_C HISPALLP_R_C HEALTH_C;
run;

proc sort data=child;
by HHX;
run;

```

```

data adult_child;
merge adult child final_weight;
by HHX;
if eligible_familyID=1;
run;

*****

*Table E: sample child as the response *
*****;

proc surveylogistic data=adult_child;
strata PSTRAT;
cluster PPSU ;
weight final_pair_weight;
class REGION URBRL HISPALLP_R_C (ref='3') SEX_C EDUC_R_A Health_A (ref='0') ;
model HEALTH_C(descending )= REGION URBRL AGE_C HISPALLP_R_C SEX_C EDUC_R_A
HEALTH_A;
domain z ;
run;

*****

*Definition of the variables: *
*HEALTH_C: health status of Sample Child *
*HEALTH_A: health status of Sample Adult *
*REGION: region *
*URBRL: 2013 NCHS Urban-Rural Classification *
*AGE_C: age of Sample Child *
*SEX_C: Sex of Sample Child *
*HISPALLP_R_C : race/ethnicity of Sample Child *
*EDUC_R_A: education of Sample Adult. *
*z: 1 = mother-child, 2 = father-child, 3=non-parent-child *
* *
*Data structure: one row each Sample Child *
*****;

```

Appendix II. Comparing Mean Estimates Using the Dyad Weights and the Sample Adult Weights

Let h be a household in the NHIS sample, and let W_h be household h 's sampling weight. Let $P_{i|h}$ be adult i 's conditional selection probability, which is the inverse of the number of eligible adults in household h ; let $P_{j|h}$ be child j 's conditional selection probability, which is the inverse of the number of children in household h . Further, assume the pair-level outcome of interest is Y and its value for pair (i, j) in household h is Y_h . To simplify the problem, assume a perfect condition where no nonresponse is observed and no poststratification is needed.

Consider two estimators for the mean of Y . The first one, denoted as $\bar{Y}_{DW}$, using the dyadic weights, can be expressed as

$$\bar{Y}_{DW} = \frac{\sum_h (W_h / P_{i|h} / P_{j|h}) y_h}{\sum_h W_h / P_{i|h} / P_{j|h}} = \frac{\sum_h W A_h C_h y_h}{\sum_h W A_h C_h},$$

where $h = 1, \dots, H$, H is the total number of households, $W A_h$ is the Sample Adult i 's sampling weight, and C_h is the total number of children in household h .

The other estimator, denoted as $\bar{Y}_{AW}$, using the Sample Adult weights, can be expressed as

$$\bar{Y}_{AW} = \frac{\sum_h W A_h y_h}{\sum_h W A_h}.$$

Let Δ be the difference of the two estimators. After some algebra:

$$\Delta = \bar{Y}_{DW} - \bar{Y}_{AW} = \frac{\sum_h \sum_{q, h < q} W A_h W A_q (C_h - C_q) (y_h - y_q)}{\sum_h \sum_q W A_h W A_q C_h}.$$

By examining the above expression, the following can be concluded:

1. In general, $\Delta \neq 0$, and the asymptote of Δ is not zero as $H \rightarrow \infty$.
2. The magnitude of Δ can be largely determined by the distributions of Sample Adult weights ($W A$), the number of children (C) in the household, and the outcome of interest (y).
3. If the number of children across households is homogeneous, that is, $C_h = C_q \forall h$ and q , then $\Delta = 0$,

which means the pair weights and the Sample Adult weights yield the same mean estimate because the two weights are perfectly correlated.

4. If the outcome of interest (y) across households is homogeneous, that is, $y_h = y_q \forall h$ and q , then $\Delta = 0$.
5. If the number of children (C) and the outcome of interest (y) are positively correlated, then Δ tends to be positive; and if C and y are negatively correlated, then Δ tends to be negative; if C and y are independent conditioning on Sample Adult weight, then $\Delta = 0$.

The comparison between analyses using the dyad weights and the Sample Child weights follow the same procedure, as a result it is not shown.

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