# 2014 NATIONAL SURVEY ON DRUG USE AND HEALTH

# METHODOLOGICAL RESOURCE BOOK SECTION 13: STATISTICAL INFERENCE REPORT



Substance Abuse and Mental Health Services Administration
Center for Behavioral Health Statistics and Quality
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# 1. Introduction

Statistical inference occurs whenever data obtained from sample observations belonging to and considered representative of a larger target population are used to make generalizations concerning the larger population. The target population for the 2014 National Survey on Drug Use and Health (NSDUH)[1] was the U.S. civilian, noninstitutionalized population aged 12 or older (at the time of their interview) in 2014. Measurements for this target population were the responses to the survey questions provided by people participating in the 2014 survey. Examples of conducting statistical inference include the use of the weighted estimate and the corresponding standard error of the number of users of illicit drugs based on a sample to make a statement about the number of users in the U.S. civilian noninstitutionalized population. Another example is conducting a significance test to determine whether the percentage of adults with serious mental illness increased over time.

Statistical inferences concerning characteristics of interest for this population and various subpopulations are presented in the form of estimates derived from the sample data collected. Examples of the inferences made from the 2014 NSDUH data are presented in the 2014 detailed tables (Center for Behavioral Health Statistics and Quality [CBHSQ], 2015b) and include estimates of the number of people who were substance users during the past month, past year, and their lifetime, as well as the associated percentages (prevalence rates) of substance use for these reference periods. Inferences also were made for such categories as substance initiation; risk and protective factors; and substance dependence, dependence or abuse, and treatment. Estimates of measures related to mental health problems are presented in the 2014 mental health detailed tables (CBHSQ, 2015c). Starting with the 2014 NSDUH, various measures of interest included in the detailed tables and mental health detailed tables were also presented in four national-level first release reports:[2] the behavioral health trends in the United States report (CBHSQ, 2015a), the suicidal thoughts and behavior among adults report (CBHSQ, 2015h), the receipt of services for behavioral health problems report (CBHSQ, 2015e), and the risk and protective factors and initiation of substance use report (CBHSQ, 2015f). Throughout the remainder of this document, these four reports will be referred to collectively as the first release reports.

The focus of this report is to describe the statistical inference procedures used to produce design-based estimates as presented in the 2014 detailed tables, the 2014 mental health detailed tables, and the 2014 first release reports.[3] The statistical procedures and information found in this report can also be generally applied to analyses based on the public use file as well as the

[1] Before 2002, the survey was called the National Household Survey on Drug Abuse (NHSDA).

[2] These four reports contain varying topics of interest and have replaced the national findings and mental health findings reports that were published in previous years.

[3] Users of the 2014 public use file (CBHSQ/Substance Abuse and Mental Health Services Administration [SAMHSA], 2015) may find inconsistencies in the variable names referenced in this report, Appendix A, the information presented in Table 5.1 in Section 5, and other specific numbers presented in this report (i.e., degrees of freedom). The specific information referenced in this report is based on the restricted-use dataset that was used to create the 2014 detailed tables (CBHSQ, 2015b), the 2014 mental health detailed tables (CBHSQ, 2015c), and the 2014 first release reports (CBHSQ, 2015a, 2015e, 2015f, 2015h).

restricted-use file available through the data portal.[4] This report is organized as follows: Section 2 provides background information concerning the 2014 NSDUH; Section 3 discusses the prevalence rates and how they were calculated, including specifics on topics such as mental illness, major depressive episode, and serious psychological distress; Section 4 briefly discusses how missing item responses of variables that are not imputed may lead to biased estimates; Section 5 discusses sampling errors and how they were calculated; Section 6 describes degrees of freedom and how they were used when comparing estimates; and Section 7 discusses how the statistical significance of differences between estimates was determined. Section 8 discusses confidence interval estimation, and Section 9 describes how past year incidence of drug use was computed. Finally, Section 10 discusses the conditions under which estimates with low precision were suppressed. Appendix A contains examples that demonstrate how to conduct various statistical procedures documented within this report using SAS® and SUDAAN® Software for Statistical Analysis of Correlated Data (RTI International, 2012) along with separate examples using Stata® software (StataCorp, 2015).

[4] NSDUH public use files and the data portal are available from a public data archive website.

# 2. Background

The respondent universe for the National Survey on Drug Use and Health (NSDUH) is the civilian, noninstitutionalized population aged 12 or older residing within the United States. The survey covers residents of households (individuals living in houses/townhouses, apartments, and condominiums; civilians living in housing on military bases, etc.) and individuals in noninstitutional group quarters (e.g., shelters, rooming/boarding houses, college dormitories, migratory workers' camps, halfway houses). Excluded from the survey are individuals with no fixed household address (e.g., homeless and/or transient people not in shelters), active-duty military personnel, and residents of institutional group quarters, such as correctional facilities, nursing homes, mental institutions, and long-term hospitals.

A coordinated design was developed for the 2014 through 2017 NSDUHs. Similar to the 1999 through 2013 surveys, the coordinated 4-year design is state based, with an independent, multistage area probability sample within each state and the District of Columbia. As a result, states are viewed as the first level of stratification and as a variable for reporting estimates. Each state was further stratified into approximately equally populated state sampling regions (SSRs). The number of SSRs varied by state and was related to the state's sample size. SSRs were contiguous geographic areas designed to yield approximately the same number of interviews within a given state.[5] There were a total of 750 SSRs for 2014. Creation of the multistage area probability sample then involved selecting census tracts within each SSR, census block groups within census tracts, and area segments (i.e., a collection of census blocks) within census block groups. Finally, dwelling units (DUs) were selected within segments, and within each selected DU, up to two residents who were at least 12 years old were selected for the interview.

The coordinated design for 2014 through 2017 includes a 50 percent overlap in third-stage units (area segments) within each successive 2-year period from 2014 through 2017. In addition to reducing costs, this designed sample overlap slightly increases the precision of estimates of year-to-year trends because of the expected small but positive correlation resulting from the overlapping area segments between successive survey years. There is no planned overlap of sampled DUs or residents.

The 2014 through 2017 design allocates more interviews to the largest 12 states (compared with the 1999 to 2013 design).[6] For the 2014 NSDUH, the target sample size for the largest 12 states was between 1,500 to 4,500 completed interviews and approximately 960 interviews in the remaining 38 states and the District of Columbia (Center for Behavioral Health Statistics and Quality [CBHSQ], 2015d). Making the sample sizes more proportional to the state population sizes improves the precision of NSDUH estimates. This change also allows for a more cost-efficient sample allocation to the largest states while slightly increasing the sample

[5] Sampling areas were defined using 2010 census geography. Counts of dwelling units and population totals were obtained from the 2010 decennial census data supplemented with revised population projections from Nielsen Claritas (see http://www.nielsen.com/us/en.html).

[6] In the 1999 to 2013 design, the eight largest states each had a target sample size of 3,600. The remaining states and the District of Columbia each had a sample size of 900. In 2014, the sample design was modified so that the sample size per state was relatively more proportional to the state population.

sizes in smaller states to improve the precision of state estimates by either direct methods (by pooling multiple years of data) or using small area estimation (SAE).[7] Population projections based on the 2010 census, data from the 2006 to 2010 American Community Surveys (ACS), and Nielsen Claritas were used to construct the sampling frame for the 2014 through 2017 NSDUHs. In contrast, projections based on the 2000 census were used in constructing the sampling frame for the 2005 to 2013 NSDUHs.

Similar to the 2005 through 2013 NSDUHs, the first stage of selection for the 2014 through 2017 NSDUHs was census tracts.[8] This stage was included to contain sample segments within a single census tract to the extent possible in order to facilitate merging to external data sources such as the ACS or the National Health Interview Survey. Within each SSR, 48 census tracts[9] were selected with probability proportional to a composite measure of size.[10] Within sampled census tracts, adjacent census block groups were combined as necessary to meet the minimum DU size requirements.[11] One census block group or second-stage sampling unit then was selected within each sampled census tract with probability proportional to population size. Compared with the selection process used for the 2005 through 2013 NSDUHs, the selection of census block groups is an additional stage of selection that was included to facilitate possible transitioning to an address-based sampling design in a future survey year. For the third stage of selection, adjacent blocks were combined within each sampled census block group to form area segments.

One area segment was selected within each sampled census block group with probability proportionate to a composite measure of size. Although only 20 segments per SSR were needed to support the coordinated 4-year sample for the 2014 through 2017 NSDUHs, an additional 28 segments per SSR were selected to support any supplemental studies that the Substance Abuse and Mental Health Services Administration may choose to field.[12] Eight sample segments per SSR were fielded during the 2014 survey year. Four of these segments were selected for the 2014 survey only; four were selected for the 2014 survey and will be used again in the 2015 survey. These sampled segments were allocated equally into four separate samples, one for each 3-month period (calendar quarter) during the year. That is, a sample of addresses was selected

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[7] SAE is a hierarchical Bayes modeling technique used to make state-level estimates for 25 measures related to substance use and mental health. For more details, see "2011–2012 NSDUH: Model-Based Prevalence Estimates (50 States and the District of Columbia)" (Tables 1 to 26, by Age Group) at http://www.samhsa.gov/data/.

[8] Census tracts are relatively permanent statistical subdivisions of counties and parishes that provide a stable set of geographic units across decennial census periods.

[9] Some census tracts had to be aggregated in order to meet the minimum DU requirement. In California, Florida, Georgia, Illinois, Michigan, New Jersey, New York, North Carolina, Ohio, Pennsylvania, Texas, and Virginia, this minimum size requirement was 250 DUs in urban areas and 200 DUs in rural areas. In the remaining states and the District of Columbia, the minimum requirement was 150 DUs in urban areas and 100 DUs in rural areas.

[10] The composite measure of size is a weighted population size where the weights are the sampling rates defined for specified age groups.

[11] The minimum DU size requirements for census tracts also were applied to census block groups. The purpose of the minimum DU size is to ensure that each sampled area has a sufficient number of DUs to field two NSDUH samples and one field test.

[12] Eight segments per SSR are needed to field the 2014 through 2017 NSDUHs (8 segments × 4 years = 32 segments per SSR). For the 2015 through 2017 NSDUHs, half of the segments are carried over from the prior year (4 segments × 3 years = 12 segments per SSR). Thus, 20 unique segments per SSR are needed to field the 4-year sample (32 – 12 = 20).

from two segments in each calendar quarter so that field data collection occurred relatively year-round.

Although the overall design remained similar, including the $30 incentive payment for participation, various design elements did change starting with the 2014 NSDUH. The 2014 NSDUH redesign did implement a change in the allocation of sample by age group. In the 2005 through 2013 NSDUHs, the sample was allocated equally between three age groups: 12 to 17, 18 to 25, and 26 or older. Starting in 2014, the allocation of the NSDUH sample is 25 percent for adolescents aged 12 to 17, 25 percent for adults aged 18 to 25, and 50 percent for adults aged 26 or older. The sample of adults aged 26 or older is further divided into three subgroups: aged 26 to 34 (15 percent), aged 35 to 49 (20 percent), and aged 50 or older (15 percent). These age allocation changes were designed to reflect more closely the actual population distributions by state and age group, so that the precision of estimates overall and for older age groups could be improved. The sample redesign is not expected to affect the prevalence estimates of outcome variables, but the nature of the design changes is expected to affect the precision of those estimates. Additionally, changes in the sample design with respect to age group and state necessitated a review of the pair sampling strategy; therefore, the number of pairs selected for the 2014 survey was reduced, but still yielded the same number of completed interviews (Chromy & Penne, 2002). The 2014 NSDUH also included a text-to-speech (TTS) field test that was conducted in late 2014 to test the comprehensibility of TTS on the NSDUH general population. The purpose of this field test was to determine the feasibility of using TTS in the audio computer-assisted self-interviewing portion of the 2015 NSDUH interview.

The final respondent sample of 67,901 people for the 2014 NSDUH provides a sufficient sample to create domain estimates for a broad range of ages and other demographic categories. Individual observations are weighted so that the weighted sample represents the civilian, noninstitutionalized population aged 12 or older for the general U.S. population and for each of the individual states. The person-level weights in NSDUH are calibrated to population estimates (or control totals) obtained from the U.S. Census Bureau. For more information on the person-level sampling weight calibration in the *2014 NSDUH Methodological Resource Book*, see CBHSQ (2016b).

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# 3. Prevalence Rates

The national prevalence rates computed using a multiprocedure package called SUDAAN® Software for Statistical Analysis of Correlated Data (RTI International, 2012). The final, nonresponse-adjusted, and poststratified analysis weights were used in SUDAAN to compute unbiased design-based estimates. Appendix A contains examples that demonstrate how to compute the prevalence rates as defined below using SUDAAN (Exhibit A.1) and Stata® (Exhibit A.2).

Prevalence rates are the proportions of the population who exhibit characteristics of interest (such as substance use). Let $\hat{p}_d$ represent the prevalence rate of interest for domain *d*. Then $\hat{p}_d$ would be defined as the ratio

$$\hat{p}_d = \frac{\hat{Y}_d}{\hat{N}_d},$$

where $\hat{Y}_d = \sum_{i \in S} w_i \delta_i y_i$ represents the estimated number of people exhibiting the characteristic of interest in domain *d*, $\hat{N}_d = \sum_{i \in S} w_i \delta_i$ represents the estimated population total for domain *d*, *S* represents the sample, $w_i$ represents the analysis weight, $\delta_i$ represents an indicator variable that is defined as 1 if the *i*th sample unit is in domain *d* and is equal to 0 otherwise, and $y_i$ represents an indicator variable that is defined as 1 if the *i*th sample unit exhibits the characteristic of interest and is equal to 0 otherwise.

For certain populations of interest, sample sizes may not be adequate to support inferences using only 1 year of survey data. In these cases, estimates were produced from annual averages based on combined data from 2 or more survey years, and they are clearly labeled in the detailed tables. The data were combined for the 2011–2012, 2013–2014, and 2010–2014 surveys to obtain annual averages, and then the prevalence rates were computed in SUDAAN as described above. The annual averages were derived by concatenating the data for the respective years and dividing the analysis weights by a factor that varied depending on the number of years of concatenated data. The weight was divided by a factor of 2 for 2 years of concatenated data and a factor of 4 for 4 years of concatenated data.

Prevalence estimates are presented in the 2014 detailed tables (Center for Behavioral Health Statistics and Quality [CBHSQ], 2015b) and in the 2014 mental health detailed tables (CBHSQ, 2015c) in the form of numbers in thousands and percentages rounded to the nearest tenth of a percent. For percentages, rounding an estimate close to zero to the nearest tenth of a percent, which has not been suppressed per the National Survey on Drug Use and Health (NSDUH) suppression rules (see Section 10), may result in an estimate of 0.0 percent being displayed in a table. Consequently, the corresponding population total presented in thousands may result in a 0 (i.e., 499 or fewer individuals) being displayed in a table. Thus, users are reminded that a percentage of 0.0 or a number in thousands of 0 are not true zeros but are

unsuppressed, nonzero estimates that should not be interpreted as no respondents in the population of interest. If an estimate is a true 0 value, both the percentage and the number in thousands will be suppressed under the NSDUH suppression rule.

## 3.1 Mental Illness

The Substance Abuse and Mental Health Services Administration (SAMHSA) has been publishing estimates of the prevalence of past year serious mental illness (SMI) and any mental illness (AMI) among adults aged 18 or older since the release of the 2008 NSDUH national findings report (Office of Applied Studies, 2009b). Originally, estimates were based on a prediction model for mental illness developed using the 2008 data from the Mental Health Surveillance Study (MHSS), which was embedded in the 2008 NSDUH (referred to as the 2008 World Health Organization Disability Assessment Schedule [WHODAS] model). Each respondent in a subsample of adults (about 1,500 in 2008) who had completed the NSDUH interview was administered the Structured Clinical Interview for DSM-IV-TR Axis I Disorders, Research Version, Non-patient Edition (SCID-I/NP) (First, Spitzer, Gibbon, & Williams, 2002).[13] For more specific information on the MHSS sample design, see the sample design report in the *2013 NSDUH Methodological Resource Book* (CBHSQ, 2014c).

The 2008 NSDUH included a split sample, in which half the respondents (approximately 750) were administered the WHODAS and the other half the Sheehan Disability Scale (SDS). Two models were used to predict SMI for 2008, one for each impairment scale (WHODAS and SDS). The 2008 models for SMI were chosen so that estimates from the WHODAS and SDS samples were approximately equal; hence, SMI estimates for 2008 were based on both samples. The WHODAS model was determined to be a better predictor of SMI than the SDS model; therefore, starting in 2009, only the WHODAS impairment scale was administered in NSDUH and used for estimating all levels of mental illness (SMI, AMI, low [mild] mental illness [LMI], moderate mental illness [MMI], and serious or moderate mental illness [SMMI]).

Although SAMHSA continued to obtain clinical interviews after 2008, estimates of mental illness from the 2009, 2010, and 2011 NSDUHs have been based on the WHODAS model developed from the 2008 clinical assessment sample. The same model was applied to each year's NSDUH data to provide consistency in mental illness comparisons across the years. Producing a new model each year based on the small annual clinical samples (only 500 interviews in 2009 and 2010) would have resulted in large changes in the model parameters and corresponding prevalence rates due to sampling error, making it impossible to detect real trends in mental illness over time. Furthermore, an evaluation of the 2008 model, using the 2009 NSDUH clinical data, found that the model could not be significantly improved with the additional 500-case 2009 clinical sample. The clinical follow-up study, which started in 2008 and continued until 2012, led to a nationally representative sample of approximately 5,000 cases assigned to the WHODAS questions that were used to develop an improved mental illness prediction model (referred to as the 2012 WHODAS model). This revised and improved model was used for estimating all levels of mental illness starting with the 2012 NSDUH and incorporates the NSDUH respondent's age and indicators of past year suicidal thoughts and

[13] DSM-IV-TR stands for the *Diagnostic and Statistical Manual of Mental Disorders*, 4th Edition, Text Revision (American Psychiatric Association, 2008).

depression, along with the variables that were specified in the 2008 model (e.g., variables for the Kessler-6 [K6] scale and the WHODAS), leading to more accurate estimates of mental illness (see below for details on the 2012 model and revised methodology).

For the 2012 through 2014 mental health detailed tables (CBHSQ, 2013, 2014b, 2015c), the 2008 and later year mental illness estimates were based on the revised model. As of October 2013, the 2008 detailed tables (Office of Applied Studies, 2009a) and the 2009–2011 mental health detailed tables (CBHSQ, 2010, 2012a, 2012c) containing estimates for past year mental illness for adults have been revised based on the 2012 model. Thus, long-term trends are available for mental illness measures from the 2008 NSDUH and onward. The addition of these mental health predictors in the 2012 model, however, affects the types of analyses that can be performed with the mental illness variables derived from the model. See the "Using Mental Illness Variables in Analysis" section below for more details. For detailed information on model revisions to the mental illness items, see Section B.4.3 in Appendix B of the 2014 methodological summary and definitions (CBHSQ, 2015d). The SMI measure available for years before 2004 is not comparable with the SMI measure based on the 2012 model similar to the 2008 model SMI measures. For NSDUH years 2004 through 2007, no mental illness measures were available at all.

***2012 SMI Prediction Model***

The 2012 model is a prediction model for mental illness, and it was used to predict SMI and to estimate prevalence of SMI for the 2014 NSDUH. The prediction model is a weighted logistic regression. The response variable $Y$ was defined so that $Y = 1$ when an SMI diagnosis was positive based on the clinical interview; otherwise, $Y = 0$. If $\mathbf{X}$ is a vector of realized explanatory variables, then the response probability $\pi = \Pr(Y = 1 \mid \mathbf{X})$ can be estimated using a weighted logistic regression model. For further technical details on the 2012 prediction models and the impact of the revised model on the 2008–2011 estimates, see the *2012 Mental Health Surveillance Study: Design and Estimation Report* (CBHSQ, 2014a) or Section B.4.3 in Appendix B of the 2014 methodological summary and definitions (CBHSQ, 2015d).

The 2012 SMI prediction model was fit with data from 4,912 WHODAS MHSS respondents from 2008 through 2012, excluding one case from 2008 and one case from 2009 that were dropped because of data errors. The final WHODAS calibration model for the 2012 prediction model for SMI was determined as

$$\begin{aligned}\text{logit}(\hat{\pi}) = \log[\hat{\pi} / (1 - \hat{\pi})] = {} & -5.972664 + 0.0873416X_k + 0.3385193X_w + 1.9552664X_s \\ & + 1.1267330\,X_m + 0.1059137X_a \end{aligned} \quad (1)$$

or

$$\hat{\pi} = \frac{1}{1 + \exp[-(-5.972664 + 0.0873416X_k + 0.3385193X_w + 1.9552664X_s + 1.1267330\,X_m + 0.1059137X_a)}},$$

where $\hat{\pi}$ refers to the estimate of the SMI response probability $\pi$. The covariates in equation (1) came from the main NSDUH interview data:

$X_k$ = *Alternative Past Year K6 Score*: Past year K6 score of less than 8 recoded as 0; past year K6 score of 8 to 24 recoded as 1 to 17.

$X_w$ = *Alternative WHODAS Score*: WHODAS item score of less than 2 recoded as 0; WHODAS item score of 2 to 3 recoded as 1, then summed for a score ranging from 0 to 8.

$X_s$ = *Serious Thoughts of Suicide in the Past Year*: Coded as 1 if "yes"; coded as 0 otherwise.

$X_m$ = *Past Year MDE*: Coded as 1 if the criteria for past year major depressive episode (MDE) were met;[14] coded as 0 otherwise.

$X_a$ = *Recoded Age*: Coded as age minus 18 if aged 18 to 30; coded as 12 otherwise.

A cut point probability $\pi_0$ was determined, so that if $\hat{\pi} \geq \pi_0$ for a particular respondent, then he or she was predicted to be SMI positive; otherwise, he or she was predicted to be SMI negative. The cut points were chosen so that the weighted numbers of false positives and false negatives in the MHSS dataset were as close to equal as possible. The predicted SMI status for all adult NSDUH respondents was used to compute prevalence estimates of SMI. In the 2012 SMI WHODAS prediction model, the respondent is classified as having past year SMI if the predicted probability of SMI is greater than or equal to 0.260573529 (SMI cutoff point). See Table 3.1 for the model specifications. Table 3.2 contains the cutoff points for other mental illness levels.

***Modified 2012 Model for the 2008 SDS Half Sample***

As noted previously, the 2008 NSDUH data included a split sample. Similar to the 2008 model, the revised 2012 model also has an alternative model for the SDS data that was fit with data from the complete 2008–2012 MHSS clinical sample that contains 5,653 MHSS respondents, excluding 4 cases from 2008 (one from the WHODAS half sample and three from the SDS half sample) and 1 case from 2009 that were dropped because of data errors.

The modified 2012 SMI prediction model for the SDS half sample was

$$\text{logit}(\hat{\pi}) = \log[\hat{\pi}/(1-\hat{\pi})] = -5.7736246 + 0.1772067X_k + 1.8392433X_s + 1.6428623X_m + 0.1231266X_a \qquad (2)$$

or

$$\hat{\pi} = \frac{1}{1+\exp[-(-5.7736246 + 0.1772067X_k + 1.8392433X_s + 1.6428623X_m + 0.1231266X_a)}.$$

All of the covariates in equation (2) also appeared in equation (1).

[14] In this situation, the past year MDE measure is from the main NSDUH interview (i.e., not from the SCID-I/NP). See Section B.4.5 of the 2014 NSDUH methodological summary and definitions (CBHSQ, 2015d).

Similar to the WHODAS model, a cut point probability $\pi_0$ was determined, so that if $\hat{\pi} \geq \pi_0$ for a particular respondent, then he or she was predicted to be SMI positive; otherwise, he or she was predicted to be SMI negative. The cut points were chosen so that the weighted numbers of false positives and false negatives in the MHSS dataset were as close to equal as possible. In the 2012 SMI SDS half sample prediction model, the respondent is classified as having past year SMI if the predicated probability of SMI is greater than or equal to 0.236434 (SMI cutoff point). Although the SDS half sample prediction model was fit across all years and the cutoff points were determined based on all years, the cutoff points were used only for the main study respondents in the 2008 sample B to predict the SMI positives. See Tables 3.1 and 3.2.

**Table 3.1 Final SMI Prediction Models in the 2008–2012 MHSS**

| | Beta | Beta SE | *T* Statistic | *P* Value | *df* | Wald *p* Value[1] |
|---|---|---|---|---|---|---|
| **WHODAS Sample (2008A–2012)** | | | | | | |
| Intercept | -5.9726640 | 0.3201 | -18.6586 | 0.0000 | | |
| Alt PY K6 | 0.0873416 | 0.0248 | 3.5247 | 0.0009 | 1 | 0.0009 |
| Alt WHODAS | 0.3385193 | 0.0349 | 9.7034 | 0.0000 | 1 | 0.0000 |
| PY Suicidal Thoughts | 1.9552664 | 0.2164 | 9.0342 | 0.0000 | 1 | 0.0000 |
| PY MDE | 1.1267330 | 0.2196 | 5.1308 | 0.0000 | 1 | 0.0000 |
| Age1830 | 0.1059137 | 0.0244 | 4.3380 | 0.0001 | 1 | 0.0001 |
| **WHODAS and SDS Samples (2008–2012)[2]** | | | | | | |
| Intercept | -5.7736246 | 0.3479 | -16.5960 | 0.0000 | | |
| Alt PY K6 | 0.1772067 | 0.0190 | 9.3251 | 0.0000 | 1 | 0.0000 |
| PY Suicidal Thoughts | 1.8392433 | 0.1941 | 9.4781 | 0.0000 | 1 | 0.0000 |
| PY MDE | 1.6428623 | 0.2119 | 7.7528 | 0.0000 | 1 | 0.0000 |
| Age1830 | 0.1231266 | 0.0259 | 4.7482 | 0.0000 | 1 | 0.0000 |

Age1830 = recoded age variable; Alt = alternative; *df* = degrees of freedom; K6 = Kessler-6, a six-item psychological distress scale; MDE = major depressive episode; MHSS = Mental Health Surveillance Study; PY = past year; SDS = Sheehan Disability Scale; SE = standard error; SMI = serious mental illness; WHODAS = eight-item World Health Organization Disability Assessment Schedule; 2008A = 2008 WHODAS half sample.

[1] The Wald *p* value is obtained from the overall model fitting.

[2] The model is fit over the WHODAS and SDS samples in 2008–2012 but is used only to produce predictions for the 2008 SDS sample.

Source: SAMHSA, Center for Behavioral Health Statistics and Quality, National Survey on Drug Use and Health, 2008–2012.

**Table 3.2 Cut Point Probabilities for SMI, AMI, and SMMI, by 2012 Model**

| | Cut Point Probability |
|---|---|
| **WHODAS Sample (2008A–2012)** | |
| SMI | 0.260573529 |
| AMI | 0.0192519810 |
| SMMI | 0.077686285365 |
| **WHODAS and SDS Samples (2008–2012)[1]** | |
| SMI | 0.236434 |
| AMI | 0.019182625 |
| SMMI | 0.06616398 |

AMI = any mental illness; SDS = Sheehan Disability Scale; SMI = serious mental illness; SMMI = serious or moderate mental illness; WHODAS = World Health Organization Disability Assessment Schedule; 2008A = 2008 WHODAS half sample.

[1] The model is fit over the WHODAS and SDS samples in 2008–2012, but the cut point predictions are only used to produce predictions for the 2008 SDS sample.

Source: SAMHSA, Center for Behavioral Health Statistics and Quality, National Survey on Drug Use and Health, 2008–2012.

### *Weights*

For the 2008 NSDUH, although SMI data for both half samples (SDS and WHODAS) could be analyzed together when using the 2008 model, the AMI, SMMI, LMI, and MMI data from the two half samples could not be combined for analysis. Under the 2012 model, both the 2008 half samples can be combined to analyze SMI and the other levels of mental illness because the 2012 models were generated so the estimates would be comparable.

Mental illness measures (i.e., SMI, AMI, SMMI, MMI, LMI, and low or moderate mental illness [LMMI])[15] that are defined based on the 2012 model should be analyzed using the standard analysis weight, ANALWT, for all survey years 2008 through 2014. With the revised 2012 model, both the WHODAS and SDS 2008 half samples can be combined to form single estimates and use ANALWT.

This differs from the initial recommendation for analyzing measures of mental illness besides SMI based on the 2008 model. Because of the 2008 split sample, an adjusted mental health sample weight, MHSAMPWT, was created so that the WHODAS and SDS half samples were separately representative of the civilian, noninstitutionalized population aged 18 or older. However, this weight should not be used to analyze 2008 mental illness data based on the 2012 model.

### *Standard Errors for Mental Illness Estimates*

For the 2014 mental health detailed tables and the first release reports (CBHSQ, 2015a, 2015c, 2015e, 2015f, 2015h), standard errors (SEs) for mental illness estimates (SMI, AMI, SMMI, MMI, LMI, and LMMI) were computed using the NSDUH dichotomous variable values without taking into account any variance introduced through using a model based on the clinical subsample data. This ignores the added error resulting from fitting the 2012 SMI model, which

[15] The mental illness measure for LMMI was added during the 2014 NSDUH and is based on the 2012 model. Because LMMI is a composite of the LMI and MMI measures, the same analysis issues apply.

can be very large. See the *2012 Mental Health Surveillance Study: Design and Estimation Report* (CBHSQ, 2014a) for details. These *conditional* SEs (conditional on the model predictions being correct) are useful when making comparisons across years and across subpopulations within years because the errors due to model fitting are nearly the same across the estimates being compared, and consequently, they roughly cancel each other out.

***Using Mental Illness Variables in Analysis***

The mental illness measures (i.e., SMI, AMI, SMMI, MMI, LMI, and LMMI) that were defined based on the 2012 model were examined to determine how they were associated with the mental health predictor variables in the 2012 model. It was found that the 2012 model significantly overestimated the proportion of adults aged 18 or older with SMI (and those with AMI) who had suicidal thoughts in the past year and the proportion of adults who had MDE in the past year (as compared with the clinical interview estimates of the same categories). Therefore, it is recommended that the mental illness measures derived from the 2012 model should not be used when analyzing past year suicidal thoughts, past year MDE, or other associated variables (including past year suicide attempts, suicide plans, medical treatment for suicide attempts, or lifetime MDE). Similarly, it is recommended that model-based mental illness measures should not be used in conjunction with the K6 variables (including serious psychological distress [SPD]) or WHODAS variables in any analyses (CBHSQ, 2014a).

## 3.2 Adult Major Depressive Episode (MDE)

The past year adult MDE estimates shown in the 2014 mental health detailed tables (CBHSQ, 2015c) are based on the full sample as was done in the 2010–2013 mental health detailed tables (CBHSQ, 2012a, 2012c, 2013, 2014b). This differs from the 2008 past year MDE estimates shown in both the 2008 detailed tables (Office of Applied Studies, 2009a) and the 2009 mental health detailed tables (CBHSQ, 2010), which were based only on the sample of adult respondents who received the WHODAS questions in the mental health questionnaire module that preceded the adult depression questionnaire module. The analysis of 2008 MDE data was restricted to only the WHODAS half sample because of apparent reporting differences (context effects) between the half sample that was administered the WHODAS and the other half sample of adult respondents who received the SDS questions (Dean & LeBaron, 2009). Both half samples have issues with context effects not seen in 2007 and previous years because of the revisions to the mental health module preceding the adult depression module. To address the break in comparability of the adult MDE data beginning in 2008 and to estimate adult MDE based on the full sample of adults from 2008, adjusted versions of lifetime and past year MDE variables for adults were created retroactively for 2005 to 2008. These variables were adjusted to make MDE estimates from the SDS half sample in 2008 and from all adult respondents for 2005 to 2007 comparable with the MDE estimates based on data from the half sample that received the WHODAS in 2008 and from all adult respondents in later years (2009 onward). The adjusted data from 2005 to 2008 can be used in conjunction with unadjusted data from later years to estimate trends in adult MDE over the entire period from 2005 to 2014.

In the 2014 mental health detailed tables (CBHSQ, 2015c), ANALWT was used to generate all estimates of adult MDE. More information about how the statistically adjusted adult MDE variables were created can be found in Section B.4.5 of the 2014 NSDUH methodological

summary and definitions (CBHSQ, 2015d) and in the report describing the adjustments (Aldworth, Kott, Yu, Mosquin, & Barnett-Walker, 2012).

## 3.3 Serious Psychological Distress (SPD)

The K6 scale, a measure of psychological distress, was used to create the SPD variable. Before 2008, the K6 consisted of one set of questions that asked adult respondents about symptoms of psychological distress in the month when they were the most depressed, anxious, or emotionally distressed in the past year. Starting in 2008, the K6 consisted of two sets of questions that asked adult respondents how frequently they experienced symptoms of psychological distress during two different periods: (1) during the past 30 days, and (2) if applicable, the month in the past year when they were at their worst emotionally. Respondents were asked about this second period only if they indicated that there was a month in the past 12 months when they felt more depressed, anxious, or emotionally stressed than they felt during the past 30 days. Because of this change, past year K6 and SPD estimates from years before 2008 were no longer comparable with estimates from 2008 onward. To address this comparability issue, adjusted versions of the past year worst K6 total score and past year SPD variables were created for each of the years from 2005 to 2007 to make the 2005–2007 past year K6 scores and past year SPD estimates comparable with their 2008–2014 counterparts.

In the 2014 mental health detailed tables (CBHSQ, 2015c), ANALWT was used to generate 2005–2014 estimates of past year SPD and 2008–2014 estimates of past month SPD. The 2014 first release reports (CBHSQ, 2015a, 2015e, 2015f, 2015h) did not present SPD estimates. More information about how the adjusted K6 and SPD variables were created can be found in the report describing these adjustments (Aldworth et al., 2012).

## 3.4 Decennial Census Effects on NSDUH Substance Use and Mental Health Estimates

As discussed in Section 2, the person-level weights in NSDUH were calibrated to population estimates (or control totals) obtained from the U.S. Census Bureau. For the weights in 2002 through 2010, annually updated control totals based on the 2000 census were used.[16] Beginning with the 2011 weights, however, the control totals from the U.S. Census Bureau are based on the 2010 census. Two investigations were implemented at the national level to assess the effects of using control totals based on the 2010 census instead of the 2000 census. One of these investigations focused specifically on measures of substance use that are used in the 2011 national findings report (CBHSQ, 2012e) and detailed tables (CBHSQ, 2012b), while a separate analysis was conducted to evaluate the impact of the weighting changes on mental health estimates in the 2011 mental health findings report (CBHSQ, 2012d) and associated mental health detailed tables (CBHSQ, 2012c). Because both the 2013 and 2014 NSDUH estimates are based on weights that were poststratified to population control totals that were in turn based on projections from the 2010 census, 2-year trend comparisons between 2013 and 2014 are not subject to census effects. However, trends between 2010 (or earlier years) and 2011 (or later

[16] In addition to the standard 2010 analysis weights poststratified to 2000 census control totals, special weights that were poststratified to 2010 census control totals are available on the 2010 NSDUH public use file (CBHSQ/SAMHSA, 2012).

years) may be influenced by census effects, especially for particular subgroups (e.g., people reporting two or more races for both investigations, people reporting American Indian or Alaska Native or Native Hawaiian or Other Pacific Islander). An additional investigation was done at the state level to evaluate the impact of census effects on model-based small area estimation (SAE).

For more information on the impact of decennial census effects on NSDUH substance use direct estimates, see Section B.4.3 in Appendix B of the 2011 national findings report (CBHSQ, 2012e). For more information on the impact of decennial census effects on NSDUH mental health direct estimates, see Appendix A of the 2011 mental health findings report (CBHSQ, 2012d). For more information on the impact of the decennial census effects on NSDUH model-based SAEs, see http://www.samhsa.gov/data/NSDUH/2k12State/NSDUHsae2012/Index.aspx. Additionally, for more information on the sampling weight calibration in the 2011 NSDUH, see the person-level sampling weight calibration report (Chen et al., 2013).

## 3.5 Using Revised Estimates for 2006 to 2010

During regular data collection and processing checks for the 2011 NSDUH, data errors were identified. These errors affected the data for Pennsylvania (2006–2010) and Maryland (2008–2009). Cases with erroneous data were removed from the data files, and the remaining cases were reweighted to provide representative estimates. The errors had minimal impact on the national estimates and no effect on direct estimates for the other 48 states and the District of Columbia. In reports where model-based SAE techniques were used, estimates for all states may have been affected, even though the errors were concentrated in only two states. In reports that did not use model-based estimates, the only estimates appreciably affected are estimates for Pennsylvania, Maryland, the mid-Atlantic division, and the Northeast region. The 2014 detailed tables (CBHSQ, 2015b), the 2014 mental health detailed tables (CBHSQ, 2015c), and the 2014 first release reports (CBHSQ, 2015a, 2015e, 2015f, 2015h) did not include state-level or model-based estimates. However, they did include estimates for the mid-Atlantic division and the Northeast region. Estimates based on 2006–2010 data may differ from previously published estimates. Tables and estimates based only on 2011 or later data are unaffected by these data errors. All affected tables, that is, tables with estimates based on 2006–2010 data, contain a note to indicate this to the user.

Caution is advised when comparing data from older reports with data from more recent reports that are based on corrected data files. As discussed above, comparisons of estimates for Pennsylvania, Maryland, the mid-Atlantic division, and the Northeast region are of most concern, whereas comparisons of national data or data for other states and regions are essentially still valid. A selected set of corrected versions of reports and tables have been produced. In particular, a set of modified detailed tables that include revised 2006–2010 estimates for the mid-Atlantic division and the Northeast region for certain key measures have been released. Given the change noted above, comparisons between unrevised 2006–2010 estimates and estimates based on 2011–2014 data for the areas of most concern are not recommended.

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# 4. Missingness

## 4.1 Potential Estimation Bias Due to Missingness

In the 2014 National Survey on Drug Use and Health (NSDUH), many variables, including core drug and demographic variables, had missing item response values imputed. See the 2014 NSDUH editing and imputation report (Center for Behavioral Health Statistics and Quality [CBHSQ], 2016a) for further details. However, the missing item responses of many other variables were not imputed, and these missing responses may lead to biased estimates in the 2014 detailed tables (CBHSQ, 2015b) and the 2014 mental health detailed tables (CBHSQ, 2015c). In addition, another source of potential uncertainty about some estimates may occur because of the way unknown item responses (e.g., blank, "don't know," "refused") were actually coded for different variables. For example, some recoded variables (i.e., variables created from one or more source variables) classified unknown item responses in the source variable(s) as missing values, whereas others did not. See Ruppenkamp, Emrich, Aldworth, Hirsch, and Foster (2006) for further details.

Recall from Section 3 that prevalence rates are defined as the proportions of the population who exhibit characteristics of interest. Let $\hat{p}_d$ represent the estimated prevalence rate of interest for domain *d*, with $\hat{p}_d$ defined as

$$\hat{p}_d = \frac{\hat{Y}_d}{\hat{N}_d},$$

where $\hat{Y}_d$ = estimated number of people exhibiting the characteristic of interest in domain *d*, and $\hat{N}_d$ = estimated population total for domain *d*.

The variable defining the characteristic of interest (e.g., illicit drug use) is referred to as the *analysis* variable, and the variable defining the domain of interest (e.g., receipt of past year mental health treatment/counseling) is referred to as the *domain* variable. Suppose that the analysis variable has all its missing values imputed, but the domain variable does not employ the imputation of missing values. In such cases, the estimates $\hat{N}_d$ and $\hat{Y}_d$ may be negatively biased, and the $\hat{p}_d$ estimates also may be biased. To see this, suppose that the domain variable has *D* levels, and define

$$\hat{N} = \sum_{d=1}^{D} \hat{N}_d + \hat{N}_m,$$

where $\hat{N}$ = estimated population total, $\hat{N}_d$ = estimated population total for domain *d*, $d = 1, 2, ..., D$, and $\hat{N}_m$ = estimated population total corresponding to the missing values of the domain variable. Thus, if $\hat{N}_m$ is positive (i.e., there are missing domain-variable responses), then

at least one of the $\hat{N}_d$ estimates will be negatively biased. The presence of negative bias in at least one of the $\hat{Y}_d$ estimates can be similarly demonstrated if $\hat{Y}_m$ is positive, where $\hat{Y}_m$ = the estimated number of people exhibiting the characteristic of interest and corresponding to the missing values of the domain variable. If either of $\hat{N}_m$ and $\hat{Y}_m$ is positive, then $\hat{p}_d$ may be biased by some unknown amount.

In the 2014 detailed tables (CBHSQ, 2015b) and the 2014 mental health detailed tables (CBHSQ, 2015c), potential bias in the $\hat{N}_d$, $\hat{Y}_d$, or $\hat{p}_d$ estimates was not treated, although footnotes included on the tables provide detailed information about which estimates were based on or excluded missing values. This problem may be illustrated by the following example, which corresponds to information presented in Tables 2.9A and 2.9B of the 2014 mental health detailed tables.

Mental health Table 2.9A presents estimates of the past year use of several types of illicit drugs among people aged 12 to 17 for 2013 and 2014. These analysis variables are grouped into a two-level domain variable that is categorized according to whether a respondent had a past year major depressive episode (MDE). In 2014, mental health Table 3.2A shows the population estimate of people aged 12 to 17 as approximately 24,875,000. However, the subdomain population estimates summed to approximately 24,212,000, resulting in an estimate of $\hat{N}_m$ = 663,000 (approximately 2.7 percent of the total population). This number represents the estimated population not assigned to either domain. This negative bias can extend to various analysis variables, such as "Illicit Drugs." In 2014, the total estimate of people aged 12 to 17 who used illicit drugs in the past year was approximately 4,336,000. However, the estimates of people aged 12 to 17 who used illicit drugs in the past year among the valid subdomains (where past year MDE status was not missing) summed to 4,171,000, resulting in an estimate of $\hat{Y}_m$ = 166,000 (approximately 3.8 percent of the total population).

Mental health Table 2.9B presents prevalence estimates of the past year use of several types of illicit drugs among people aged 12 to 17 for 2013 and 2014. Because $\hat{N}_m$ is positive and $\hat{Y}_m$ is positive for the analysis variable, "Illicit Drugs," the prevalence estimates for this variable may be biased by some unknown amount across the two domains. The 2014 prevalence estimates reported in mental health Table 2.9B for youths who had or did not have past year MDE are 33.0 and 15.2 percent, respectively. It can be shown that the approximate range of possible bias values for each of these estimates is as follows: between -5.05 and 3.81 percent and between -0.34 and 0.65 percent, respectively.

As mentioned above, some recoded variables classify unknown item responses in source variables as missing values, whereas others do not. Respondents with missing data are generally excluded from the relevant analyses. For the 2014 NSDUH, an investigation was completed to look at missing data rates in the 2014 detailed tables (CBHSQ, 2015b) and 2014 mental health detailed tables (CBHSQ, 2015c). This investigation concluded that missing data are not a concern for most topics presented in these tables. However, items on perceived availability of various illicit drugs in the detailed tables did have larger rates of missing data. For example, the

rates of missing data for the perceived availability questions ranged from 3.5 to 7.4 percent in 2014. With the mental health detailed tables, a few items have missing data (e.g., items on suicidal thoughts and behavior among adults). For the estimates that are presented in the 2014 NSDUH first release report on suicide (CBHSQ, 2015h), however, less than 1 percent of adult respondents had missing data for suicidal thoughts and behavior. In general, missing data rates for all data elements used in this report were lower than 5 percent.

## 4.2 Variance Estimation in the Presence of Missingness

SUDAAN® Software for Statistical Analysis of Correlated Data (RTI International, 2012) uses the number of strata and number of primary sampling units (PSUs) in its variance calculations, even if there are some PSUs in which a variable is entirely missing for all sample members associated with that PSU. The rationale behind this approach is that there may be individuals in the target population who have nonmissing values in PSUs where no sample members have nonmissing values.

To illustrate how this is operationalized in SUDAAN, consider the following example. Suppose there is interest in calculating the mean of some variable (say, $X$), but there are missing values associated with $X$. SUDAAN then creates an internal subpopulation indicator variable (say, $\delta$), where $\delta = 1$ if $X$ is not missing, and $\delta = 0$ if $X$ is missing. SUDAAN then internally calculates the mean and variance of $X$ by using $\delta X$, assuming the full sample mean is the same as the nonmissing sample mean.

For the variance estimator based on the Taylor series linearization approach, one of the terms in the variance estimator consists of the sum of squared deviations of PSU-level totals about their stratum-level means, divided by the number of PSUs in the stratum minus 1. Therefore, if SUDAAN encounters an incorrect number of PSUs within a stratum, then this term is incorrectly calculated. In addition, if there is only one PSU in a stratum, then the denominator for the variance term associated with that stratum becomes 0, and this causes the overall variance estimate to return an error message in SUDAAN. By including all PSUs in a stratum, whether or not the PSU has reported values, SUDAAN computes the variances appropriately; that is, PSUs with nothing but missing values for a variable should never be excluded from an input file.

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# 5. Sampling Error

In sampling, statistics from different samples will vary and can differ from the true population parameter. Sampling error is the error caused by the use of statistics based on a sample instead of a complete census. Standard errors (SEs) are commonly used to measure how much these statistics differ from the true parameter. This measure is incorporated in common statistical methods such as significance testing (see Section 7) and confidence intervals (see Section 8). As were the prevalence rates, all of the variance estimates for prevalence (including those for prevalence based on annual averages from combined data) were calculated using a method in SUDAAN® that is unbiased for linear statistics. This method is based on multistage clustered sample designs where the first-stage (primary) sampling units are drawn with replacement.

Because of the complex nature of the sampling design for the National Survey on Drug Use and Health (NSDUH) (specifically the use of stratified cluster sampling), key nesting variables were created for use in SUDAAN to capture explicit stratification and to identify clustering. Starting with the 2005 NSDUH,[17] a change was made in the way the key nesting variables were defined. Each state sampling region (SSR) appears in a different variance estimation stratum every quarter. This method had the effect of assigning the regions to strata in a pseudo-random fashion while ensuring that each stratum consists of four SSRs from four different states.

Two replicates per year are defined within each variance stratum (VEREP). Each variance replicate consists of four segments, one for each quarter of data collection. One replicate consists of those segments that are "phasing out" or will not be used in the next survey year. The other replicate consists of those segments that are "phasing in" or will be fielded again the following year, thus constituting the 50 percent overlap between survey years. A segment stays in the same VEREP for the 2 years it is in the sample. This simplifies computing SEs for estimates based on combined data from adjacent survey years.

Although the SEs of estimates of means and proportions can be calculated appropriately in SUDAAN using a Taylor series linearization approach, SEs of estimates of totals may be underestimated in situations where the domain size is poststratified to data from the U.S. Census Bureau. Because of this underestimation, alternatives for estimating SEs of totals were implemented in all of the 2014 detailed tables (Center for Behavioral Health Statistics and Quality [CBHSQ], 2015b) and the 2014 mental health detailed tables (CBHSQ, 2015c), where appropriate.

[17] The new design variables were created retroactively for 1999 through 2004; however, the old design variables continue to be used to generate 2002–2004 estimates in multiyear trend detailed tables, mental health detailed tables, and first release reports for consistency with previously published estimates. Analyses beyond the detailed tables, mental health detailed tables, and first release reports typically use the new design variables for all available years.

Estimates of means or proportions, $\hat{p}_d$, such as drug use prevalence rates for a domain *d*, can be expressed as a ratio estimate:

$$\hat{p}_d = \frac{\hat{Y}_d}{\hat{N}_d},$$

where $\hat{Y}_d$ is a linear statistic estimating the number of substance users in the domain *d*, and $\hat{N}_d$ is a linear statistic estimating the total number of people in domain *d* (both users and nonusers). The SUDAAN software package is used to calculate direct estimates of $\hat{Y}_d$ and $\hat{N}_d$ and can be used to estimate their respective SEs. A Taylor series approximation method implemented in SUDAAN provides estimates for $\hat{p}_d$ and its SE.

When the domain size, $\hat{N}_d$, is free of sampling error, an appropriate estimate of the SE for the total number of substance users is

$$\mathrm{SE}(\hat{Y}_d) = \hat{N}_d \mathrm{SE}(\hat{p}_d).$$

This approach is theoretically correct when the domain size estimates, $\hat{N}_d$, are among those forced to match their respective U.S. Census Bureau population estimates through the weight calibration process. In these cases, $\hat{N}_d$ is not subject to a sampling error induced by the NSDUH design. For more information on the person-level sampling weight calibration in the 2014 NSDUH, see CBHSQ (2016b).

For estimated domain totals, $\hat{Y}_d$, where $\hat{N}_d$ is not fixed (i.e., where domain size estimates are not forced to match the U.S. Census Bureau population estimates), this formulation still may provide a good approximation if it can be assumed that the sampling variation in $\hat{N}_d$ is negligible relative to the sampling variation in $\hat{p}_d$. This is a reasonable assumption for most estimates in this study.

For various subsets of estimates, the above approach yielded an underestimate of the variance of a total because $\hat{N}_d$ was subject to considerable variation. In 2000, an approach was implemented to reflect more accurately the effects of the weighting process on the variance of total estimates. This approach consisted of calculating SEs of totals for all estimates in a particular detailed table using the formula above when a majority of estimates in a table were among domains in which $\hat{N}_d$ was fixed during weighting or if it could be assumed that the sampling variation in $\hat{N}_d$ was negligible. Detailed tables in which the majority of estimates were among domains where $\hat{N}_d$ was subject to considerable variability were calculated directly in SUDAAN.

To improve on the accuracy of the SEs, a "mixed" method approach was implemented in which tables might include more than one method of SE estimation. This mixed approach was applied to selected tables in the 2004 NSDUH, and it was implemented across all tables starting with the 2005 NSDUH and continuing in the 2014 NSDUH. This approach assigns the method of SE calculation to domains within tables so that all estimates among a select set of domains with fixed $\hat{N}_d$ were calculated using the formula above, and all other estimates were calculated directly in SUDAAN, regardless of other estimates within the same table. The set of domains considered controlled (i.e., those with a fixed $\hat{N}_d$) was restricted to main effects and two-way interactions to maintain continuity between years. Domains consisting of three-way interactions may be controlled in one year but not necessarily in preceding or subsequent years. The use of such SEs did not affect the SE estimates for the corresponding proportions presented in the same sets of tables because all SEs for means and proportions are calculated directly in SUDAAN. Appendix A contains SAS®, SUDAAN, and Stata® code examples that demonstrate how to compute SEs of proportions as well as both types of SEs of totals (controlled or uncontrolled; see Exhibits A.1 to A.4.

Table 5.1 contains a list of domains with a fixed $\hat{N}_d$ for the restricted-use data file.[18] This table includes both the main effects and two-way interactions and may be used to identify the method of SE calculation employed for estimates of totals in the 2014 detailed tables (CBHSQ, 2015b) and the 2014 mental health detailed tables (CBHSQ, 2015c). For example, Table 1.23 of the 2014 detailed tables presents estimates of illicit drug use among people aged 18 or older within the domains of gender, Hispanic or Latino (referred to as "Hispanic" hereafter) origin and race, education, and current employment. Estimates among the total population (age main effect), males and females (age by gender interaction), and Hispanics and non-Hispanics (age by Hispanic origin interaction) were treated as controlled in this table, and the formula above was used to calculate the SEs. The SEs for all other estimates, including white and black or African American (age by Hispanic origin by race interaction), were calculated directly from SUDAAN. It is important to note that estimates presented in the 2014 detailed tables and 2014 mental health detailed tables for racial groups are among non-Hispanics, unless noted otherwise. For instance, the domain for whites is actually non-Hispanic whites and is therefore a two-way interaction. Although not reported on in the 2014 detailed tables or the 2014 mental health detailed tables, additional geographic interactions are also treated as domains with fixed $\hat{N}_d$ for other NSDUH analyses. Similar to geographic region and division, a state is considered a controlled domain, and two-way interactions with state and gender, Hispanic origin, quarter, and age group (12-17, 18-25, and 26 or older) are all treated as domains with fixed $\hat{N}_d$.

[18] See the estimation of totals section in the 2014 public use data file introduction for a list of domains with fixed $\hat{N}_d$ (CBHSQ/SAMHSA, 2015).

**Table 5.1 Demographic and Geographic Domains Forced to Match Their Respective U.S. Census Bureau Population Estimates through the Weight Calibration Process, 2014**

| Main Effects | Two-Way Interactions |
|---|---|
| **Age Group** | |
| 12-17 | |
| 18-25 | **Age Group** × **Gender** |
| 26-34 | (e.g., Males Aged 12 to 17) |
| 35-49 | |
| 50-64 | |
| 65 or Older | **Age Group** × **Hispanic Origin** |
| All Combinations of Groups Listed Above[1] | (e.g., Hispanics or Latinos Aged 18 to 25) |
| **Gender** | |
| Male | |
| Female | **Age Group** × **Race** |
| **Hispanic Origin** | (e.g., Whites Aged 26 or Older) |
| Hispanic or Latino | |
| Not Hispanic or Latino | |
| **Race** | **Age Group** × **Geographic Region** |
| White | (e.g., People Aged 12 to 25 in the Northeast) |
| Black or African American | |
| **Geographic Region** | |
| Northeast | **Age Group** × **Geographic Division** |
| Midwest | (e.g., People Aged 65 or Older in New England) |
| South | |
| West | |
| **Geographic Division** | **Gender** × **Hispanic Origin** |
| New England | (e.g., Not Hispanic or Latino Males) |
| Middle Atlantic | |
| East North Central | |
| West North Central | **Hispanic Origin** × **Race** |
| South Atlantic | (e.g., Not Hispanic or Latino Whites) |
| East South Central | |
| West South Central | |
| Mountain | |
| Pacific | |

[1] Combinations of the age groups (including but not limited to 12 or older, 18 or older, 26 or older, 35 or older, and 50 or older) also were forced to match their respective U.S. Census Bureau population estimates through the weight calibration process.

Source: SAMHSA, Center for Behavioral Health Statistics and Quality, National Survey on Drug Use and Health, 2014.

# 6. Degrees of Freedom

## 6.1 Background

To determine whether the observed difference between estimates is statistically significant, the degrees of freedom (*df*) are needed to locate the corresponding probability level (*p* value) of the test statistic. The test statistic is computed from the sample data and represents a numerical summary of the difference between the estimates under consideration; it is a random variable that has a predetermined distribution (such as Student's *t*, chi-square, or *F*). The *df* characterize the amount of variation expected in the estimation of sampling error and are used in conjunction with the test statistic to determine probabilities and evaluate statistical significance. In statistics, the number of *df* refers to the number of independent units of information in a sample relevant to the estimation of a parameter or calculation of a statistic. In general, the *df* of a parameter estimate are equal to the number of independent observations that go into the estimate minus the number of other parameters that need to be estimated as an intermediate step. The *df* are also used to compute the confidence intervals (CIs) discussed in Section 8. The upper and lower limits of the CIs are defined by a constant value that is chosen to yield a level of confidence based on the *df*.

In practice, beyond a certain value, which *df* value is used has little impact. The 97.5th percentile of the *t* distribution does not change much once there are about 50 *df*. Thus, results with 50 *df* are similar to results with the 900 *df* used for the 2002–2013 National Surveys on Drug Use and Health (NSDUHs) and the 750 *df* used for the 2014 NSDUH (Figure 6.1). In addition, Table 6.1 shows the large sample 95 percent CI for a "typical" estimate—for example, the percentage of past month users of illicit drugs in 2012—for different *df*. The CIs are similar.

The *df* for NSDUH vary based on the sample design. Table 6.2 shows the *df* for specific states per the NSDUH sample designs.[19] Starting with the 2005 NSDUH, a change in the definition of the variance estimation strata had the effect of increasing the number of *df* for the state-level estimates fourfold while preserving the number of *df* for the national estimates. Revised design variables were created retroactively for years before 2005 (see footnote 17). When producing 2002–2013 NSDUH estimates at the national level, there are 900 *df*. If an analysis involves individual states, the *df* are determined by the number of strata in which the state is included. In the 2002–2013 surveys, there were two sample size groups. Large sample states (i.e., California, Florida, Illinois, Michigan, New York, Ohio, Pennsylvania, and Texas) have 192 *df* because each large state is in 192 strata. Small sample states (i.e., all other states including the District of Columbia) have 48 *df* because each small state is in 48 different strata.

[19] Users of the 2014 public use file (Center for Behavioral Health Statistics and Quality [CBHSQ]/Substance Abuse and Mental Health Services Administration [SAMHSA], 2015) may find inconsistencies with the specific *df* presented in this report because the specific information referenced is based on the restricted-use dataset that was used to create the 2014 detailed tables (CBHSQ, 2015b), the 2014 mental health detailed tables (CBHSQ, 2015c), and the 2014 first release reports (CBHSQ, 2015a, 2015e, 2015f, 2015h).

**Figure 6.1 Results for 97.5th Percentile of *t* Distributions**

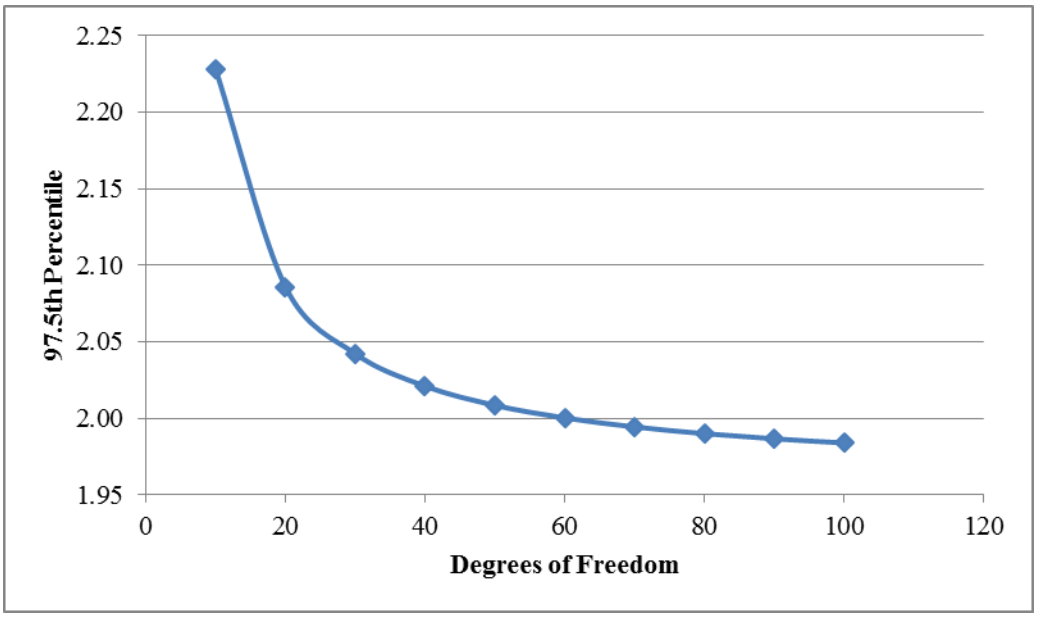


**Table 6.1 Ninety-Five Percent Confidence Intervals for the Percentage of Past Month Users of Illicit Drugs, Using Different Degrees of Freedom, 2012**

| Degrees of Freedom | 97.5th Percentile | 95% Confidence Interval | |
|---|---|---|---|
| | | Lower Limit | Upper Limit |
| 10 | 2.2281 | 8.75 | 9.60 |
| 20 | 2.0860 | 8.78 | 9.57 |
| 30 | 2.0423 | 8.79 | 9.56 |
| 40 | 2.0211 | 8.79 | 9.56 |
| 50 | 2.0086 | 8.80 | 9.56 |
| 60 | 2.0003 | 8.80 | 9.55 |
| 70 | 1.9944 | 8.80 | 9.55 |
| 80 | 1.9901 | 8.80 | 9.55 |
| 90 | 1.9867 | 8.80 | 9.55 |
| 100 | 1.9840 | 8.80 | 9.55 |
| 500 | 1.9647 | 8.80 | 9.55 |
| 750 | 1.9631 | 8.80 | 9.55 |
| 900 | 1.9626 | 8.80 | 9.55 |
| 1,800 | 1.9613 | 8.80 | 9.55 |

NOTE: The percentage of past month users of illicit drugs used to produce the data in this table is 9.1761 with a corresponding standard error of 0.1893.

Source: SAMHSA, Center for Behavioral Health Statistics and Quality, National Survey on Drug Use and Health, 2012.

Changes were made to the 2014 through 2017 sample allocation in order to increase the sample in the original 43 small states to improve precision of the state and substate estimates while moving close to a proportional allocation in the larger states. This design change moved the sample from two state sample size groups (large and small) to five state sample size groups. In the revised design, sampling strata called state sampling regions (SSRs) were formed within

each state. The partitioning divided the United States into a total of 750 SSRs, which results in 750 *df* for national estimates. States in sample size group 1 (i.e., California) have 144 *df*, states in sample size group 2 (i.e., Florida, New York, and Texas) have 120 *df*, states in sample size group 3 (i.e., Illinois, Michigan, Ohio, and Pennsylvania) have 96 *df*, states in sample size group 4 (i.e., Georgia, New Jersey, North Carolina, and Virginia) have 60 *df*, and states in sample size group 5 (i.e., the remaining 38 states and the District of Columbia) have 48 *df*.

Appendix A contains examples that demonstrate how to define the *df* within SUDAAN (RTI International, 2012) or Stata® to compute design-based estimates.

**Table 6.2 Degrees of Freedom for Specific States per the NSDUH Sample Design Based on the Restricted-Use Dataset**

| States | Sample Design Years[1] | Degrees of Freedom[2] |
|---|---|---|
| California | 2014 | 144 |
| | 2005–2013 | 192 |
| | 2002–2004 | 192 |
| Florida, New York, and Texas | 2014 | 120 |
| | 2005–2013 | 192 |
| | 2002–2004 | 192 |
| Illinois, Michigan, Ohio, and Pennsylvania | 2014 | 96 |
| | 2005–2013 | 192 |
| | 2002–2004 | 192 |
| Georgia, New Jersey, North Carolina, and Virginia | 2014 | 60 |
| | 2005–2013 | 48 |
| | 2002–2004 | 48 |
| Remaining 38 states and the District of Columbia | 2002–2014 | 48 |

[1] The NSDUH sample design variables were revised in 2005 and 2014. The 2005 revisions were applied retroactively to the 1999 through 2004 NSDUHs. Because of survey improvements in the 2002 NSDUH, the 2002 data constitute a new baseline, so this table does not include information before 2002.

[2] The degrees of freedom in this table are based on the new sample design variables. If using the old sample design variables for NSDUH years 2002–2004, the state degrees of freedom listed in this table would be divided by 4.

Source: SAMHSA, Center for Behavioral Health Statistics and Quality, National Survey on Drug Use and Health, 2002–2014.

Under the NSDUH sample designs, for an analysis of a group of states, the *df* would be less than or equal to the sum of the *df* for each individual state due to overlap of strata. Therefore, the specific number of *df* should be computed by counting the unique values of VESTR (variance estimation [pseudo] stratum) for the particular geographic area of interest. For these types of specific state analyses (or other subpopulations of interest), the *df* can be calculated outside of SUDAAN® and this value entered manually into SUDAAN for use in testing (RTI International, 2012); otherwise, the *df* are computed using the entire dataset. Similar methods can be used to compute appropriate *df* for any geographic region comprising counties. Using this technique with the public use file will give similar, but not always exact, results.

The technique of counting the number of unique values of VESTR (see above) can also be used to compute the number of *df* for analyses based on combining survey data across years. An alternative technique for computing the *df* for analyses that use data combined (or pooled) across NSDUH sample design years involves summing the *df* from each sample design year (see Table 6.2 to determine the *df* for the NSDUH years and states of interest) because each sample design (i.e., 2002–2004, 2005–2013, 2014–2017) contains unique variance strata. For example, when pooling 2013 and 2014 NSDUH data, the *df* for California would be 192 (2013) + 144 (2014) = 336 because the years being pooled come from two different sample designs. However, if pooling 2012 and 2013 NSDUH data, which both come from the same sample design, the *df* would simply be 192.

## 6.2 Degrees of Freedom Used in Key NSDUH Analyses

The current practices for applying *df* to NSDUH data depends on the type of analyses. Table 6.3 summarizes key types of NSDUH analyses and the *df* used for these analyses for the various survey design years. The detailed tables, mental health detailed tables, and first release reports use the national *df* for the most current survey year (including census region and division and estimates for all years including pooled years), with the exception of the mean age of first use (AFU) estimates. The current year *df* is used because when conducting significance testing between estimates with different *df* (e.g., 2014 vs. 2013), the lower *df* provide a more conservative test and are used. For all of the currently analyzed years of NSDUH data, the current year's *df* have always been less than or equal to the previous years.

AFU estimates are treated differently because of the possibility of smaller sample sizes (i.e., the sample sizes are typically the number of past year initiates), and therefore belong to fewer variance estimation strata. Based on the NSDUH suppression rules, the sample size threshold for suppression of a mean age at first use estimate is 10, whereas for prevalence rates, it is 100. Thus, it is possible for nonsuppressed AFU estimates to have smaller sample sizes than prevalence rates. The subpopulation for estimates of mean AFU includes only lifetime users of each specific drug, which could be small for drugs with low prevalence rates of use. An impact assessment was done using 2012–2013 data to determine whether the results of statistical comparisons between the means for the 2 years would be affected if the *df* were changed from the national *df* (900 in 2013) to the number of nonempty strata (the number of strata containing respondents with valid data to each specific question within the subpopulation). This latter value would produce more conservative tests. After the impact assessment, a decision was made to use the number of nonempty strata as the *df* for the five detailed tables that include estimates of mean AFU.

Unlike the detailed tables, mental health detailed tables, and the first release reports which use the national *df* for estimates by geographic subgroups (census region and division), special analyses and methodological reports follow the procedures described in Section 6.1 for these subgroups. The *df* used for key NSDUH analyses are summarized in Table 6.3. For NSDUH analyses that compare two subpopulations (including those that compare subpopulations with the full population), standard practice is to use the smaller of the two values for *df* to err on the side of being conservative. For analyses where the subpopulation is not geographic in nature (e.g., members of a certain race or age category, past year users of a certain

drug), standard practice is to use the same *df* value that is used for analyses involving the whole population.

**Table 6.3 Key NSDUH Analyses and Degrees of Freedom for the Restricted-Use Data File and the Public Use Data File, by Sample Design Years, 2002–2014**

| Analyses | Sample Design Years[1] | Degrees of Freedom for Restricted-Use (Public Use) Data File[2] |
|---|---|---|
| Special analyses involving the whole population or a nongeographic subpopulation[3] | 2014 | 750 (50) |
| | 2005–2013 | 900 (60) |
| | 2002–2004 | 900 (60) |
| Special analyses involving a single state | See Table 6.2 | See Table 6.2 |
| Special analyses involving other geographic subpopulations[3] | Any | Count of the unique values of VESTR (variance estimation [pseudo] stratum) for the particular geographic area of interest[4] |
| Detailed tables or first release reports with estimates of mean age at first use | 2014 | Number of nonempty[5] strata (for each estimate/subpopulation) |
| | 2005–2013 | 900 (60) |
| | 2002–2004 | 900 (60) |
| All other detailed tables, mental health detailed tables, and first release reports (including geographic subpopulations) | 2014 | 750 (50) |
| | 2005–2013 | 900 (60) |
| | 2002–2004 | 900 (60) |

[1] The NSDUH sample design variables were revised in 2005 and 2014. The 2005 revisions were applied retroactively to the 1999 through 2004 NSDUHs. Because of survey improvements in the 2002 NSDUH, the 2002 data constitute a new baseline, so this table does not include information before 2002.

[2] The degrees of freedom shown first in this column are based on the restricted-use data files, and the degrees of freedom in parentheses are based on the public use data file.

[3] Some analyses capped the degrees of freedom at 900, regardless of year combinations across the study year groups. This rule is not consistently applied to all special analyses and reports.

[4] Users of the 2014 public use file (CBHSQ/SAMHSA, 2015) may find inconsistencies in the counts when comparing them with published data. The degrees of freedom for the corresponding public use data files are found in the degrees of freedom column in parentheses in Table 6.2.

[5] A stratum or primary sampling unit (PSU) is *empty* for a given subpopulation if the respondent pool contains no subpopulation members in the stratum or PSU.

Source: SAMHSA, Center for Behavioral Health Statistics and Quality, National Survey on Drug Use and Health, 2002–2014.

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# 7. Statistical Significance of Differences

Once the degrees of freedom (*df*) have been determined, various methods used to compare prevalence estimates may be employed. This section describes the impact of the 2014 sample redesign on significance testing, the methods used to compare prevalence estimates, examples showing how to compute the comparison of estimates between years, and the impact of rounding in interpreting testing results.

Customarily, the observed difference between estimates is evaluated in terms of its statistical significance. Statistical significance is based on the size of the test statistic and its corresponding *p* value, which refers to the probability that a difference as large as that observed would occur because of random variability in the sample estimates if there were no differences in the prevalence rates being compared. The significance of observed differences is generally reported at the .05 and .01 levels when the *p* value is defined as less than or equal to the designated significance level.

Significance tests were conducted on differences between prevalence estimates from the 2014 National Survey on Drug Use and Health (NSDUH) and previous years of NSDUH back to 2002. Because of survey design changes implemented in 2002, data from the 2002–2014 NSDUHs should not be compared with data from earlier survey years. Significance tests were also conducted on differences between prevalence estimates from combined 2011–2012 survey data and those from combined 2013–2014 survey data. Within-year tests were conducted on differences between prevalence estimates for various populations (or subgroups) of interest using data from the 2014 survey. In addition to comparing subpopulations, linear trend tests for all data points across all years of interest were performed.

## 7.1 Impact of Sample Redesign on Significance Testing between Years

In 2014, the NSDUH sample was redesigned, and this sample design will continue to be used in 2015 and future survey years. The primary purpose of the redesign was to redistribute the sample sizes by state and by age group, so the sample size in each state was more proportional to the state population, and similarly for age groups (i.e., youths aged 12 to 17 and young adults aged 18 to 25 were oversampled less, and older adults aged 50 or older were undersampled less). The change in sample design with regard to states resulted in greater precision (i.e., smaller standard errors) overall, and the change in sample design with regard to age groups resulted in slightly decreased precision for youths and young adults, but increased precision for older adults; the increase in precision for older adults was much larger than the decrease in precision for youths and younger adults.

Other sample design changes in 2014 included the following: the use of the 2010 census data (instead of projections from the 2000 census), the 2006 to 2010 American Community Surveys, and Nielsen Claritas to provide more up-to-date information for constructing the sampling frame and thereby slightly increasing precision; reducing the number of state sampling regions so that national, regional, and state *df* were typically reduced (e.g., from 900 in 2013 and earlier to 750 in 2014 for national estimates), but the effect on critical values of the *t*-distribution was small (i.e., relative changes all less than 1 percent); the average cluster (i.e., segment) size

was increased while simultaneously reducing the number of clusters, which did not result in a significant loss of precision.

Changes (mainly reductions) in the precision of estimates due to the 2014 sample redesign are likely to affect significance testing. For example, suppose an estimate in 2013 is identical to that of 2014, but the 2014 estimate is more precise; then it is possible that a test between 2013 and 2012 estimates may not be significant, but the same test between 2014 and 2012 estimates may be significant because the 2014 estimate has a smaller standard error.

## 7.2 Comparing Prevalence Estimates between Years

When comparing prevalence estimates, one can test the null hypothesis (no difference between rates) against the alternative hypothesis (there is a difference in prevalence rates) using the standard *t* test (with the appropriate *df*) for the difference in proportions test, expressed as

$$t_{df} = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\text{var}(\hat{p}_1) + \text{var}(\hat{p}_2) - 2\text{cov}(\hat{p}_1, \hat{p}_2)}}, \quad (1)$$

or

$$t_{df} = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\text{var}(\hat{p}_1) + \text{var}(\hat{p}_2) - 2\rho(\hat{p}_1, \hat{p}_2)\text{SE}(\hat{p}_1)\text{SE}(\hat{p}_2)}} \quad (2)$$

where in both formulas, $df$ = the appropriate degrees of freedom, $\hat{p}_1$ = the first prevalence estimate, $\hat{p}_2$ = the second prevalence estimate, $\text{var}(\hat{p}_1)$ = the variance of the first prevalence estimate, and $\text{var}(\hat{p}_2)$ = the variance of the second prevalence estimate. In the first formula, $\text{cov}(\hat{p}_1, \hat{p}_2)$ = covariance between $\hat{p}_1$ and $\hat{p}_2$. In the second formula, the covariance between $\hat{p}_1$ and $\hat{p}_2$ is displayed as the product of the correlation between $\hat{p}_1$ and $\hat{p}_2$ and the standard errors (SEs) of $\hat{p}_1$ and $\hat{p}_2$, where $\rho(\hat{p}_1, \hat{p}_2)$ = the correlation between $\hat{p}_1$ and $\hat{p}_2$ and $\text{SE}(\hat{p}_1)\text{SE}(\hat{p}_2)$ = the product of the standard errors for $\hat{p}_1$ and $\hat{p}_2$ (i.e., the two formulas are equivalent; the first formula is defined in terms of the covariance, and the second is defined in terms of the correlations and SEs). Generally, the correlations between estimates in adjacent years are very small and positive; thus, ignoring the correlation in the second formula will usually result in a slightly more conservative test outcome, which is a test that is less likely to reject the null hypothesis that there is no difference in the two estimates. However, a negative correlation is possible and would result in a liberal test, which means it would be more likely to reject the null hypothesis that there is no difference in the two estimates. Additionally, the second (simplified) formula can be used in the case of two independent (i.e., uncorrelated) samples, like in the case of comparing two nonadjacent year estimates. Note that the first and second prevalence estimates may take the form of prevalence estimates from two different survey years (e.g., 2013 and 2014, respectively), prevalence estimates from sets of combined survey data (e.g., 2011–2012 annual averages and 2013–2014 annual averages, respectively), or prevalence estimates for populations of interest within a single survey year. Quick tests (where the correlation of 0 is assumed) are

great tools for gaining a better understanding of published estimates; however, the results of these quick tests should be confirmed using NSDUH data and appropriate software.

Under the null hypothesis, the test statistic $t$ is a random variable that asymptotically follows a $t$-distribution. Therefore, calculated values of $t$, along with the appropriate $df$, can be used to determine the corresponding probability level (i.e., $p$ value). Whether testing for differences between years or from different populations within the same year, the covariance term in the formula for $t$ (see formula 1 above) will, in general, not be equal to 0. SUDAAN® is used to compute estimates of $t$ along with the associated $p$ values such that the covariance term is calculated by taking the sample design into account (RTI International, 2012). A similar procedure and formula for $t$ are used for estimated totals; however, it should be noted that because it was necessary to calculate the SE outside SUDAAN for domains forced by the weighting process to match their respective U.S. Census Bureau population estimates, the corresponding test statistics also were computed outside SUDAAN. SAS®, SUDAAN, and Stata® examples showing the computational methods for generating $p$ values of estimates of $t$ and estimated totals can be found in Appendix A (Exhibits A.7 through A.18).

Under the null hypothesis, the test statistic with known variances asymptotically follows a standard normal ($Z$) distribution. However, because the variances of the test statistic are estimated, its distribution is more accurately described by the $t$-distribution for finite sample sizes. A sufficiently large sample size is required for the asymptotic properties to take effect, and this is usually determined through the suppression criteria applied to the estimates (see Section 10). As the $df$ approach infinity, the $t$-distribution approaches the $Z$ distribution. That is, because most of the statistical tests performed have 750 $df$ (see Section 6), the $t$ tests performed produce approximately the same numerical results as if a $Z$ test had been performed.

If SUDAAN is not available to compute the standard $t$ test, using published estimates can provide similar pairwise testing results. When comparing prevalence rates shown in the detailed tables with their SEs, independent $t$ tests for the difference of proportions can be performed and usually will provide the same results as tests performed in SUDAAN (see Sections 7.4 and 7.5). However, where the $p$ value is close to the predetermined level of significance, results may differ for two reasons: (1) the covariance term is included in the SUDAAN tests, whereas it is not included in independent $t$ tests; and (2) the reduced number of significant digits shown in the published estimates may cause rounding errors in the independent $t$ tests.

## 7.3 Example of Comparing Prevalence Estimates between Years

The following example reproduces the difference in the proportions tested between 2013 and 2014 for a measure shown in Table 1.1B of the 2014 detailed tables (Center for Behavioral Health Statistics and Quality [CBHSQ], 2015b). Table1.1B displays the prevalence for lifetime, past year, and past month illicit drug use. This example will test the difference between 2013 and 2014 past month marijuana use. Marijuana use shown in Table 1.1B has a prevalence rate of 7.5 percent in 2013 and 8.4 percent in 2014. The corresponding SEs shown in Table 1.1D are 0.17 percent for 2013 and 0.16 percent for 2014. Assuming that the source data are not available and/or the user does not have access to appropriate software (i.e., SUDAAN), the second $t$ test formula provided earlier in this section can be used with the assumption that the correlation is 0.

Note that

$$\text{var}(\hat{p}_i) = (\text{SE}(\hat{p}_i))^2,$$

$$t_{750} = \frac{7.5 - 8.4}{\sqrt{0.17^2 + 0.16^2 - 2(0)(0.17)(0.16)}} = 3.8552.$$

Using a *t* test to find the corresponding *p* value when *t* = -3.8552 and *df* = 750, results in *p* value = 0.0001. This is very close to the SUDAAN-calculated *p* value of 0.0004 provided in Table 1.1P. This example confirms that the difference between the 2013 estimate of 7.5 percent and the 2014 estimate of 8.4 percent is statistically significant at the 0.01 level as indicated by footnote b included on the 2013 estimate in Table 1.1B. Note that the calculated *p* value assuming the correlation is 0 is smaller than the actual *p* value, which seems to contradict the earlier assertion that assuming the correlation is 0 results in a more conservative *p* value. However, this example produces a smaller *p* value due to the use of rounded estimates from the table (if the unrounded estimates had been available, the formula would yield a slightly larger *p* value than what is published in the tables). For 2014, note that because there was a sample design change, the correlation for all tests between years is 0. This is not usually the case. Next year, when testing 2015 versus 2014, there will be a correlation greater than 0 because the sample design will be the same between the 2 years.

Below is an example using the same formula with the unrounded estimates and the covariance from SUDAAN. The extra digits, along with the 0 covariance for 2014, change the *t*-score slightly, resulting in the published *p* value of 0.0004.

$$t_{750} = \frac{7.54996387 - 8.36886162}{\sqrt{(0.16861815)^2 + (0.15983236)^2 - 2(0)\ (0.16861815)(0.15983236)}} = -3.52468$$

Also note that the correlations between estimates in adjacent years are generally very small and positive, but a negative correlation is possible. Estimates with negative correlations will also be close to 0; thus, the differences in SUDAAN-calculated *p* values and *p* values calculated from published estimates using the second *t* test formula provided earlier in this section (where the correlation is assumed to be 0) would still be minimal, such as the small differences shown in this section. However, where the *p* value is close to the predetermined level of significance, results may differ.

## 7.4 Example of Comparing Prevalence Estimates between Years in Excel

Using the same numbers presented in Section 7.4, this example uses Excel functions to produce the same *p* value produced in the previous example. The same assumption is made about the correlation (i.e., it is 0) and that $\text{var}(\hat{p}_i) = (\text{SE}(\hat{p}_i))^2$. The correlation of 0 results in the simplified formula shown below (additionally, the variances have been replaced by SEs squared).

$$t_{df} = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{(\text{SE}(\hat{p}_1))^2 + (\text{SE}(\hat{p}_2))^2}}$$

Excel can be used to set up a simple table (shown below) to compare prevalence estimates. Cells A2 through E2 are the known values input by the user. Cells F2 and G2 contain functions. This table could extend over several rows to aid in comparing many different pairs of prevalence estimates (i.e., data for columns A through E would have to be entered for each row, and then the formulas in columns F and G could be copied for all rows).

| | A | B | C | D | E | F | G |
|---|---|---|---|---|---|---|---|
| 1 | $p_1$ | $p_2$ | SE($p_1$) | SE($p_2$) | *df* | *t* | *p* value |
| 2 | 7.5 | 8.4 | 0.17 | 0.16 | 750 | -3.8552 | 0.0001 |

The standardized test statistic is found using the simplified formula for $t_{df}$.

| | A | B | C | D | E | F | G |
|---|---|---|---|---|---|---|---|
| 1 | $p_1$ | $p_2$ | SE($p_1$) | SE($p_2$) | *df* | *t* | *p* value |
| 2 | 7.5 | 8.4 | 0.17 | 0.16 | 750 | =(A2-B2)/SQRT(C2^2+D2^2) | 0.0001 |

The Excel T.DIST.2T function then calculates the two-tailed Student's *T*-Distribution, a continuous probability distribution.

| | A | B | C | D | E | F | G |
|---|---|---|---|---|---|---|---|
| 1 | $p_1$ | $p_2$ | SE($p_1$) | SE($p_2$) | *df* | *t* | *p* value |
| 2 | 7.5 | 8.4 | 0.17 | 0.16 | 750 | -3.8552 | =T.DIST.2T(ABS(F2),E2) |

Alternatively, the Excel NORM.S.DIST function can be used to calculate the Standard Normal Cumulative Distribution Function because the *t*-distribution approaches the *Z* distribution as the *df* approach infinity. Tests performed having 750 *df* produce approximately the same numerical results as if a *Z* test had been performed. Note that this function refers to the test statistic as *Z* and does not require the *df* input.

| | A | B | C | D | E | F | G |
|---|---|---|---|---|---|---|---|
| 1 | $p_1$ | $p_2$ | SE($p_1$) | SE($p_2$) | *df* | *Z* | *p* value |
| 2 | 7.5 | 8.4 | 0.17 | 0.16 | 750 | -3.8552 | =2*(1-NORMSDIST(ABS(F2))) |

Both the T.DIST.2T and NORM.S.DIST functions yield the same *p* value, 0.0001. Although not generated in all NSDUH publications, some publications do include sampling error in the form of 95 percent confidence intervals (CIs). In terms of testing for differences between prevalence rates shown with 95 percent CIs, it is important to note that two overlapping 95 percent CIs do not imply that their rates are statistically equivalent at the 5 percent level of significance. For additional information, see Schenker and Gentleman (2001) and Payton, Greenstone, and Schenker (2003).

## 7.5 Comparing Prevalence Estimates in Categorical Subgroups

In addition to examining estimates between years, significance testing is also used when comparing population subgroups defined by three or more levels of a categorical variable within a given year. In this type of situation, log-linear chi-square tests of independence of the subgroup and the prevalence variables were conducted first to control the error level for multiple comparisons. Although these tests are generally not published in the detailed tables, they can aid in report writing for NSDUH publications to verify statements implying significance such as claiming that the prevalence for a measure of interest varies by age groups. In Appendix A, see Exhibit A.27 for example SUDAAN code and Exhibit A.28 for example Stata code showing this type of testing. If Shah's Wald *F* test (transformed from the standard Wald chi-square) indicated overall significant differences, the significance of each particular pairwise comparison of interest was tested using SUDAAN analytic procedures to properly account for the sample design (RTI International, 2012). Individual pairwise tests are also used in report writing for NSDUH publications to verify statements implying significance such as claiming that a particular age group has the highest prevalence for a measure of interest. In Appendix A, see Exhibit A.27 for example SUDAAN code and Exhibit A.28 for example Stata code showing this type of testing.

## 7.6 Comparing Prevalence Estimates to Identify Linear Trends

In addition to comparing subpopulations or one year versus another year, it can also be useful to test the linear trend for all data points, across all years of interest. Linear trend testing can inform users about whether prevalence use has decreased, increased, or remained steady over the entire span of the years of interest or about changes in specific measures. Various methods can be used to test linear trend. Linear trend testing is produced for the detailed tables and mental health detailed tables as applicable, but it is only used to aid in NSDUH report writing and is not published. These linear trend tests are implemented using the SUDAAN procedure DESCRIPT with CONTRAST statements looking across years to evaluate change over time. In Appendix A, see Exhibit A.31 for example SUDAAN code and Exhibit A.32 for example Stata code showing this type of linear trend testing.

For linear testing within the detailed tables, the DESCRIPT procedure is used in the mass production of detailed tables *only* to aid in report writing regarding whether a particular measure has remained stable, increased, or decreased over time. This method uses the *t* test, similar to the pairwise method used when testing means between years and between demographic levels within the detailed tables. Instead of using PAIRWISE statements, type I errors (incorrectly producing significant differences) are controlled through the use of orthogonal polynomial coefficients in the CONTRAST statement. Although pairwise testing gives detailed information for testing

between 2 years, it does not perform as well for overall trend information and increases type I errors.

The DESCRIPT procedure for linear testing within the detailed tables is a good approximation to a model-based approach. The 2014 redesign impact assessment report (RIAR) (CBHSQ, 2015g) also includes linear trend testing and implemented the testing using a model-based approach, specifically linear regression, logistic regression, and multinomial logistic regression models to determine whether there were breaks in trends for the most current year. Models were also run and stratified by age and state group. The more complex model-based approach was used to incorporate more information about the outcome into the models (i.e., what type of data are being modeled) and to allow for multiple covariates, which helped determine whether there was a break in trend for 2014. This model-based approach was specific to the 2014 RIAR. In Appendix A, see Exhibit A.33 for example SUDAAN code and Exhibit A.34 for example Stata code showing the model-based linear trend testing.

The model-based method used in the RIAR is more flexible to measure a change in measurement over time when controlling for multiple covariates as needed. The modeling method can be used to estimate more specific measures, such as testing a year effect in a trend model that adjusts for seasonal effects and redesign effects, or comparing an estimate with an estimated forecast using data up to a specified year. The modeling method may yield a slightly different result than the DESCRIPT method under similar settings. Because the purpose of the testing for the detailed tables is to test whether any observed difference across years is significant without consideration of other covariates, the DESCRIPT method was used for its simplicity to be incorporated into the table generation software under the given time constraints.

## 7.7 Impact of Rounding in Interpreting Testing Results

Prevalence estimates in the form of percentages are presented in the detailed tables, mental health detailed tables, and first release reports rounded to the nearest tenth of a percent. Testing between two rounded prevalence estimates can indicate significant or nonsignificant differences involving seemingly identical estimates. Examples are provided below to aid users in interpreting significance testing results:

1. Differences between the estimate in a given year (e.g., 2013) and the estimate in the current year (e.g., 2014) are shown as statistically significant, but the percentages appear to be identical. For example, in Table 1.1B of the 2014 detailed tables (CBHSQ, 2015b), the estimate for past year heroin use among people aged 12 or older was 0.3 percent for both 2013 and 2014 and was indicated as significantly different. Although the rounded estimates appear the same, the unrounded estimates were 0.2595 percent for 2013 and 0.3446 percent for 2014.
2. Difference between the estimate in prior year A (e.g., 2002) and the estimate in the current year (e.g., 2014) is statistically significant, but the difference between the estimate in prior year B (e.g., 2003) and the estimate in the current year (e.g., 2014) is not significant, but the estimates for prior years A and B appear to be identical. For example, in Table 7.3B of the 2014 detailed tables (CBHSQ, 2015b), the estimate for past month crack use among people aged 12 or older is 0.2 percent for 2007, 2009, and 2012, but only the 2007 estimate is significantly different from the 2014 estimate

of 0.1 percent. Although the rounded estimates for 2007, 2009, and 2012 appear the same, the unrounded estimates were 0.2464 percent for 2007, 0.1973 percent for 2009, and 0.1705 percent for 2012.

# 8. Confidence Intervals

In some National Survey on Drug Use and Health (NSDUH) publications, sampling error has been quantified using 95 percent confidence intervals (CIs). CIs provide a scale to judge how close the sample statistic is likely to be to the true population parameter under repeated sampling. A 95 percent CI, which varies for each sample, is expected to capture the true population parameter in 95 percent of samples. The interval provides a value above and below the estimate and is determined by using the sampling distribution and standard error. The sampling distribution translates the confidence level into the appropriate multiplier, and the standard error measures how much statistics differ from the parameter due to sampling variability. Samples with more variability will result in a larger spread in the CI. Symmetric CIs for small proportions may lead to the undesirable result of a lower CI limit that is less than 0. Frequently, NSDUH estimates are small percentages (i.e., are close to 0), and in that case, a logit transformation of the estimate provides favorable properties. For example, the logit transformation yields asymmetric interval boundaries between 0 and 1 that are more balanced with respect to the true probability that the true value falls below or above the interval boundaries. This is partly because for values close to 0, the distribution of a logit-transformed estimate approximates the normal distribution more closely than the standard estimate.

To illustrate the method, let the proportion $P_d$ represent the true prevalence rate for a particular analysis domain *d*. Then the logit transformation of $P_d$ , commonly referred to as the "log odds," is defined as

$$L = \ln[P_d / (1 - P_d)],$$

where "1n" denotes the natural logarithm.

Letting $\hat{p}_d$ be the estimate of the domain proportion, the log odds estimate becomes

$$\hat{L} = \ln[\hat{p}_d / (1 - \hat{p}_d)].$$

The lower and upper confidence limits of *L* are formed as

$$A = \hat{L} - K\left[\frac{\sqrt{\text{var}(\hat{p}_d)}}{\hat{p}_d(1 - \hat{p}_d)}\right],$$

$$B = \hat{L} + K\left[\frac{\sqrt{\text{var}(\hat{p}_d)}}{\hat{p}_d(1 - \hat{p}_d)}\right],$$

where $\text{var}(\hat{p}_d)$ is the variance estimate of $\hat{p}_d$, the quantity in brackets is a first-order Taylor series approximation of the standard error of $\hat{L}$, and *K* is the critical value of the *t*-distribution associated with a specified level of confidence and degrees of freedom (*df*). For example, to produce 95 percent confidence limits for 2014 national estimates, the value of *K* would be 1.96

based on 750 *df*. See Section 6 for more details on what *df* should be used for various subpopulations in order to determine *K* appropriately.

Although the distribution of the logit-transformed estimate, $\hat{L}$, is asymptotically normal, the variance term in the CI is estimated, and a critical value from the *t*-distribution is therefore appropriate when calculating CIs. A sufficiently large sample size is required for the asymptotic properties to take effect, and this is usually determined through the suppression criteria applied to the estimates (see Section 10).

Applying the inverse logit transformation to *A* and *B* above yields a CI for $\hat{p}_d$ as follows:

$$\hat{p}_{d,lower} = \frac{1}{1+\exp(-A)},$$

$$\hat{p}_{d,upper} = \frac{1}{1+\exp(-B)},$$

where "exp" denotes the inverse log transformation. The lower and upper CI endpoints for percentage estimates are obtained by multiplying the lower and upper endpoints of $\hat{p}_d$ by 100.

The CI for the estimated domain total, $\hat{Y}_d$, as estimated by

$$\hat{Y}_d = \hat{N}_d \cdot \hat{p}_d,$$

is obtained by multiplying the lower and upper limits of the proportion CI by $\hat{N}_d$. For domain totals $\hat{Y}_d$, where $\hat{N}_d$ (weighted population total) is not fixed, the CI approximation assumes that the sampling variation in $\hat{N}_d$ is negligible relative to the sampling variation in $\hat{p}_d$.

Examples below illustrate how to compute and use CIs of prevalence rates. Note that CIs of totals cannot be computed using published data from the detailed tables and mental health detailed tables because this computation requires the weighted sum of the measures, which is not a published estimate. In Appendix A, see Exhibit A.21 for example SUDAAN code and Exhibit A.22 for example Stata code on how to compute the confidence intervals of the totals. The example in Section 8.1 computes CIs using the formulas shown above, the Section 8.2 example computes CIs using Excel, the Section 8.3 example shows how to use the CIs to compute standard errors, and the Section 8.4 example shows how to use Excel to compute the standard error from the CIs.

## 8.1 Example of Calculating Confidence Intervals Using Published Prevalence Estimates and Standard Errors

The following example illustrates how to determine the 95 percent CI using the prevalence estimates and standard errors provided for measures shown in the detailed tables and mental health detailed tables. This example will use estimates from Table 1.1B of the 2014 detailed tables (Center for Behavioral Health Statistics and Quality, 2015b), which displays the prevalence for lifetime, past year, and past month illicit drug use. This example will focus on 2014 past year pain reliever use. Pain reliever use shown in Table 1.1B has a prevalence rate of 3.9 percent in 2014. The corresponding standard error shown in Table 1.1D is 0.10 percent for 2014. This example uses the formulas shown above to determine the 95 percent CI for the prevalence rate of past year pain reliever use in 2014. Note that

$$\text{var}(\hat{p}_d) = (SE(\hat{p}_d))^2; \textit{thus}, \sqrt{\text{var}(\hat{p}_d)} = SE(\hat{p}_d).$$

Define log odds estimate:

$$\hat{L} = \ln[0.039/(1-0.039)] = 3.2044$$

Define the upper and lower confidence limits of the log odds:

$$A = -3.2044 - 1.96\left[\frac{0.0010}{0.0375}\right] = -3.2567$$

$$B = -3.2044 + 1.96\left[\frac{0.0010}{0.0375}\right] = -3.1521$$

Apply inverse logit transformation to yield CIs $p$:

$$\hat{p}_{d,lower} = \frac{1}{1+\exp(3.2567)} = 0.0371$$

$$\hat{p}_{d,upper} = \frac{1}{1+\exp(3.1521)} = 0.0410$$

Rounding to two significant digits, the 95 percent CI is 3.7 percent to 4.1 percent.

The same CI calculated using SUDAAN® is also 3.7 percent to 4.1 percent, but note that the reduced number of significant digits shown in the published estimates may sometimes cause rounding errors when producing CIs. However, the results are usually close. Producing the CIs for totals requires the weighted sum, which is generally not published. For examples using SUDAAN or Stata® to calculate CIs for means and totals, see Exhibits A.21 and A.22, respectively.

## 8.2 Example of Calculating Confidence Intervals in Excel Using Published Prevalence Estimates and Standard Errors

Using the same estimates presented in Section 8.1, this example uses Excel functions to produce the same CIs produced in the previous example. Recall that $\text{var}(\hat{p}_d) = (\text{SE}(\hat{p}_d))^2$; thus, $\sqrt{\text{var}(\hat{p}_d)} = \text{SE}(\hat{p}_d)$. Excel can be used to set up a simple table (shown below) to produce the CI. Cells A2 through D2 are the known values input by the user. Cells E2 and F2 contain functions. This table could extend over several rows to aid in producing many CIs (i.e., data for columns A through D would have to be entered for each row, and then the formulas in columns E and F could be copied for all rows).

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | $p_d$ | SE($p_d$) | α | *df* | $p_{d,lower}$ | $p_{d,upper}$ |
| 2 | 0.039 | 0.0010 | 0.05 | 750 | 0.0371 | 0.0410 |

The lower confidence limit is determined using the extended formula for $\hat{p}_{d,lower}$.

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | $p_d$ | SE($p_d$) | α | *df* | $p_{d,lower}$ | $p_{d,upper}$ |
| 2 | 0.039 | 0.0010 | 0.05 | 750 | =1/(1+EXP(-(LN(A2/(1-A2)) - T.INV.2T(C2,D2)*(B2/(A2*(1-A2))))))) | 0.0410 |

The upper limit is determined using the extended formula for $\hat{p}_{d,upper}$.

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | $p_d$ | SE($p_d$) | α | *df* | $p_{d,lower}$ | $p_{d,upper}$ |
| 2 | 0.039 | 0.0010 | 0.05 | 750 | 0.0371 | =1/(1+EXP(-(LN(A2/(1-A2)) + T.INV.2T(C2,D2)*(B2/(A2*(1-A2))))))) |

The 95 percent CI is 3.7 percent to 4.1 percent.

In the Excel formulas for $\hat{p}_{d,lower}$ and $\hat{p}_{d,upper}$, the Excel function T.INV.2T calculates the inverse of the two-tailed Student's *T*-Distribution, a continuous probability distribution. The function arguments are T.INV.2T (probability, *df*), where probability is the probability (between 0 and 1) for which you want to evaluate the inverse of the two-tailed Student's *T*-Distribution. This is also sometimes referred to as the alpha level. For 95 percent CIs, the alpha level is always 0.05. The example uses 750 *df* for a national estimate, but this could be adjusted for smaller areas of estimation.

## 8.3 Example of Calculating Standard Errors Using Published Confidence Intervals

This example illustrates how to determine the standard error for an estimate when only the prevalence and 95 percent CI are provided. If a NSDUH publication provided only the prevalence rate for 2014 past year pain reliever use (3.9 percent) and the 95 percent CI (3.7 percent to 4.1 percent), the reader may want to determine the standard error for use in

significance testing. This example uses the formulas above to determine the standard error for the prevalence rate of past year pain reliever use in 2014. Note that

$$\text{var}(\hat{p}_d) = (\text{SE}(\hat{p}_d))^2; \text{ thus, } \sqrt{\text{var}(\hat{p}_d)} = \text{SE}(\hat{p}_d).$$

Following is the formula to calculate A (lower CI for log odds estimate) using the lower CI of the prevalence rate ($p$).

$$\hat{p}_{d,lower} = \frac{1}{1+\exp(-A)}; \text{ thus, } A = \ln\left(\frac{\hat{p}_{d,lower}}{1-\hat{p}_{d,lower}}\right).$$

$$\text{Ln}\left(\frac{0.037}{1-0.037}\right) = -3.2591$$

Below is the formula for A (lower limit of the log odds ratio. To get the standard error, convert this formula as follows.

$$\text{A} = \hat{\text{L}} - \text{K}\left[\frac{\sqrt{\text{var}(\hat{\text{p}}_\text{d})}}{\hat{\text{p}}_\text{d}(1-\hat{\text{p}}_\text{d})}\right]; \textit{thus}, SE(\hat{\text{p}}_\text{d}) = \frac{(\text{A}-\hat{\text{L}})(\hat{\text{p}}_\text{d}(1-\hat{\text{p}}_\text{d}))}{-\text{K}}.$$

Recall from the Section 8.1 example that $\hat{\text{L}} = -3.2044$. Thus, the standard error is computed as follows:

$$SE(\hat{P}_d) = \frac{(-3.2591+3.2044)(0.039(1-0.039))}{-1.96} = 0.0010 \text{ or } 0.10\%$$

Using similar steps, the standard error can be produced from the upper CI with the formulas below. Note that the denominator is positive in the standard error formula when using the upper CI.

$$\text{B} = \ln\left(\frac{\hat{\text{p}}_{\text{d,upper}}}{1-\hat{\text{p}}_{\text{d,upper}}}\right) \textit{ and } SE(\hat{\text{p}}_\text{d}) = \frac{(\text{B}-\hat{\text{L}})(\hat{\text{p}}_\text{d}(1-\hat{\text{p}}_\text{d}))}{\text{K}}$$

$$\text{B} = -3.1523 \text{ and } SE\left(\hat{\text{p}}_\text{d}\right) = 0.0010, \text{ or } 0.10 \text{ percent}$$

As previously mentioned, Table 1.1D shows that the actual standard error when calculated in SUDAAN is 0.10 percent, which is the same as the calculated 0.10 percent. Note that the reduced number of significant digits shown in the published estimates may cause rounding errors when producing standard errors from the lower or upper limits of the CIs. This can result in standard error estimates that differ when compared with the SUDAAN-calculated standard error. However, standard errors calculated from the lower or upper limits usually will provide the same testing results as tests performed in SUDAAN, except results may differ when the $p$ value is close to the predetermined level of significance.

## 8.4 Example of Calculating Standard Errors in Excel Using Published Confidence Intervals

Using the same estimates presented in Section 8.3, this example uses Excel functions to produce the same standard errors from the previous example (i.e., the SUDAAN-generated standard error from Table 1.1D). Recall that $\text{var}(\hat{p}_d) = (\text{SE}(\hat{p}_d))^2$; thus, $\sqrt{\text{var}(\hat{p}_d)} = \text{SE}(\hat{p}_d)$. Excel can be used to set up a simple table (shown below) to produce the standard error from the upper and lower limits of the CI. Cells A2 through D2 are the known values input by the user. Cell E2 contains the function to determine the standard error. This table could extend over several rows to aid in producing many standard errors (i.e., data for columns A through D would have to be entered for each row, and then the formula in column E could be copied for all rows). Note that once the methods used in this example have determined the standard error from the CI, the methods shown in the Section 7.2 example can be used to perform independent *t* tests for differences of reported estimates in Excel.

Calculate the standard error from the lower limit of the CI:

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | $p_d$ | $p_{d,lower}$ | α | *df* | $SE(p_d)$ |
| 2 | 0.039 | 0.037 | 0.05 | 750 | 0.001 |

$\text{SE}(\hat{p}_d) = 0.0010$, or 0.10 percent

Similar to the Section 8.2 example, the Excel function T.INV.2T is used in the formula to determine the standard error.

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | $p_d$ | $p_{d,lower}$ | α | *df* | $SE(p_d)$ |
| 2 | 0.039 | 0.037 | 0.05 | 750 | =(((LN(B2/(1-B2)))-(LN(A2/(1-A2))))*(A2*(1-A2)))/(-T.INV.2T(C2,D2)) |

Calculate the standard error from the upper limit of the CI:

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | $p_d$ | $p_{d,upper}$ | α | *df* | $SE(p_d)$ |
| 2 | 0.039 | 0.041 | 0.05 | 750 | 0.0010 |

$\text{SE}(\hat{p}_d) = 0.0010$, or 0.10 percent.

This also requires the use of the Excel function T.INV.2T (see details in Section 8.2).

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | $p_d$ | $p_{d,upper}$ | α | *df* | $SE(p_d)$ |
| 2 | 0.039 | 0.041 | 0.05 | 750 | =(((LN(B2/(1-B2)))-(LN(A2/(1-A2))))*(A2*(1-A2)))/(T.INV.2T(C2,D2)) |

Remember that the reduced number of significant digits shown in the published estimates may cause rounding errors when producing standard errors. This can result in standard error estimates that differ when using the lower or upper limit when compared with the SUDAAN-calculated standard error. However, standard errors calculated from the lower or upper limits usually will provide the same testing results as tests performed in SUDAAN, except results may differ when the *p* value is close to the predetermined level of significance.

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# 9. Incidence Estimates

In epidemiological studies, incidence is defined as the number of new cases of a disease occurring within a specific period of time. Similarly, in substance use studies, incidence refers to the first use of a particular substance.

Starting with the 2004 National Survey on Drug Use and Health (NSDUH) data, the evaluation of trends in the initiation of drug use was presented by estimates of past year drug use incidence or initiation (i.e., the number of users whose first use was within the 12 months before their interview date). This incidence measure, termed "past year initiation," is determined by self-reported past year use, age at first use, year and month of most recent new use, and the interview date.

Since 1999, the NSDUH questionnaire allowed for the collection of year and month of first use for recent initiates (i.e., people who used a particular substance for the first time in a given survey year). Month, day, and year of birth also were obtained directly or imputed for item nonrespondents as part of the data processing. In addition, the questionnaire call record provided the date of the interview. By imputing a day of first use within the year and month of first use, a specific date of first use, $(\text{MM/DD/YYYY})_{\text{First Use of Substance}}$, can be used for estimation purposes.

Past year initiation among people using a substance in the past year can be viewed as an indicator variable defined as follows:

$$I_{(\text{Past Year Initiate})} \text{ if } [(\text{MM/DD/YYYY})_{\text{Interview}} - (\text{MM/DD/YYYY})_{\text{First Use of Substance}}] \leq 365,$$

where $(\text{MM/DD/YYYY})_{\text{Interview}}$ denotes the month, day, and year of the interview, and $(\text{MM/DD/YYYY})_{\text{First Use of Substance}}$ denotes the date of first use.

Note that the 12-month reference period (i.e., 365 days) is set up on the calendar at the beginning of the audio computer-assisted self-interviewing portion of the computer-assisted interview. For example, if the date of the interview (DOI) is December 1, 2014 (12/01/2014), then 365 days earlier would be December 1, 2013 (12/01/2013). If a respondent's date of first use is the same as the DOI, then the respondent is considered a past year initiate (because I = 0). Additionally, in this example, a respondent interviewed on 12/01/2014 could have used for the first time as far back as 12/01/2013 and be considered a past year initiate.

The calculation of past year initiation does not take into account whether the respondent initiated substance use while a resident of the United States. This method of calculation has little effect on past year estimates and provides direct comparability with other standard measures of substance use because the populations of interest for the measures will be the same (i.e., both measures examine all possible respondents and do not restrict to those only initiating substance use in the United States).

One important note for incidence estimates is the relationship between a main substance category and subcategories of substances (e.g., illicit drugs would be a main category, and

inhalants and marijuana would be examples of subcategories in relation to illicit drugs). For most measures of substance use, any member of a subcategory is by necessity a member of the main category (e.g., if a respondent is a past month user of a particular drug, then he or she is also a past month user of illicit drugs in general). However, this is not the case with regard to incidence statistics. Because an individual can only be an initiate of a particular substance category (main or sub) a single time, a respondent with lifetime use of a subcategory may not, by necessity, be included as an initiate of the corresponding main category, even if he or she were an initiate for a different subcategory.

In addition to estimates of the number of people initiating use of a substance in the past year, estimates of the mean age of past year first-time users of these substances were computed. Unless specified otherwise, estimates of the mean age at initiation in the past 12 months have been restricted to people aged 12 to 49 so that the mean age estimates reported are not influenced by those few respondents who were past year initiates at age 50 or older. As a measure of central tendency, means are influenced heavily by the presence of extreme values in the data, and this constraint should increase the utility of these results to health researchers and analysts by providing a better picture of the substance use initiation behaviors among the civilian, noninstitutionalized population in the United States. This constraint was applied only to estimates of mean age at first use and does not affect estimates of incidence.

Because NSDUH is a survey of people aged 12 or older at the time of the interview, younger individuals (under 12 years of age) in the sample dwelling units are not eligible for selection into the NSDUH sample. Some of these younger people may have initiated substance use during the past year. As a result, past year initiate estimates suffer from undercoverage when one can think of the estimates as reflecting all initial users regardless of current age. For earlier years, data can be obtained retrospectively based on the age at and date of first use. As an example, people who were 12 years old on the date of their interview in the 2014 survey may have reported initiating use of cigarettes between 1 and 2 years ago; these people would have been past year initiates reported in the 2013 survey had people who were 11 years old on the date of the 2013 interview been allowed to participate in the survey. Similarly, estimates of past year use by younger people (aged 10 or younger) can be derived from the current survey, but they apply to initiation in prior years—not the survey year.

To get a rough estimate of the potential undercoverage of individuals younger than 12 years in the current year, reports of substance use initiation reported in 2014 by people aged 12 or older were estimated for the years in which these people would have been 1 to 11 years younger. These estimates do not necessarily reflect behavior by people who were 1 to 11 years younger in 2014. Instead, the data for the 11-year-olds reflect initiation in the year before the 2014 survey, the data for the 10-year-olds reflect behavior between the 12th and 23rd month before the 2014 survey, and so on. A crude way to adjust for the difference in the years that the estimate pertains to without considering changes to the population is to apply an adjustment factor to each age-based estimate of past year initiates. The adjustment factor can be based on a ratio of lifetime users aged 12 to 17 in 2014 to the same estimates for the prior applicable survey year. To illustrate the calculation, consider past year use of alcohol. In the 2014 survey, 58,041 people who were 12 years old were estimated to have initiated use of alcohol between 1 and 2 years earlier. These people would have been past year initiates in the 2013 survey conducted on the same dates had the 2013 survey covered younger people. The estimated number of lifetime

users currently aged 12 to 17 was 7,375,125 for 2014 and 7,669,220 for 2013, indicating fewer overall initiates of alcohol use among people aged 17 or younger in 2014. Thus, an adjusted estimate of initiation of alcohol use by people who were 11 years old in 2014 is given by

$$(\text{Estimated Past Year Initiates Aged } 11)_{2013} \times \frac{(\text{Estimated Lifetime Users Aged } 12 \text{ to } 17)_{2014}}{(\text{Estimated Lifetime Users Aged } 12 \text{ to } 17)_{2013}}$$

This yielded an adjusted estimate of 55,815 people who were 11 years old on a 2014 survey date and initiated use of alcohol in the past year:

$$58,041 \times \frac{7,375,125}{7,669,220} = 55,815$$

A similar procedure was used to adjust the estimated number of past year initiates among 2014 respondents who would have been 10 years old on the same month and day of the month as the interview date in 2012. This is applied similarly for younger people in earlier years. The overall adjusted estimate for past year initiates of alcohol use by people aged 11 or younger on the date of the interview was 112,059, or about 2.4 percent of the estimate based on past year initiation by people aged 12 or older only (112,059 ÷ 4,655,448 = 0.0241). Based on similar analyses, the estimated undercoverage of past year initiates was 2.7 percent for cigarettes, 0.7 percent for marijuana, and 19.7 percent for inhalants.

The undercoverage of past year initiates aged 11 or younger also affects the mean age-at-first-use estimate. An adjusted estimate of the mean age at first use was calculated using a weighted estimate of the mean age at first use based on the current survey and the numbers of people aged 11 or younger in the past year obtained in the aforementioned analysis for estimating undercoverage of past year initiates. Analysis results showed that the mean age at first use was changed from 17.3 to 17.1 for alcohol, from 18.6 to 18.3 for cigarettes, from 18.5 to 18.4 for marijuana, and from 18.2 to 16.5 for inhalants. The decreases reported above are comparable with results generated in prior survey years.

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# 10. Suppression of Estimates with Low Precision

Direct survey estimates that were considered to be unreliable because of unacceptably large sampling errors were not reported, but rather were noted by an asterisk (*). The criteria used to assess the need to suppress direct survey estimates were based on prevalence (for proportion estimates), the relative standard error (RSE) (defined as the ratio of the standard error [SE] over the estimate), nominal (actual) sample size, and effective sample size for each estimate.

Proportion estimates ( $\hat{p}$ ), or rates, within the range $0 < \hat{p} < 1$, and corresponding estimated numbers of users were suppressed if

$$\text{RSE}[-\ln(\hat{p})] > .175 \text{ when } \hat{p} \leq .5$$

or

$$\text{RSE}[-\ln(1-\hat{p})] > .175 \text{ when } \hat{p} > .5 .$$

The choice of .175 is arbitrary, but it roughly marks the tails of the distribution.

Based on a first-order Taylor series approximation of $\text{RSE}[-\ln(\hat{p})]$ and $\text{RSE}[-\ln(1-\hat{p})]$, the following equation was derived and used for computational purposes when applying a suppression rule dependent on effective sample sizes:

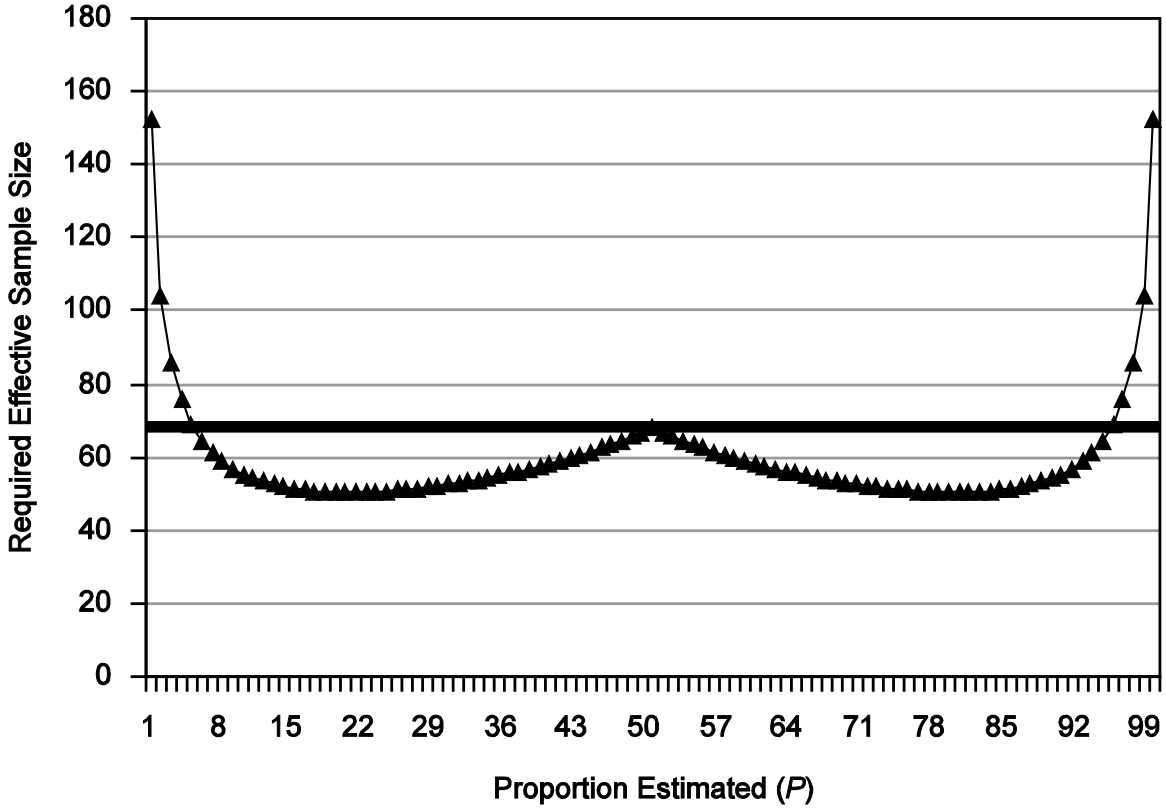
$$\frac{\text{SE}(\hat{p})/\hat{p}}{-\ln(\hat{p})} > .175 \text{ when } \hat{p} \leq .5,$$

or

$$\frac{\text{SE}(\hat{p})/(1-\hat{p})}{-\ln(1-\hat{p})} > .175 \text{ when } \hat{p} > .5 .$$

The separate formulas for $\hat{p} \leq .5$ and $\hat{p} > .5$ produce a symmetric suppression rule; that is, if $\hat{p}$ is suppressed, $1-\hat{p}$ will be suppressed as well. See Figure 10.1 for a graphical representation of the required minimum effective sample sizes as a function of the proportion estimated. When $.05 < \hat{p} < .95$, the symmetric properties of the rule produce local minimum effective sample sizes at $\hat{p} = .2$ and again at $\hat{p} = .8$, such that an effective sample size of greater than 50 is required; this means that estimates would be suppressed for these values of $\hat{p}$ unless the effective sample sizes were greater than 50. Within this same interval of $.05 < \hat{p} < .95$, a local maximum effective sample size of 68 is required at $\hat{p} = .5$.

**Figure 10.1 Required Effective Sample in the 2014 NSDUH as a Function of the Proportion Estimated**




These varying effective sample size requirements sometimes produced unusual occurrences of suppression for a particular combination of prevalence rates. For example, in some cases, lifetime prevalence rates near $\hat{p}$ = .5 were suppressed (effective sample size was less than 68 but greater than 50), while not suppressing the corresponding past year or past month estimates near $\hat{p}$ = .2 (effective sample sizes greater than 50). To reduce the occurrence of this type of inconsistency and to maintain a conservative suppression rule, estimates of $\hat{p}$ between .05 and .95, which had effective sample sizes below 68, were suppressed starting with the 2000 National Survey on Drug Use and Health (NSDUH).

The effective sample size for a domain is a function of the nominal sample size and the design effect (i.e., nominal sample size/design effect). During the original development of this suppression rule, the design effect was calculated outside SUDAAN® (RTI International, 2012) in SAS®. Since the 2005 NSDUH analysis, the direct SUDAAN design effect was used to provide a more precise and accurate reflection of the design effect (due to the removal of several possible rounding errors) when compared with the SAS method used in the past. The differences between the direct SUDAAN design effects and the SAS-calculated design effects occur only at approximately the tenth decimal place or later; however, previously published estimates that were on the borderline of being suppressed or unsuppressed due to the effective sample size suppression rule may potentially change from suppressed to unsuppressed, or vice versa.

Design effects range widely among the measures and domains found in the detailed tables and mental health detailed tables. Potential problems with suppression only occur if large design effects are combined with small domains. Large estimates of design effects when resulting from small sample sizes (variability of the variance estimate) should be suppressed on sample size alone, and the current rule achieves this. But to protect against unreliable estimates caused by small design effects and small nominal sample sizes, a minimum nominal sample size suppression criterion ($n$ = 100) was employed starting with the 2000 NSDUH. Table 10.1 shows a formula for calculating design effects. Prevalence estimates also were suppressed if they were close to 0 or 100 percent (i.e., if $\hat{p} < .00005$ or if $\hat{p} \geq .99995$).

**Table 10.1 Summary of 2014 NSDUH Suppression Rules**

| Estimate | Suppress if: |
|---|---|
| Prevalence Rate, $\hat{p}$, with Nominal Sample Size, $n$, and Design Effect, *deff* $\left( deff = \frac{n[\mathrm{SE}(\hat{p})]^2}{\hat{p}(1-\hat{p})} \right)$ | (1) The estimated prevalence rate, $\hat{p}$, is < 0.00005 or ≥ 0.99995, or<br>(2) $\frac{\mathrm{SE}(\hat{p}) \ / \ \hat{p}}{-\ln(\hat{p})} > 0.175$ when $\hat{p} \leq 0.5$, or<br>$\frac{\mathrm{SE}(\hat{p}) \ / \ (1-\hat{p})}{-\ln(1-\hat{p})} > .175$ when $\hat{p} > 0.5$, or<br>(3) Effective $n$ < 68, where $Effective\ n = \frac{n}{deff} = \frac{\hat{p}(1-\hat{p})}{\left[\mathrm{SE}(\hat{p})\right]^2}$, or<br>(4) $n$ < 100.<br>Note: The rounding portion of this suppression rule for prevalence rates will produce some estimates that round at one decimal place to 0.0 or 100.0 percent but are not suppressed from the tables.[1] |
| Estimated Number (Numerator of $\hat{p}$) | The estimated prevalence rate, $\hat{p}$, is suppressed.<br>Note: In some instances when $\hat{p}$ is not suppressed, the estimated number may appear as a 0 in the tables. This means that the estimate is greater than 0 but less than 500 (estimated numbers are shown in thousands).<br>Note: In some instances when totals corresponding to several different means that are displayed in the same table and some, but not all, of those means are suppressed, the totals will not be suppressed. When all means are suppressed, the totals will also be suppressed. |
| Means not bounded between 0 and 1 (i.e., Mean Age at First Use, Mean Number of Drinks), $\bar{x}$, with Nominal Sample Size, $n$ | (1) $\mathrm{RSE}(\bar{x}) > 0.5$, or<br>(2) $n$ < 10. |

*deff* = design effect; RSE = relative standard error; SE = standard error.

[1] See Sections 3 and 7 of this report for more information on rounding.

Source: SAMHSA, Center for Behavioral Health Statistics and Quality, National Survey on Drug Use and Health, 2014.

Beginning with the 1991 survey, the suppression rule for proportions based on $\mathrm{RSE}[-\ln(\hat{p})]$ described above replaced an older rule in which data were suppressed whenever

RSE( $\hat{p}$ ) > .5. This rule was changed because the older rule imposed a very stringent application for small $\hat{p}$, but a very lax application for large $\hat{p}$. The new rule ensured a more uniformly stringent application across the whole range of $\hat{p}$ (i.e., from 0 to 1). The old rule also was asymmetric in the sense that suppression only occurred in terms of $\hat{p}$; that is, there was no complementary rule for (1 – $\hat{p}$), which the new suppression rules now account for.

Estimates of totals were suppressed if the corresponding prevalence rates were suppressed. Estimates of means not bounded between 0 and 1 (e.g., mean age at first use, mean number of drinks consumed) were suppressed if the RSEs of the estimates were larger than .5 or if the sample sizes were smaller than 10 respondents. This rule was based on an empirical examination of the estimates of mean age of first use and their SEs for various empirical sample sizes. Although arbitrary, a sample size of 10 appears to provide sufficient precision and still allow reporting by year of first use for many substances. In these cases, the totals (e.g., total number of drinks consumed) were suppressed if the corresponding mean estimates were suppressed.

Section 4 of the detailed tables demonstrates an exception to the rule that indicates the totals are suppressed when their corresponding means are suppressed. Some tables in Section 4 of the detailed tables show estimates of incidence among different populations. Specifically, these Section 4 tables display the number of initiates among three different populations: the total population, people at risk for initiation, and past year users. In these tables, some mean estimates may be suppressed while the total estimate is not suppressed. When at least one mean estimate in the table is not suppressed, one can assume that the numerator (or total estimate) is not the cause for the suppression and the total estimate will not be suppressed. In contrast, when all mean estimates are suppressed, the total will also be suppressed.

Tables that show sample sizes and population counts do not incorporate the suppression rule for several reasons. One reason is that no mean is associated with these estimates; thus, most of the components of the suppression criteria are not applicable. Also, because no behavior associated with the numbers is displayed, there is no risk of behavior disclosure.

The suppression criteria for various NSDUH estimates are summarized in Table 10.1, and sample SAS and Stata® code demonstrating how to implement these rules can be found in Appendix A (Exhibits A.5 and A.6).

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# Appendix A: Documentation for Conducting Various Statistical Procedures: SAS®, SUDAAN®, and Stata® Examples

This appendix provides guidance concerning various options that should be specified in both SUDAAN® and Stata® to correctly analyze the National Survey on Drug Use and Health (NSDUH) data. Additionally, example SAS®, SUDAAN® Software for Statistical Analysis of Correlated Data (RTI International, 2012), and Stata code is provided to illustrate how the information in this report is applied to generate estimates (means, totals, and percentages along with the standard errors [SEs]), implement the suppression rule, perform statistical tests of differences, handle missing data, calculate confidence intervals, test between overlapping domains, test independence of two variables, perform pairwise tests, and perform linear trend tests. Specifically, the examples produce estimates of past month alcohol use by year (2013 and 2014) and gender (males and females) using the statistical procedures documented within this report and implemented in the 2014 detailed tables (Center for Behavioral Health Statistics and Quality [CBHSQ], 2015b) and the 2014 mental health detailed tables (CBHSQ, 2015c). The examples below are created using variable names found on the restricted-use dataset; thus, some variable names may differ when using the public use file (see footnote 3 for more detail). Note that all the detailed tables and mental health detailed tables are produced using SAS and SUDAAN code. However, the Stata code below replicates results from these tables. The exhibit number for each example, a description of the example, and a reference to the report section that addresses the example are provided in Table A.1.

**Table A.1 Summary of SAS, SUDAAN, and Stata Exhibits**

| SAS/SUDAAN Exhibit | Stata Exhibit | Description | Report Section |
|---|---|---|---|
| A.1 | A.2 | Produces estimates (including means, totals, and the respective standard errors). | Sections 3, 5, and 6 |
| A.3 | A.4 | Calculates the standard error of the total for controlled domains using the estimates produced in Exhibits A.1 and A.2. | Section 5 |
| A.5 | A.6 | Creates suppression indicators for each estimate (i.e., suppression rule). | Section 10 |
| A.7 | A.8 | Performs statistical tests of differences between means. | Section 7 |
| A.9 | A.10 | Calculates the *p* value for the test of differences between uncontrolled totals (using estimates produced in Exhibits A.7 and A.8). | Section 7 |
| A.11, A.13, A.15, and A.17 | A.12, A.14, A.16, and A.18 | Calculates the *p* value for the test of differences between controlled domains by producing the covariance matrix, pulling the relevant covariance components, and calculating the variances. | Section 7 |
| A.19 | A.20 | Produces estimates where the variable of interest has missing values. | Section 4 |
| A.21 | A.22 | Calculates a confidence interval using estimates produced in Exhibits A.1 and A.2. | Section 8 |

**Table A.1 Summary of SAS, SUDAAN, and Stata Exhibits (continued)**

| SAS/SUDAAN Exhibit | Stata Exhibit | Description | Report Section |
|---|---|---|---|
| A.23 | A.24 | Calculates percentages and the associated standard errors. | Sections 3 and 5 |
| A.25 | A.26 | Performs statistical tests of differences between two groups when the two groups overlap. | Section 7 |
| A.27 | A.28 | Performs tests of the independence of the prevalence variable and subgroup variable. | Section 7 |
| A.29 | A.30 | Performs pairwise tests for each subgroup variable found significant in Exhibits A.27 and A.28. | Section 7 |
| A.31 | A.32 | Performs linear trend test of significance across years using test statements. | Section 7 |
| A.33 | A.34 | Performs linear trend test of significance across years using modeling. | Section 7 |

## Guide for Defining Options for Analyzing NSDUH Data

Before running the SUDAAN procedures, the input dataset must be sorted by the nesting variables (VESTR and VEREP), or the NOTSORTED option must be used for SUDAAN to create an internal copy of the input dataset properly sorted by the nesting variables. The SUDAAN procedure DESCRIPT can then be run to produce weighted (using ANALWT for restricted use and ANALWT_C for public use files) and unweighted sample sizes, means, totals, SEs of means and totals, and *p* values for testing of the means and totals.

Stata commands can be run without the data being sorted. The Stata commands svy: mean and svy: total will be used throughout in these exhibits (note that Stata still uses VESTR and VEREP, but the data do not need to be sorted).

The following options are specified within the SUDAAN and Stata examples to correctly produce estimates using NSDUH data.

### Design

Because of the NSDUH sample design, estimates are calculated using a method in SUDAAN that is unbiased for linear statistics. This method is based on multistage clustered sample designs where the first-stage (primary) sampling units are drawn with replacement. In SUDAAN, a user must specify DESIGN=WR (meaning with replacement). Note that with Stata, the design does not need to be indicated, because the svyset command uses Taylor linearized variance estimation as a default.

### Nesting Variables

The nesting variables (VESTR and VEREP) are used to capture explicit stratification and to identify clustering with the NSDUH data, which are needed to compute the variance estimates correctly. Two replicates per year were defined within each variance stratum (VESTR). Each variance replicate (VEREP) consists of four segments, one for each quarter of data collection. One replicate consists of those segments that are "phasing out" or will not be used in the next

survey year. The other replicate consists of those segments that are "phasing in" or will be fielded again the following year, thus constituting the 50 percent overlap between survey years. A segment stays in the same VEREP for the 2 years it is in the sample. This simplifies computing SEs for estimates based on combined data from adjacent survey years. In SUDAAN, users must use the NEST statement within one of the appropriate SUDAAN procedures. In the NEST statement, the variable for the variance stratum should be listed first, followed by the primary sampling unit variable; that is, the VESTR variable should be listed first, followed by the VEREP variable. In Stata, the nesting variables are specified in the svyset command. Unlike the svyset command in Stata, the NEST statement will need to be used each time a user calls one of the appropriate SUDAAN procedures.

**Degrees of Freedom**

As described in Section 6 of this report, the degrees of freedom (DDF in SUDAAN and dof in Stata) are 750 for the 2014 national estimates, 144 in California; 120 each in Florida, New York, and Texas; 96 each in Illinois, Michigan, Ohio, and Pennsylvania; 60 each in Georgia, New Jersey, North Carolina, and Virginia; and 48 each in the remaining 38 states and the District of Columbia. For an analysis of a group of states, the degrees of freedom can be less than or equal to the sum of the degrees of freedom for each individual state due to overlap of variance strata. The specific number of degrees of freedom can be computed by counting the unique values of VESTR for the particular geographic area of interest. The technique of counting the number of unique values of VESTR can also be used for analyses combining survey data across years. When combining any years of data from 2005 through 2013, the degrees of freedom remain the same as if it were a single year (e.g., 750 for national estimates) because these years are part of the same sample design. When comparing estimates in two domains with different degrees of freedom, err on the conservative side and use the smaller degrees of freedom. To specify the degrees of freedom in SUDAAN, the DDF = option on the procedure statement is used. This option should be used each time one of the appropriate SUDAAN procedures is called to ensure correct calculations. In Stata, the degrees of freedom are specified as a design option in the svyset command (i.e., "dof(750)"). If switching from national estimates to state estimates, the svyset command would need to be rerun with the updated degrees of freedom. More information about which degrees of freedom to use can be found in Section 6.

**Design Effect**

The option DEFT4 within SUDAAN provides the correct measure of variance inflation due to stratification (or blocking), clustering, and unequal weighting in NSDUH estimation. Requesting deff srssubpop in Stata gives the same result as using DEFT4 in SUDAAN.

The following SAS, SUDAAN, and Stata examples apply the specific NSDUH options described previously to compute estimates, apply the suppression rule, and perform significance testing by using the data produced by the examples in Exhibit A.1 (using SUDAAN code) and Exhibit A.2 (using Stata code).

## Generation of Estimates

Exhibits A.1 and A.2 demonstrate how to compute various types of estimates for past month alcohol use by year and gender using the SUDAAN descript procedure and the Stata svy: mean and svy: total commands, respectively. The SUDAAN example includes code to compute the prevalence estimate (MEAN), SE of the mean (SEMEAN), weighted sample size (WSUM), unweighted sample size (NSUM), weighted total (TOTAL), and SE of the totals (SETOTAL). The Stata svy: mean and svy: total commands will produce the same estimates. Whether the SETOTAL is taken directly from SUDAAN or Stata depends on whether the specified domain (i.e., gender in this example) is among those forced to match their respective U.S. Census Bureau population estimates through the weight calibration process. See the Standard Errors section below for additional information.

**Exhibit A.1 SUDAAN DESCRIPT Procedure (Estimate Generation)**

```
PROC SORT DATA=DATANAME; /*SAS code to sort output dataset by
Nesting Variables*/
BY VESTR VEREP;
RUN;
PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS DEFT4;
NEST VESTR VEREP;
WEIGHT ANALWT;   /*Standard single-year, person-level analysis
weight*/

VAR ALCMON;   /*Past month alcohol analysis variable*/
SUBGROUP YEAR IRSEX;
     /*Year variable, where 2013=1 & 2014=2*/
     /*Gender variable, where male=1 & female=2*/
LEVELS 2 2;
TABLES YEAR*IRSEX; /*Gender by year*/

PRINT WSUM NSUM MEAN SEMEAN TOTAL SETOTAL / REPLACE STYLE=NCHS;
OUTPUT WSUM MEAN SEMEAN TOTAL SETOTAL NSUM DEFFMEAN /REPLACE
   NSUMFMT=F8.0 WSUMFMT=F12.0 MEANFMT=F15.10 SEMEANFMT=F15.10
   DEFFMEANFMT=F15.10 TOTALFMT=F12.0 SETOTALFMT=F12.0
   FILENAME="OUT.SUDFILE";
TITLE "ESTIMATES OF PAST MONTH ALCOHOL BY YEAR AND GENDER";
RUN;
```

```
Note: The following CLASS statement could be used in place of SUBGROUP
and LEVELS statements in the above example:
     CLASS YEAR IRSEX;
```

**Exhibit A.2 Stata COMMANDS svy: mean and svy: total (Estimate Generation)**

```
use using ".\\dataname.dta", clear

/*Ensure all variables are lower case*/
rename *, lower

/*ID Nesting variables (VESTR and VEREP) and weight variable (ANALWT -
standard single-year, person-level analysis weight*/
svyset verep [pw=analwt], strata(vestr) dof(750)

gen total_out=.
gen setotal=.
gen mean_out=.
gen semean=.
gen nsum=.
gen wsum=.
gen deffmean=.

/*Estimated means of past month alcohol use by year and gender*/

  /*Year variable, where 2013=1 & 2014=2*/
  /*Gender variable, where male=1 & female=2*/
svy: mean alcmon, over(year irsex)
matrix M=e(b) /*Store mean estimates in matrix M*/
matrix S=e(V) /*Store variances in matrix S*/
matrix N=e(_N) /*Store sample size in matrix N*/
matrix W=e(_N_subp) /*Store weighted sample size in matrix W*/

estat effects, deff srssubpop/*Obtain design effect*/
matrix D=e(deff) /*Store design effect in matrix D*/

/*Extract values stored in the M, S, N, W, and D matrices defined
above to the mean_out, semean, nsum, wsum, and deffmean variables. The
loop ensures that the appropriate values are extracted for each value
of year and gender.*/
  local counter=1
    forvalues i=1/2 { /*number of years*/
      forvalues j=1/2 { /* number of gender categories*/
        replace mean_out=(M[1,`counter']) if year==`i' & irsex==`j'
        replace semean=(sqrt(S[`counter',`counter'])) ///
if year==`i' & irsex==`j'
        replace nsum=(N[1,`counter']) if year==`i' & irsex==`j'
        replace wsum=(W[1,`counter']) if year==`i' & irsex==`j'
        replace deffmean=(D[1,`counter']) if year==`i' & irsex==`j'
  local counter=`counter'+1
      }
    }
```

**Exhibit A.2 Stata COMMANDS svy: mean and svy: total (Estimate Generation) (continued)**

```
/*Estimated Totals*/
svy: total alcmon, over(year irsex)

  matrix M=e(b) /*Store total estimates in matrix M*/
  matrix S=e(V) /*Store variances in matrix S*/

/*Extract values stored in the M and S matrices defined above to the
total_out and setotal variables. The loop ensures that the appropriate
values are extracted for value of year and gender.*/

  local counter=1
    forvalues i=1/2 { /*number of years*/
      forvalues j=1/2 { /* number of gender categories*/
        replace total_out=(M[1,`counter']) if year==`i' & irsex==`j'
        replace setotal=(sqrt(S[`counter',`counter'])) ///
if year==`i' & irsex==`j'
   local counter=`counter'+1
      }
    }

keep wsum mean_out semean total_out setotal nsum deffmean year irsex

duplicates drop year irsex, force /*keep one record per subpopulation
                                    of interest*/

/*Format wsum, mean_out, semean, total_out, setotal, nsum, and
deffmean variables to control appearance in output.*/

format wsum %-12.0fc
format mean_out %-15.10f
format semean %-15.10f
format total_out %-12.0fc
format setotal %-12.0fc
format nsum %-8.0fc
format deffmean %-15.10f

/*Estimates of past month alcohol by year and gender*/
list year irsex wsum nsum mean_out semean total_out setotal

/*The output from this exhibit will be utilized in Exhibit A.16. Users
can either rerun the code presented in this exhibit or save the output
from this exhibit to a dataset using the following command.*/
save ".\\EXa2.dta" , replace
```

### Standard Errors

As discussed in Section 5 of this report, the SE for the mean (or proportion) comes directly out of SUDAAN in the output variable SEMEAN (Exhibit A.1), and the SEMEAN is calculated in Stata by taking the square root of the variance (Exhibit A.2). However, to compute the SE of the totals, NSDUH implements different methods depending on whether the specified

domain (i.e., gender in this example) is controlled or uncontrolled through poststratification during the weighting process. If a domain is uncontrolled (i.e., it is not one of the domains described in Table 5.1 in Section 5), then the SE of the total comes directly out of SUDAAN in the output variable SETOTAL. If the domain is controlled (i.e., it is one of the domains described in Table 5.1), then the SE of the total is calculated as SETOTAL (SE of controlled domain) = WSUM (weighted sample size) × SEMEAN (SE for the mean/proportion). Because gender is controlled, the SE of the totals would not be taken directly from the examples in Exhibits A.1 and A.2 but rather would be computed using the formula shown in Exhibits A.3 and A.4 (note that the formula is the same in both exhibits) (Exhibits A.1 and A.3 using SUDAAN/SAS code and Exhibits A.2 and A.4 using Stata code).

**Exhibit A.3 SAS Code (Calculation of Standard Error of Totals for Controlled Domains)**

```
DATA ESTIMATE;
SET OUT.SUDFILE; /*input the output file from above SUDAAN
                  procedure*/
/************************************************************
  Define SETOTAL for gender because it is a controlled domain.
   In the SUDAAN procedure in Exhibit A.1, IRSEX is in the
subgroup
     Statement with 2 levels indicated. Therefore, values for
     0=total male & females, 1=males, and 2=females are
     automatically produced.
************************************************************/

IF IRSEX IN (0,1,2) THEN SETOTAL=WSUM*SEMEAN;

RUN;
```

**Exhibit A.4 Stata Code (Calculation of Standard Error of Totals for Controlled Domains)**

```
generate setotal2=wsum*semean
replace setotal = setotal2 if inlist(irsex,1,2)
/*Note, Stata does not automatically produce overall estimates,
i.e., irsex=0*/
```

## Suppression Rule

As described in Section 10 of the report, each published NSDUH estimate goes through a suppression rule to detect if the estimate is unreliable because of an unacceptably large sampling error. The suppression rules as they apply to different types of estimates are shown in Table 10.1 in Section 10. The examples in Exhibits A.5 (SAS code) and A.6 (Stata code) show both the prevalence rate rule and the rule for means not bounded by 0 and 1 (i.e., averages). The average suppression rule is commented out for these examples, but it would replace the prevalence rate suppression rule if averages were shown in the examples in place of means bounded by 0 and 1.

For tables that display totals along with multiple means from differing populations (e.g., incidence tables in Section 4 of the 2014 detailed tables [CBHSQ, 2015b]), suppression is not as straightforward as coding the rule in the SAS/SUDAAN or Stata programs. As discussed in

Section 10, perhaps some means are suppressed and others are not suppressed. In that instance, suppression of the total estimate is based on the level of suppression present across all corresponding mean estimates. If all mean estimates associated with a total estimate are suppressed, the total estimate should also be suppressed. If at least one mean estimate is not suppressed, the total estimate is also not suppressed. The best way to ensure that this happens is to program the total estimate in the table to be suppressed if, and only if, the mean with the largest denominator is suppressed. The analyst should also check the final table to ensure that the suppression follows the rule after the program has been run.

**Exhibit A.5 SAS Code (Implementation of Suppression Rule)**

```
DATA ESTIMATE;
SET OUT.SUDFILE; /*input the output file from above SUDAAN
                  procedure*/

/******APPLY THE PREVALENCE RATE SUPPRESSION RULE*******/

/* CALCULATE THE RELATIVE STANDARD ERROR */
      IF MEAN GT 0.0 THEN RSE=SEMEAN/MEAN;

/* CALCULATE THE RELATIVE STANDARD ERROR OF NATURAL LOG P */
      IF 0.0 LT MEAN LE 0.5 THEN RSELNP=RSE/ABS(LOG(MEAN)); ELSE
      IF 0.5 LT MEAN LT 1.0 THEN
      RSELNP=RSE*(MEAN/(1-MEAN))/(ABS(LOG(1-MEAN)));

/*CALCULATE THE EFFECTIVE SAMPLE SIZE*/
      EFFNSUM=NSUM/DEFFMEAN;

/*SUPPRESSION RULE FOR PREVALENCE RATES*/
IF (MEAN LT .00005) OR (MEAN GE 0.99995) OR (RSELNP GT 0.175) OR
(EFFNSUM < 68) OR (NSUM <100) THEN SUPRULE=1;

/*SUPPRESSION RULE FOR MEANS NOT BOUNDED BY 0 AND 1, I.E.
AVERAGES (COMMENTED OUT FOR THIS EXAMPLE)*/
/*IF (RSELNP GT 0.5) OR (NSUM < 10) THEN SUPRULE=1;*/

RUN;
```

**Exhibit A.6 Stata Code (Implementation of Suppression Rule)**

```
/******APPLY THE PREVALENCE RATE SUPPRESSION RULE*******/

/*CALCULATE THE RELATIVE STANDARD ERROR*/
generate rse=.
replace rse=semean/mean_out ///
if mean_out > 0.0 & !missing(mean_out)
```

**Exhibit A.6 Stata Code (Implementation of Suppression Rule) (continued)**

```
/* CALCULATE THE RELATIVE STANDARD ERROR OF NATURAL LOG P */
generate rselnp=.
replace rselnp=rse/(abs(log(mean_out))) ///
if mean_out <= 0.5 & mean_out > 0.0
replace rselnp=rse*(mean_out/(1-mean_out)) ///
/(abs(log(1-mean_out))) if mean_out < 1.0 & mean_out > 0.5

/*CALCULATE THE EFFECTIVE SAMPLE SIZE*/
generate effnsum=nsum/deffmean

/*SUPPRESSION RULE FOR PREVALENCE RATES*/
generate suprule1a=1 if rselnp > 0.175 & !missing(rselnp)
generate suprule1b=1 if mean_out < .00005 & !missing(mean)
generate suprule1c=1 if mean_out >= .99995 & !missing(mean)
generate suprule2=1 if effnsum < 68 & !missing(nsum)
generate suprule3=1 if nsum < 100 & !missing(nsum)

generate supress=0
replace supress=1 if suprule1a==1 | suprule1b==1 | ///
suprule1c==1 | suprule2==1 | suprule3==1

/*SUPPRESSION RULE FOR MEANS NOT BOUNDED BY 0 AND 1, I.E.
AVERAGES
(COMMENTED OUT FOR THIS EXAMPLE)*/
/*generate suprule=1 if (nsum < 100 & !missing(nsum))///
| (effnsum < 68 & !missing(nsum))*/
```

**Statistical Tests of Differences**

As described in Section 7 of this report, significance tests were conducted on differences of prevalence estimates between the 2014 NSDUH and previous years of NSDUH back to 2002, as well as differences of prevalence estimates between combined 2011–2012 survey data and combined 2013–2014 survey data. Note that for year-to-year tests of differences, if the estimate for either year is suppressed, then the resulting *p* value is also suppressed. This is the rule used when creating the detailed tables and mental health detailed tables; however, this code does not show this rule being implemented.

For the SUDAAN example (Exhibit A.7), testing of differences requires a separate PROC DESCRIPT run from the initial DESCRIPT run that produces the corresponding yearly estimates. Tests of differences can be generated using DESCRIPT's CONTRAST, PAIRWISE, or DIFFVAR statements. The SUDAAN example (Exhibit A.7) uses the DIFFVAR statement to test for differences between the 2013 and 2014 past month alcohol use estimates for all people aged 12 or older (IRSEX=0), all males (IRSEX=1), and all females (IRSEX=2). It also includes an example of using multiple DIFFVAR statements to test for differences between each year (2002–2013) and 2014. Similarly, for the Stata example (Exhibit A.8), a separate svy: mean command is needed.

Similar to computing the SEs of the totals, calculating *p* values for tests of differences of totals differs depending on whether an estimate is considered to be from a controlled domain or an uncontrolled domain. Both ways are described as follows with accompanying example code: Exhibits A.7 and A.9 show example code for uncontrolled domains using SUDAAN and SAS, and Exhibits A.8 and A.10 show the same examples using Stata. Exhibits A.7, A.11, A.13, A.15, and A.17 show example code for controlled domains using SUDAAN and SAS, and Exhibits A.8, A.12, A.14, A.16, and A.18 show the same examples using Stata.

**Exhibit A.7 SUDAAN DESCRIPT Procedure (Tests of Differences)**

```
PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS;
NEST VESTR VEREP;
WEIGHT ANALWT;
VAR ALCMON;
SUBGROUP YEAR IRSEX;
LEVELS 2 2;
TABLES IRSEX;
DIFFVAR YEAR=(1 2); / NAME="2013 vs 2014";
                      PRINT WSUM NSUM MEAN SEMEAN TOTAL SETOTAL
T_MEAN P_MEAN /
   REPLACE STYLE=NCHS;
OUTPUT WSUM MEAN SEMEAN TOTAL SETOTAL NSUM T_MEAN P_MEAN /
    REPLACE
    NSUMFMT=F8.0 WSUMFMT=F12.0 MEANFMT=F15.10 SEMEANFMT=F15.10
    TOTALFMT=F12.0 SETOTALFMT=F12.0 FILENAME="OUT.SUDTESTS";
TITLE "TESTS OF DIFFERENCES BETWEEN 2013 AND 2014 ESTIMATES OF
PAST MONTH ALCOHOL BY GENDER";
RUN;
```

Note: For testing of multiple years vs the current year as shown in Multiyear Detailed Tables, more years could be included in the data (and LEVELS statement) and several DIFFVAR statements as shown below could be used in place of the single DIFFVAR statement in the above example:

```
LEVELS 13 2;
DIFFVAR YEAR=(1 13)  /NAME="2002 vs 2014)";
DIFFVAR YEAR=(2 13)  /NAME="2003 vs 2014)";
DIFFVAR YEAR=(3 13)  /NAME="2004 vs 2014)";
DIFFVAR YEAR=(4 13)  /NAME="2005 vs 2014)";
DIFFVAR YEAR=(5 13)  /NAME="2006 vs 2014)";
DIFFVAR YEAR=(6 13)  /NAME="2007 vs 2014)";
DIFFVAR YEAR=(7 13)  /NAME="2008 vs 2014)";
DIFFVAR YEAR=(8 13)  /NAME="2009 vs 2014)";
DIFFVAR YEAR=(9 13)  /NAME="2010 vs 2014)";
DIFFVAR YEAR=(10 13) /NAME="2011 vs 2014)";
DIFFVAR YEAR=(11 13) /NAME="2012 vs 2014)";
DIFFVAR YEAR=(12 13) /NAME="2013 vs 2014)";

TITLE "TESTS OF DIFFERENCES BETWEEN EACH YEAR AND 2014 ESTIMATES
OF PAST MONTH ALCOHOL BY GENDER";
```

**Exhibit A.7 SUDAAN DESCRIPT Procedure (Tests of Differences) (continued)**

```
Note: The following CLASS statement could be used in place of SUBGROUP
and LEVELS statements in the above examples:
      CLASS YEAR IRSEX;
```

When one or more contrasts are specified in SUDAAN, as in the DIFFVAR statement above, the output variable MEAN becomes the contrast mean where the number assigned to the output variable, CONTRAST, represents the tests in order of appearance in the SAS code, and SEMEAN becomes the SE of the contrast mean. The examples above also output the *t*-statistic (T_MEAN) and the corresponding *p* value (P_MEAN).

SUDAAN does not test differences in the corresponding totals explicitly. However, it will output the contrast total (TOTAL) and the SE of the contrast total (SETOTAL). With these statistics and the correct degrees of freedom (750 in this example), the *p* value (PVALT) for the test of differences between totals for uncontrolled domains can be calculated as indicated in Exhibit A.9. The SAS function PROBT returns the probability from a *t*-distribution.

**Exhibit A.8 Stata COMMANDS svy: mean and svy: total (Tests of Differences)**

```
use using ".\\dataname.dta", clear

/*Ensure all variables are lower case*/
rename *, lower

/*ID Nesting variables (VESTR and VEREP) and weight variable
(ANALWT - standard single-year, person-level analysis weight*/
svyset verep [pweight=analwt], strata(vestr) dof(750)
{
svy: mean alcmon, over(year irsex)
local max=2*2 /*number of years*number of gender categories. This
is the total number of supops*/
local range=2 /*number of gender categories. This is the number
of subpops per year*/
local compmin=`max'-`range'
gen pmean=. /*P-value T-test Cont. Mean=0*/
local counter=1
forvalues i=1/1 { /*number of contrasts needed to compare year==1
vs year==2*/
      local counter2=1
      forvalues j=1/2 { /*number of gender categories*/
            local stop=`counter2'+`compmin'
            test [alcmon]_subpop_`counter' = ///
            [alcmon]_subpop_`stop', nosvyadjust
            replace pmean=r(p) if year==`i' & irsex==`j' /*p-value
      t-test cont. mean=0*/
            local counter=`counter'+1
            local counter2=`counter2'+1
      }
            }
      }
```

**Exhibit A.8 Stata COMMANDS svy: mean and svy: total (Tests of Differences) (continued)**

```
svy: total alcmon, over(year irsex)
      {
matrix M = e(b) /*The totals for each subpopulation are stored in
here*/
local max=2*2     /*number of years*number of gender categories.
This is the total number of supops*/
local range=2    /*number of gender categories. This is the number
of subpops per year*/
local compmin=`max'-`range'
gen total_out=. /*Contrast total*/
gen setotal=.    /*Total Standard error*/
      local counter=1
      forvalues i=1/1 {  /*number of contrasts needed to compare
year==1 vs year==2*/
            local counter2=1
            forvalues j=1/2 {     /*number of gender categories*/
                  local stop=`counter2'+`compmin'
                  test [alcmon]_subpop_`counter' = ///
      [alcmon]_subpop_`stop', nosvyadjust matvlc(test`counter')

                  replace setotal= sqrt((test`counter'[1,1])) ///
      if year==`i' & irsex==`j'
                  replace total_out=M[1,`counter']-M[1,`stop'] ///
      if year==`i' & irsex==`j' /*Calculating the difference
between the totals of the subpopulation*/
                  local counter=`counter'+1
                  local counter2=`counter2'+1
                  }
            }
      }

      *Keeping variables that matches SUDAAN
      keep irsex total_out setotal pmean
      duplicates drop irsex total_out setotal pmean, force /*keep
one record per contrast*/

      drop if total_out == . /* drop the rows where there is no
information */
      format pmean %-15.10f
      format total_out %-12.0fc
      format setotal %-12.0fc

      /* Output the dataset*/
      list irsex total_out setotal pmean
```

**Exhibit A.8 Stata COMMANDS svy: mean and svy: total (Tests of Differences) (continued)**

Note: For testing of multiple years vs the current year as shown in Multiyear Detailed Tables, more years could be included in the data and the number of tests conducted can be increased by changing the number of for loops as shown below. The first block of code applies to means while the second block of code applies to totals. Note, this only demonstrates how the for loops would change. The svy: statements demonstrated above would still need to be utilized.

```
local max=13*2 /*number of years*number of gender categories.
This is the total number of subpops*/
local range=2 /*number of gender categories. This is the number
of subpops per year*/
local compmin=`max'-`range'
gen pmean=. /*P-value T-test Cont. Mean=0*/
local counter=1
forvalues i=1/12 { /*number of contrasts needed to compare each
year to the current year*/
      local counter2=1
      forvalues j=1/2 { /*number of gender categories*/
            local stop=`counter2'+`compmin'
            test [alcmon]_subpop_`counter' = ///
            [alcmon]_subpop_`stop', nosvyadjust
            replace pmean=r(p) if year==`i' & irsex==`j' /*p-value
      t-test cont. mean=0*/
            local counter=`counter'+1
            local counter2=`counter2'+1
      }
            }
      }

local max=13*2 /*number of years*number of gender categories.
This is the total number of subpops.*/
local range=2 /*number of gender categories. This is the number
of subpops per year.*/
local compmin=`max'-`range'
gen total=. /*Contrast total*/
gen setotal=. /*Total Standard error*/
local counter=1
forvalues i=1/12 {  /*number of contrasts needed to compare each
year to the current year*/
      local counter2=1
      forvalues j=1/2 { /*number of gender categories*/
            local stop=`counter2'+`compmin'
            test [alcmon]_subpop_`counter' = ///
            [alcmon]_subpop_`stop', nosvyadjust ///
            matvlc(test`counter')
            replace setotal= sqrt((test`counter'[1,1])) if ///
            year==`i' & irsex==`j'
            replace total=M[1,`counter']-M[1,`stop'] if ///
```

**Exhibit A.8 Stata COMMANDS svy: mean and svy: total (Tests of Differences) (continued)**

```
            year==`i' & irsex==`j' /*Calculating the difference
between the totals of the subpopulation*/
            local counter=`counter'+1
            local counter2=`counter2'+1
            }
      }
}
```

**Exhibit A.9 SAS Code (Calculation of the *P* Value for the Test of Differences between Totals for Uncontrolled Domains)**

```
IF SETOTAL GT 0.0 THEN DO; /*SETOTAL and TOTAL come from
Exhibit A.7*/
   PVALT=2*(1-PROBT(ABS(TOTAL/SETOTAL),750));
END;
```

**Exhibit A.10 Stata Code (Calculation of the *P* Value for the Test of Differences between Totals for Uncontrolled Domains)**

```
generate pvalt = tprob(750,abs(total_out /setotal)) ///
if setotal > 0 & !missing(setotal) /* two-tail*/
/*total_out and setotal come from Exhibit A.8*/
```

In Exhibits A.1 and A.2, all people aged 12 or older and gender are annually controlled totals. For controlled domains like these, additional steps are needed to compute similar *p* values for tests of differences. One approach uses an additional DESCRIPT procedure in SUDAAN to output the appropriate covariance matrix (Exhibit A.11), and an additional svy: mean command in Stata outputs a similar matrix (Exhibit A.12). Then, through further SAS or Stata data manipulations, the weighted sample sizes (WSUM), variances, and the covariance of the two means (obtained from the covariance matrix) are used to generate the standard *t* test statistic. The corresponding *p* value can once again be produced using the SAS PROBT function or Stata TPROB function and calculated *t* test statistic.

**Exhibit A.11 SUDAAN DESCRIPT Procedure (Covariance Matrix)**

```
PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS DEFT4;
NEST VESTR VEREP;
WEIGHT ANALWT;
VAR ALCMON;
SUBGROUP YEAR IRSEX;
LEVELS 2 2;
TABLES IRSEX*YEAR;
PRINT COVMEAN / STYLE = NCHS;
OUTPUT / MEANCOV = DEFAULT REPLACE FILENAME="OUT.SUDCOV";
TITLE "Variance Covariance Matrices ";
RUN;
```

**Exhibit A.11 SUDAAN DESCRIPT Procedure (Covariance Matrix) (continued)**

```
Note: The following CLASS statement could be used in place of SUBGROUP
and LEVELS statements in the above example:
     CLASS YEAR IRSEX;
```

**Exhibit A.12 Stata COMMAND svy: mean (Covariance Matrix)**

```
use using ".\\dataname.dta", clear

/*Ensure all variables are lower case*/
rename *, lower

/*ID Nesting variables (VESTR and VEREP) and weight variable
(ANALWT - standard single-year, person-level analysis weight*/

svyset verep [pweight=analwt], strata(vestr) dof(750)
svy: mean alcmon, over(year irsex)
*Save and display the Covariance Matrix
matrix M = e(V)
matrix list M
```

The covariances of the estimated means can be obtained from the output of the DESCRIPT procedure (Exhibit A.11) and svy: mean command (Exhibit A.12). The covariance matrix in SUDAAN consists of a row and column for each gender (total, male, female) and year (both years, 2013, and 2014) combination with each cell corresponding to a particular variance component (i.e., a 9 x 9 matrix). Because the rows and columns of the matrix are identical, the cells in the top half (above the diagonal) and the bottom half (below the diagonal) are identical. Table A.2 shows a shell for what the SUDAAN covariance matrix would look like for this example. The Stata matrix would look similar but with a few exceptions: total rows and columns would not be included (i.e., year=0 and irsex=0), and the order would be reversed (i.e., year would be listed first, followed by irsex). Table A.3 presents the Stata matrix shell.

**Table A.2 SUDAAN Matrix Shell**

| | | | IRSEX=0 | | | IRSEX=1 | | | IRSEX=2 | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | YEAR=0 | YEAR=1 | YEAR=2 | YEAR=0 | YEAR=1 | YEAR=2 | YEAR=0 | YEAR=1 | YEAR=2 |
| | | ROWNUM | B01 | B02 | B03 | B04 | B05 | B06 | B07 | B08 | B09 |
| IRSEX=0 | YEAR=0 | 1 | | | | | | | | | |
| | YEAR=1 | 2 | | | | | | | | | |
| | YEAR=2 | 3 | | | | | | | | | |
| IRSEX=1 | YEAR=0 | 4 | | | | | | | | | |
| | YEAR=1 | 5 | | | | | | | | | |
| | YEAR=2 | 6 | | | | | | | | | |
| IRSEX=2 | YEAR=0 | 7 | | | | | | | | | |
| | YEAR=1 | 8 | | | | | | | | | |
| | YEAR=2 | 9 | | | | | | | | | |

**Table A.3 Stata Matrix Shell**

| OVER: | YEAR | IRSEX |
|---|---|---|
| _subpop_1: | 1 | 1 |
| _subpop_2: | 1 | 2 |
| _subpop_3: | 2 | 1 |
| _subpop_4: | 2 | 2 |

| | alcmon: _subpop_1 | alcmon: _subpop_2 | alcmon: _subpop_3 | alcmon: _subpop_4 |
|---|---|---|---|---|
| alcmon:_subpop_1 | | | | |
| alcmon:_subpop_2 | | | | |
| alcmon:_subpop_3 | | | | |
| alcmon:_subpop_4 | | | | |

In the SUDAAN output, each cell of the variance-covariance matrix is identified by a separate variable of the form B0*x*, where *x* is a particular cell number. (Cells are numbered left to right.) The variable *ROWNUM* is an additional output variable that simply identifies the matrix row. The covariance data needed for a particular significance test can be pulled out of the matrix using SAS code. For this example, the covariance for IRSEX=0 between YEAR=1 and YEAR=2, would be either B03 from ROWNUM2 or B02 from ROWNUM3. These two values would be the same in this case. The needed covariances are kept in the SAS code shown in Exhibit A.13.

The three SAS datasets created by the following examples, one containing the covariances (Exhibit A.13) and two containing the variances (Exhibit A.15), are then merged with the output dataset from the DESCRIPT procedure that generated the tests of differences (Exhibit A.7). With the proper statistics contained in one dataset, the corresponding *p* value for the tests of differences between controlled totals can be produced using the SAS PROBT function and calculated *t* test statistic (Exhibit A.17). Interwoven with these three SAS code examples are Exhibits A.14, A.16, and A.18, which show Stata code performing the same functions.

**Exhibit A.13 SAS Code (Identification of Covariance Components)**

```
DATA COV(KEEP=IRSEX COV1);
  SET OUT.SUDCOV;
    IF ROWNUM=2 THEN DO; IRSEX=0; COV1=B03; END;
  ELSE IF ROWNUM=8 THEN DO; IRSEX=2; COV1=B09; END;
  ELSE IF ROWNUM=5 THEN DO; IRSEX=1; COV1=B06; END;

  IF ROWNUM IN (2,5,8) THEN OUTPUT;

RUN;

PROC SORT DATA=COV; BY IRSEX; RUN;
```

**Exhibit A.14 Stata Code (Identification of Covariance Components)**

```
local max=2*2         /*number of years*number of gender
categories. This is the total number of supops*/
local range=2         /*number of gender categories. This is the
number of subpops per year*/
local compmin=`max'-`range'

gen cov1=1
local counter=1
forvalues i=1/1 {  /*number of contrasts needed to compare year=1
vs year=2*/
      local counter2=1
      forvalues j=1/2 {     /*number of gender categories*/
            local stop=`counter2'+`compmin'
            replace cov1=M[`j', `stop'] if irsex==`j'
            local counter=`counter'+1
            local counter2=`counter2'+1
            }
      }

duplicates drop irsex cov1, force
      list irsex cov1
      keep irsex cov1
/* Save data to network*/
save ".\\cov.dta" , replace  /*Need to save dataset since Stata
can only work with one at a time*/
```

The variances of the means are calculated in separate data steps shown in Exhibits A.15 and A.16. The variance is simply the square of the SE of the mean. The SEs of the means were output in the original procedure that generated the estimates (DESCRIPT for the SUDAAN/SAS example and svy: mean for the Stata example; see Exhibits A.1 and A.2).

**Exhibit A.15 SAS Code (Calculation of Variances)**

```
DATA EST1(KEEP=WSUM1 VAR1 YEAR IRSEX);
 SET OUT.SUDFILE;
 WHERE YEAR=1;
 WSUM1=WSUM;
 VAR1=SEMEAN**2; /*THE variance is the SEMEAN squared*/
RUN;

DATA EST2(KEEP=WSUM2 VAR2 YEAR IRSEX);
 SET OUT.SUDFILE;
 WHERE YEAR=2;
 WSUM2=WSUM;
 VAR2 = SEMEAN**2;
      RUN;
```

**Exhibit A.16 Stata Code (Calculation of Variances)**

```
/*Run code from Exhibit A.2 or save the output from that exhibit
into a dataset then read in that dataset here then run the
remaining code.*/
/*Note: The remaining code for this exhibit will need to be run as
a block to avoid errors.*/
preserve  /*keep dataset in memory*/


keep if year ==1
gen wsum1 = wsum
gen var1  = semean^2
keep wsum1 var1 year irsex

duplicates drop year irsex, force /*keep one record per
subpopulation of interest*/

save ".\\est1.dta" , replace  //Need to save dataset since Stata
could only work with one at a time

restore, preserve /*restore dataset back to normal and edit for
second dataset*/


keep if year==2
gen wsum2 = wsum
gen var2  = semean^2
keep wsum2 var2 year irsex

duplicates drop year irsex, force /*keep one record per
subpopulation of interest*/

save ".\\est2.dta" , replace  /*Need to save dataset since Stata
could only work with one dataset at a time*/

restore, preserve
```

**Exhibit A.17 SAS Code (Calculation of the *P* Value for the Test of Differences between Totals for Controlled Domains)**

```
DATA P_VALUE;
 MERGE EST1 EST2 OUT.SUDTESTS COV;
 BY IRSEX;

  PVALT=2*(1-PROBT(ABS(TOTAL/SQRT(WSUM1**2*VAR1+WSUM2**2*VAR2-
       2*WSUM1*WSUM2*COV1)),750));
RUN;
```

**Exhibit A.18 Stata Code (Calculation of the *P* Value for the Test of Differences between Totals for Controlled Domains)**

```
/*Run code from Exhibits A.8, A.14, and A.16 then run the
remaining code to calculate the p values*/

keep irsex total_out

*merge by irsex for dataset est1 est2 cov
merge m:m irsex using ".\\est1.dta", generate(_merge1)
merge m:m irsex using ".\\est2.dta", generate(_merge2)
merge m:m irsex using ".\\cov.dta", generate(_merge3)
generate pvalt = tprob(750,abs(total_out ///
/sqrt(wsum1^2*var1+wsum2^2*var2-2*wsum1*wsum2*cov1))) /*
 two-tail*/

drop _merge1 _merge2 _merge3
list irsex year wsum1 var1 wsum2 var2 cov1 pvalt
```

## Recoding and Missing Values

In the example in Exhibit A.19 (using SAS and SUDAAN) and A.20 (using Stata), the mean age of first use of marijuana will be calculated in two ways within each exhibit. Respondents who have never used marijuana are assigned IRMJAGE=991, and if this level is included in the analysis, then the mean age calculated will be too high. Thus, two methods are shown on how to omit this level in calculating mean age of first use of marijuana using SAS and SUDAAN or Stata.

**Exhibit A.19 SAS Code (Recoding a Variable) and SUDAAN DESCRIPT Procedure (Estimate Generation with (1) Missing Values and (2) Using Subpopulation)**

```
/* Method 1, recoding unused values to missing*/

DATA DATANAME;
 SET DATANAME;
 IF IRMJAGE=991 THEN IRMJAGE_R=.;
 ELSE IRMJAGE_R=IRMJAGE;
 RUN;
 PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR
 FILETYPE=SAS DEFT4;
 NEST VESTR VEREP;
 WEIGHT ANALWT;   /*Standard single-year, person-level
 analysis weight*/
 VAR IRMJAGE_R;   /*Marijuana Age of First Use recoded
 analysis variable*/
 SUBGROUP IRSEX;
 /*Gender variable, where male=1 & female=2*/
 LEVELS 2;
 TABLES IRSEX; /*Gender*/
```

**Exhibit A.19 SAS Code (Recoding a Variable) and SUDAAN DESCRIPT Procedure (Estimate Generation with (1) Missing Values and (2) Using Subpopulation) (continued)**

```
  PRINT MEAN SEMEAN / REPLACE STYLE=NCHS;
  TITLE "ESTIMATES OF AGE OF FIRST USE OF MARIJUANA BY
  GENDER";
RUN;

/* Method 2, using subpopulation to omit the unused values*/

PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS DEFT4;
NEST VESTR VEREP;
WEIGHT ANALWT;   /*Standard single-year, person-level analysis
weight*/
SUBPOPN MRJFLAG=1; /*Sub setting to omit those respondents who
had never used marijuana, i.e., omitting respondents where
IRMJAGE=991*/
VAR IRMJAGE;   /*Marijuana Age of First Use analysis variable*/
SUBGROUP IRSEX;
     /*Gender variable, where male=1 & female=2*/
LEVELS 2;
TABLES IRSEX; /*Gender*/
PRINT MEAN SEMEAN / REPLACE STYLE=NCHS;
TITLE "ESTIMATES OF AGE OF FIRST USE OF MARIJUANA BY GENDER";
RUN;
```

**Exhibit A.20 Stata Code (Recoding a Variable, Estimate Generation with (1) Missing Values and (2) Using Subpopulation)**

```
/*Read in data*/
use using ".\\dataname.dta", clear
/*Ensure all variables are lower case*/
rename *, lower

generate irmjage_r = irmjage
replace irmjage_r = . if irmjage == 991
/*Method 1, recoding unused values to missing*/
svyset verep [pweight=analwt], strata(vestr) dof(750)
svy: mean  irmjage_r, over(irsex)
/*marijuana age of first use analysis variable, gender variable*/

/*Method 2, using subpopulation to omit the unused values*/
svyset verep [pweight=analwt], strata(vestr) dof(750)
svy, subpop(mrjflag): mean  irmjage, over(irsex)
```

## Confidence Intervals

As discussed in Section 8 of this report, confidence intervals can be calculated using means (MEAN) and SEs (SEMEAN) from PROC DESCRIPT in SUDAAN or svy: mean in Stata. After the means and standard errors are obtained (Exhibits A.1 and A.2), the code in Exhibits A.21 and A.22 can be used to create the 95 percent confidence intervals for means and totals.

**Exhibit A.21 SAS Code (Calculating a 95 Percent Confidence Interval)**

```
      DATA CI;
      SET OUT.SUDFILE; /*output data from Exhibit A.1*/
T_QNTILE=TINV(0.975,750); /*define t-statistic*/
            NUMBER=SEMEAN/(MEAN*(1-MEAN));
            L=LOG(MEAN/(1-MEAN));

            A=L-T_QNTILE*NUMBER;
            B=L+T_QNTILE*NUMBER;

            PLOWER=1/(1+EXP(-A));
            PUPPER=1/(1+EXP(-B));
/*PLOWER AND PUPPER ARE THE 95% CIS ASSOCIATED WITH MEAN FROM SUDAAN*/
            TLOWER=WSUM*PLOWER;
            TUPPER=WSUM*PUPPER;
/*TLOWER AND TUPPER ARE THE 95% CIS ASSOCIATED WITH TOTAL FROM
SUDAAN*/
            RUN;
```

**Exhibit A.22 Stata Code (Calculating a 95 Percent Confidence Interval for a Mean)**

```
      /*Run code from Exhibit A.2 or save output dataset from
      Exhibit A.2 and use that as input to this code.*/
      generate t_qntile = invt(750,0.975)
      generate number = semean/(mean_out*(1-mean_out))
      generate l=log(mean_out/(1-mean_out))
      generate a = l-t_qntile*number
      generate b = l+t_qntile*number
      generate plower = 1/(1+exp(-a))
      generate pupper = 1/(1+exp(-b))

      /*plower and pupper are the 95% CIs associated with mean_out from
      Stata*/

      generate tlower = wsum*plower
      generate tupper = wsum*pupper

      /*tlower and tupper are the 95% CIs associated with total_out
      from Stata*/

      duplicates drop year irsex, force /*keep one record per
      subpopulation of interest*/
```

**Exhibit A.22 Stata Code (Calculating a 95 Percent Confidence Interval for a Mean) (continued)**

```
keep year irsex nsum wsum mean_out semean total_out setotal
///t_qntile number l a b plower pupper tlower tupper
```

## Calculating Percentages for Categories

Exhibits A.23 and A.24 demonstrate how to compute estimates corresponding to levels of a categorical variable. This example uses the number of days used marijuana in the past month among past month marijuana users. The variable that will be analyzed (MRJDAYS) is a categorical variable with days grouped into four levels (1=1-2 days, 2=3-5 days, 3=6-19 days, 4=20+ days). Because SUDAAN now needs to estimate percentages and SEs for each level of the variable instead of computing only one estimate for the variable overall, the CATLEVEL statement is introduced, and the PERCENT and SEPERCENT keywords replace the MEAN and SEMEAN keywords. Note that the suppression rule for percentages is the same as the suppression rule for means shown in Exhibit A.5, except PERCENT and SEPERCENT have to be divided by 100 (and thus are equivalent to MEAN and SEMEAN in the formulas). In Stata, the output will be proportions that can be directly used in the suppression rule formulas. However, if for reporting purposes, percentages need to be shown, then these proportions would need to be multiplied by 100.

**Exhibit A.23 SAS Code (Frequency of Use, i.e., Number of Days Used Substance in the Past Month among Past Month Users)**

```
PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS DEFT4;
   NEST VESTR VEREP;
   WEIGHT ANALWT;   /*Standard single-year, person-level analysis
   weight*/
   VAR MRJMDAYS MRJMDAYS MRJMDAYS MRJMDAYS;   /*Marijuana Use
   frequency in the past month variable: 1=1-2 days, 2=3-5 days,
   3=6-19 days, 4=20+ days, 5=did not use in the past month*/
   CATLEVEL 1 2 3 4;  /*levels of MRJMDAYS to be shown in table*/
   SUBGROUP MRJMON;
   /*Past month marijuana use variable, where used in past month=1 &
   did not use in past month=0*/
   LEVELS 1;
   TABLES MRJMON; /*Tables will show percents among marijuana
   users*/
   PRINT WSUM NSUM PERCENT SEPERCENT TOTAL SETOTAL / REPLACE
   STYLE=NCHS;
   OUTPUT WSUM PERCENT SEPERCENT TOTAL SETOTAL NSUM  /REPLACE
   FILENAME="OUT.SUDFILE_FREQ";
   TITLE "FREQUENCY OF MARIJUANA USE BY PAST MONTH MARIJUANA
USERS";RUN;
```

**Exhibit A.24 Stata Code (Frequency of Use, i.e., Number of Days Used Substance in the Past Month among Past Month Users)**

```
use using ".\\dataname.dta", clear
/*Ensure all variables are lower case*/
rename *, lower

svyset verep [pw=analwt], strata(vestr) dof(750)
svy: proportion  mrjmdays, subpop( mrjmon)
/*This code will produce output showing proportions for marijuana
use frequency in the past month, to get percentages, these proportions
would need to be multiplied by 100*/
```

## Testing Between Overlapping Domains

In addition to testing between-year differences shown in Exhibits A.7 and A.8, Exhibits A.25 and A.26 demonstrate testing between two overlapping domains. Specifically, these exhibits show how to use a stacked dataset to test whether past month cigarette use among the full population aged 18 or older is different from cigarette use among people aged 18 or older who are employed full time.

This code will apply when one domain is completely contained in another or when there is only partial overlap. The example below uses two domains, where one domain is completely contained in the other (i.e., comparing unemployed adults to all adults—the unemployed group is completely contained by the all adults group). Note that the correlations between the two estimates are accounted for in this test (i.e., correlation between past month cigarette use among people aged 18 or older and past month cigarette use among people aged 18 or older employed full time).

**Exhibit A.25 SAS Code (Test of Difference when Two Groups Overlap Using Stacked Data)**

```
DATA STACKED;
      SET DATANAME(IN=A) DATANAME(IN=B); /*reading in data
twice*/
      IF A THEN DO;
INDIC=1;
IF EMPSTAT4 IN (1,2,3,4) THEN EMPLOY=1;
/*EMPSTAT4 is a four level employment variable for adults, where
level 1 is those employed full time, 2 is those employed part
time, 3 are those unemployed, and 4 are all other adults.
Respondents aged 12 to 17 are coded as level 99*/
ELSE EMPLOY=0;
      END;
      ELSE IF B THEN DO;
INDIC=2;
IF EMPSTAT4=1 THEN EMPLOY=1;
ELSE EMPLOY=0;
      END;
/*create an indicator variable for the stacked data, this will be
used in the diffvar statement in PROC DESCRIPT
```

**Exhibit A.25 SAS Code (Test of Difference when Two Groups Overlap Using Stacked Data) (continued)**

```
When indic=1, employ=1 represents the full population
When indic=2, employ=1 represents those employed full time*/
RUN;

PROC SORT DATA=STACKED;
BY VESTR VEREP;
RUN;
PROC DESCRIPT DATA=STACKED DDF=750 DESIGN=WR FILETYPE=SAS;
NEST VESTR VEREP;
WEIGHT ANALWT;
VAR CIGMON;
SUBGROUP INDIC;
LEVELS 2
DIFFVAR INDIC=(1 2); /*Since subsetting in the next line to
employ=1, this is testing all persons 18+ vs. employed persons
18+*/
SUBPOPN CATAG18=1 AND EMPLOY=1;
PRINT WSUM NSUM MEAN SEMEAN TOTAL SETOTAL T_MEAN P_MEAN /
   REPLACE STYLE=NCHS;

OUTPUT WSUM MEAN SEMEAN TOTAL SETOTAL NSUM T_MEAN P_MEAN /
   REPLACE
   NSUMFMT=F8.0 WSUMFMT=F12.0 MEANFMT=F15.10 SEMEANFMT=F15.10
   TOTALFMT=F12.0 SETOTALFMT=F12.0 FILENAME="OUT.SUDTESTS";
TITLE "TESTS OF DIFFERENCES BETWEEN ALL PERSONS 18 OR OLDER AND
EMPLOYED PERSONS 18 OR OLDER";
RUN;
```

**Exhibit A.26 Stata Code (Test of Difference when Two Groups Overlap Using Stacked Data)**

```
/*Creating the first dataset*/
/*Read in data */
use using ".\\dataname.dta", clear
/*Ensure all variables are lower case*/
rename *, lower

gen indic = 1
gen employ = 0
replace employ = 1 if inlist(empstat4,1,2,3,4)
/*Save the dataset*/
save ".\\a26_a.dta" , replace  /*Need to save dataset since Stata
can only work with one at a time*/

/*Creating the second dataset*/
/*Read in data a second time*/
use using ".\\dataname.dta", clear
/*Ensure all variables are lower case*/
rename *, lower
```

**Exhibit A.26 Stata Code (Test of Difference when Two Groups Overlap Using Stacked Data) (continued)**

```
gen indic = 2
gen employ = 0
replace employ = 1 if inlist(empstat4,1)
*Save the dataset
save ".\\a26_b.dta" , replace  /*Need to save dataset since Stata
could only work with one at a time*/

/*Need to stack the dataset together */
use using ".\\a26_a.dta", clear
append using ".\\a26_b.dta"

/*Create the subpopulation variable*/
generate subpop = 1 if catag18 == 1 & employ == 1
svyset verep [pweight=analwt], strata(vestr) dof(750)
svy, subpop(subpop): mean cigmon, over(indic)
test [cigmon]1 = [cigmon]2
/*Since subsetting to employ=1, this is testing all persons 18+
vs. employed persons 18+ for past month cigarette use*/
/* employ is defined earlier in this exhibit and catag18=1 for
persons 18 or older and 0 otherwise    */
```

## Testing Independence of Two Variables when One Variable Has Three or More Levels

When comparing population subgroups defined by three or more levels of a categorical variable, log-linear chi-square tests of independence of the subgroup and the prevalence variables are conducted first to control the error level for multiple comparisons (i.e., if the goal is to compare cigarette use among several levels of employment, first test whether cigarette use is associated with employment). Exhibits A.27 and A.28 show the code for calculating the Wald *F* test to determine whether cigarette use is associated with employment status. If Shah's Wald *F* test (transformed from the standard Wald chi-square) indicated overall significant differences, the significance of each particular pairwise comparison of interest can be tested using the SUDAAN procedure DESCRIPT (as shown in Exhibit A.25) or Stata (Exhibit A.26). The additional pairwise testing can determine which levels of employment status show significant differences in cigarette use compared with other levels of employment.

**Exhibit A.27 SAS Code (Test for Independence Based on a Log-Linear Model)**

```
PROC CROSSTAB DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS DEFT4;
   NEST VESTR VEREP;
   WEIGHT ANALWT;
   CLASS CIGMON;
   SUBGROUP EMPSTAT4; /*four level employment status variable*/
   LEVELS   4;
   SETENV DECWIDTH=6 COLWIDTH=17;
   TABLES   EMPSTAT4*CIGMON;
   TEST LLCHISQ / WALDF;   /*log linear hypothesis test, wald F
   test statistic, if test statistic is significant, then reject
   null hypothesis of no interaction*/
```

**Exhibit A.27 SAS Code (Test for Independence Based on a Log-Linear Model) (continued)**

```
 SETENV DECWIDTH=4 COLWIDTH=15;
 PRINT  NSUM WSUM TOTPER ROWPER COLPER STESTVAL SPVAL SDF /
        REPLACE STYLE=NCHS;
 OUTPUT  STESTVAL SPVAL SDF / REPLACE FILENAME="TEST_CHI";
RUN;
```

**Exhibit A.28 Stata Code (Test for Independence Based on a Log-Linear Model)**

```
use using ".\\dataname.dta", clear
/*Ensure all variables are lower case*/
rename *, lower


/*Need to subset to just 4 levels of empstat4*/
generate subpop = 1 if inlist(empstat4,1,2,3,4)
/*four level employment status variable*/

svyset verep [pw=analwt], strata(vestr) dof(750)

svy, subpop(subpop): tab cigmon empstat4, llwald noadjust

/*This will give you both the adjusted and non-adjusted Wald F,
the non-adjusted test statistic will match SUDAAN*/
```

**Exhibit A.29 SUDAAN DESCRIPT Procedure (Pairwise Testing)**

```
PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS;
NEST VESTR VEREP;
WEIGHT ANALWT;
VAR CIGMON;
SUBGROUP EMPSTAT4;
LEVELS 4;
PAIRWISE EMPSTAT4 / NAME="Tests of differences for all levels";
PRINT WSUM NSUM MEAN SEMEAN TOTAL SETOTAL T_MEAN P_MEAN /
   REPLACE STYLE=NCHS;
OUTPUT WSUM MEAN SEMEAN TOTAL SETOTAL NSUM T_MEAN P_MEAN /
   REPLACE
   NSUMFMT=F8.0 WSUMFMT=F12.0 MEANFMT=F15.10 SEMEANFMT=F15.10
   TOTALFMT=F12.0 SETOTALFMT=F12.0 FILENAME="OUT.SUDTESTS";
TITLE "TESTS OF DIFFERENCES IN PAST MONTH CIGARETTE USE AMONG ALL
LEVELS OF EMPLOYMENT STATUS";
RUN;
```

**Exhibit A.30 Stata Code (Pairwise Testing)**

```
use using ".\\dataname.dta", clear
/*Ensure all variables are lower case*/
rename *, lower


/*Need to subset to just 4 levels of empstat4*/
generate subpop = 1 if inlist(empstat4,1,2,3,4)
/*four level employment status variable*/

svyset verep [pw=analwt], strata(vestr) dof(750)

/*Estimated means of past month cigarette use by employment
status*/
svy: mean cigmon, over(empstat4)
matrix Me = e(b)

local max=4  /*number of empstat4 categories*/
matrix output = J(6,7,.) /*empty matrix to store results - the
number of rows should match the number of contrasts needed*/

local counter1 = `max' - 1
local counter2 = `max' - 1
local contrast = 0

forvalues i=1/`counter1' {
  local stop = `max' - `i' + 1
  forvalues j=1/`counter2' {
    local contrast = `contrast' + 1
    test [cigmon]`j' = [cigmon]`stop', nosvyadjust ///
      matvlc(mtest`contrast')
   matrix output[`contrast', 1] = `j'
   matrix output[`contrast', 2] = `stop'
   matrix output[`contrast',7]=r(p)
   matrix output[`contrast',4]=sqrt((mtest`contrast'[1,1]))
   matrix output[`contrast',3]=Me[1,`j']-Me[1,`stop']
  }
  local counter2 = `counter2' - 1
}

/*Estimated Totals*/
svy: total cigmon, over(empstat4)

matrix M = e(b) /*Store total estimates in matrix M*/
local max=4  /*number of categories*/

local counter1 = `max' - 1
local counter2 = `max' - 1
local contrast = 0
```

**Exhibit A.30 Stata Code (Pairwise Testing) (continued)**

```
forvalues i=1/`counter1' {
  local stop = `max' - `i' + 1
  forvalues j=1/`counter2' {
    local contrast = `contrast' + 1
    test [cigmon]`j' = [cigmon]`stop', nosvyadjust ///
      matvlc(test`contrast')
    matrix output[`contrast',6]=sqrt((test`contrast'[1,1]))
    matrix output[`contrast',5]=M[1,`j']-M[1,`stop']
  }
  local counter2 = `counter2' - 1
}
matrix colnames output = level1 level2 mean semean total_out ///
  setotal mean_pval
matrix list output
```

## Testing of Linear Trends

As users, it can also be useful to test the linear trend for all data points, across all years of interest. The linear trend test can inform users about whether prevalence use has decreased, increased, or remained steady over the entire span of the years of interest. This type of test can be done using either SUDAAN (as shown in Exhibits A.31 and A.33) or Stata (Exhibits A.32 and A.34). This linear trend test can be performed using a *t* test (Exhibits A.31 and A.32) or modeling (Exhibits A.33 or A.34), depending on the analysis.

## Contrast Method

The *t* test method for testing linear trends is more simplistic and better suited for large-scale table production similar to that used in the detailed tables and mental health detailed tables if the primary purpose is to test whether any observed differences across years are significant without consideration of other covariates. This method is also consistent with the method used in the detailed tables and mental health detailed tables to test means between years and between demographic levels as shown in Exhibits A.7 and A.8. In SUDAAN, the *t* test method would be implemented using the CONTRAST statement in the DESCRIPT procedure as shown in Exhibit A.31. The corresponding Stata code using test statements is shown in Exhibit A.32. Both approaches are based on orthogonal polynomial coefficients. The code in Exhibits A.31 and A.32 includes two placeholders that need to be specified by the user. For each year of data the user wants to include in the test, an additional contrast is required to account for that year. Certain variables are available for only a subgroup of NSDUH years, and sometimes the analysis of interest involves only a subgroup of years. For this reason, Table A.4 is provided to help users specify the needed information for linear trend tests involving from 3 to 14 years of data. Recall that 2 years of data would be the same as the comparison shown in Exhibits A.7 and A.8. Thus, Exhibits A.31 and A.32 are for tests across a combination of 3 or more years of data.

**Table A.4 Contrast Statements for Exhibits A.31 and A.32**

| Number of Years (X) | Contrast Statement (Y) |
|---|---|
| 14 | (-13 -11 -9 -7 -5 -3 -1 1 3 5 7 9 11 13) |
| 13 | (-6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6) |
| 12 | (-11 -9 -7 -5 -3 -1 1 3 5 7 9 11) |
| 11 | (-5 -4 -3 -2 -1 0 1 2 3 4 5) |
| 10 | (-9 -7 -5 -3 -1 1 3 5 7 9) |
| 9 | (-4 -3 -2 -1 0 1 2 3 4) |
| 8 | (-7 -5 -3 -1 1 3 5 7) |
| 7 | (-3 -2 -1 0 1 2 3) |
| 6 | (-5 -3 -1 1 3 5) |
| 5 | (-2 -1 0 1 2) |
| 4 | (-3 -1 1 3) |
| 3 | (-1 0 1) |

Note: Replace the placeholders (X) and (Y) in Exhibits A.31 and A.32 per the information in this table. Replace (X) with the numbers of years included in the linear trend test and (Y) with the corresponding contrast statement.

**Exhibit A.31 SUDAAN Code (Test of Linear Trends with DESCRIPT)**

```
PROC DESCRIPT DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS;
NEST VESTR VEREP;
WEIGHT ANALWT;
VAR ALCMON;
SUBGROUP YEAR IRSEX;
LEVELS X 2; /*define X as the # of years*/
TABLES IRSEX;
CONTRAST YEAR = Y / NAME="LINEAR TREND TEST"; /*define Y as the
coefficients according to the number of years see Table A.4*/
PRINT WSUM NSUM MEAN SEMEAN TOTAL SETOTAL T_MEAN P_MEAN /
   REPLACE STYLE=NCHS;
OUTPUT WSUM MEAN SEMEAN TOTAL SETOTAL NSUM T_MEAN P_MEAN /
    REPLACE
    NSUMFMT=F8.0 WSUMFMT=F12.0 MEANFMT=F15.10 SEMEANFMT=F15.10
    TOTALFMT=F12.0 SETOTALFMT=F12.0 FILENAME="OUT.SUDTESTS";
TITLE " TEST OF LINEAR TREND IN PAST MONTH ALCOHOL USE BY
GENDER";
RUN;
```

**Exhibit A.32 Stata Code (Test of Linear Trends with TEST Statements)**

```
use using ".\\dataname.dta", clear
/*Ensure all variables are lower case*/
rename *, lower

svyset verep [pw=analwt], strata(vestr) dof(750)

svy: mean alcmon, over(year irsex)
matrix Me = e(b)

matrix coeff = (Y)  /*define Y as the coefficients according to
the # of years see Table A.4*/
local max=X*2  /*total number of subpops - # of years(X)*# levels
of irsex(2)*/
local counter1 = 2 /*number of categories, i.e. number of levels
of irsex*/

generate pmean=.
generate mean=.
generate semean=.
forvalues i=1/`counter1' {   /*number of categories, i.e. number
of levels of irsex*/
  local stop = `max' / `counter1'
  local test
  local mean
  forvalues j=1/`stop' {  /*stop should be equal to the # of
coefficients defined in coeff*/
    local sub = `i' + `counter1'*(`j'-1)
    local co = coeff[1,`j']
    local test = "`test' (`co')*[alcmon]_subpop_`sub'"
    local mean = "`mean' `co'*Me[1,`sub']"
    if (`j' < `stop') {
      local test = "`test' + "
       local mean = "`mean' + "
      }
  }
  test`test' = 0, nosvyadjust matvlc(mtest`counter')
  replace pmean=r(p) if irsex==`i'
  replace semean = sqrt((mtest`counter'[1,1])) if irsex==`i'
  replace mean = `mean' if irsex==`i'
}

/*Estimated Totals*/

svy: total alcmon, over(year irsex)
matrix M = e(b)

generate total_out=.
generate setotal=.
local counter=1
```

**Exhibit A.32 Stata Code (Test of Linear Trends with TEST Statements) (continued)**

```
forvalues i=1/`counter1' {   /*number of categories, i.e. number
of levels of irsex*/
  local stop = `max' / `counter1'
  local test
  local total
  forvalues j=1/`stop' {  /*stop should be equal to the # of
coefficients defined in coeff*/
    local sub = `i' + `counter1'*(`j'-1)
    local co = coeff[1,`j']
    local test = "`test' (`co')*[alcmon]_subpop_`sub'"
    local total = "`total' `co'*M[1,`sub']"
     if (`j' < `stop') {
       local test = "`test' + "
          local total = "`total' + "
     }
  }
  test `test' = 0, nosvyadjust matvlc(test`counter')
  replace setotal= sqrt((test`counter'[1,1])) if irsex==`i'
  replace total_out=`total' if irsex==`i' /*Calculating the
difference between the totals of the subpopulation*/
local counter = `counter'+1
}

/*Keeping variables that matches SUDAAN*/
keep irsex mean semean total_out setotal pmean
duplicates drop irsex mean semean total_out setotal pmean, force
/*keep one record per contrast*/

drop if total_out == . /* drop the rows where there is no
information */
format pmean %-15.10f
format total_out %-12.0fc
format setotal %-12.0fc

/* Output the dataset*/
list irsex mean semean total_out setotal pmean
```

## Modeling Method

The model-based method is more complex and flexible. This method, which was used in the analyses for the 2014 redesign impact assessment report (RIAR) (CBHSQ, 2015g), can measure a change in a variable over time while controlling for covariates. The modeling method can be used for more specific tests, such as controlling for the linear year trend across years to determine a break in trend for the current year. In the examples below, the variable YEAR should be defined as a continuous variable (i.e., 1 to X with X being the number of years included in the test), and the variable YEARIND should be defined as a categorical variable (i.e., 1 if in current year of interest or 2 if not in current year of interest). The SUDAAN modeling method shown in Exhibit A.33 uses the procedure RLOGIST for logistic regression, and the

Stata modeling example shown in Exhibit A.34 uses the svy: logit command for logistic regression.

The models shown below were used in the 2014 RIAR (CBHSQ, 2015g) to determine change, but a simpler model could be run to test overall trend across years similar to Exhibits A.31 and A.32 by removing the YEARIND variable from the code below. Note that the simplified modeling method may give a slightly different result than the DESCRIPT method under similar settings.

**Exhibit A.33 SUDAAN Code (Modeling Test of Linear Trends)**

Note: The input dataset includes 2002–2014 NSDUH data, so YEAR = 1 to 13 and YEARIND = 1 if in 2014 and YEARIND = 2 if not in 2014.

```
/*Overall model, no subpopulations*/

PROC RLOGIST DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS;
NEST VESTR VEREP;
WEIGHT ANALWT;
REFLEVEL YEARIND=2;  /*Not in Current Year is Reference Level*/
SUBGROUP YEARIND;
LEVELS 2;
MODEL ALCMON=YEARIND YEAR;  /*Model controlling for linear trend of
year to determine change in the current year*/
SETENV DECWIDTH=6 COLWIDTH=18;
PRINT BETA="BETA" SEBETA="STDERR" DEFT="DESIGN EFFECT"
T_BETA="T:BETA=0" P_BETA="P-VALUE"/ RISK=ALL TESTS=DEFAULT
T_BETAFMT=F8.2 WALDCHIFMT=f6.2 ORFMT=f10.2 LOWORFMT=f10.2
UPORFMT=f10.2 DFFMT=f7.0;
OUTPUT BETA SEBETA T_BETA P_BETA / REPLACE
FILENAME="OUT.MODEL_OUTPUT";
TITLE "MAIN MODEL OF ALCMON - OVERALL";
RUN;

/*model below is subset for Gender where IRSEX=1 is Males. Similar
model can be run for IRSEX=2 for Females*/

PROC RLOGIST DATA=DATANAME DDF=750 DESIGN=WR FILETYPE=SAS;
NEST VESTR VEREP;
WEIGHT ANALWT;
REFLEVEL YEARIND=2; /*Not in Current Year is Reference Level*/
SUBGROUP YEARIND;
LEVELS 2;
MODEL ALCMON=YEARIND YEAR;  /*Model controlling for linear trend of
year to determine change in the current year*/
SUBPOPN IRSEX=1;  /*Subset for Males*/
SETENV DECWIDTH=6 COLWIDTH=18;
PRINT BETA="BETA" SEBETA="STDERR" DEFT="DESIGN EFFECT"
T BETA="T:BETA=0" P BETA="P-VALUE"/ RISK=ALL TESTS=DEFAULT
T BETAFMT=F8.2 WALDCHIFMT=f6.2 ORFMT=f10.2 LOWORFMT=f10.2
UPORFMT=f10.2 DFFMT=f7.0;
OUTPUT BETA SEBETA T BETA P BETA / REPLACE
FILENAME="OUT.MODEL_OUTPUT";

TITLE "MAIN MODEL OF ALCMON - MALES";
RUN;
```

**Exhibit A.34 Stata Code (Modeling Test of Linear Trends)**

Note: The input dataset includes 2002–2014 NSDUH data, so YEAR = 1 to 13 and YEARIND = 1 if in 2014 and YEARIND = 2 if not in 2014.

```
use using ".\\dataname.dta", clear

svyset verep [pw=analwt], strata(vestr) dof(750)

/*Overall model controlling for linear trend of year to determine
change in the current year.*/
svy: logit alcmon ib2.yearind year

/*Create a subsetting variable, irsex_1 that will be 1 for males
(IRSEX=1) and zero otherwise. A similar variable can be created to
subset for females (IRSEX=2)*/
generate irsex_1 = 0
replace irsex_1 = 1 if irsex == 1

/*Model subsetting by gender and controlling for linear trend of year
to determine change in the current year. A similar model can be run
for females(IRSEX=2).*/
svy, subpop (irsex_1): logit alcmon ib2.yearind year
```

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