Methodology Used to Estimate the Bayes Significance Level for the Null Hypothesis of No Change between the 2022-2023 and 2023-2024 State Population Percentages

This methodology document is a companion piece to the *National Surveys on Drug Use and Health: Comparison of the 2022-2023 and 2023-2024 Population Percentages (50 States and the District of Columbia)* tables. These tables can be found on the NSDUH State Releases web page. These tables present the 2022-2023 and 2023-2024 National Surveys on Drug Use and Health (NSDUHs) state estimates and an indication of the statistical significance of the difference or change (*p* value). These tables were produced for outcomes that were consistently defined across the two time periods and for which 2022-2023 and 2023-2024 state-level small area estimates were available.[1] The moving average state estimates for the overlapping 2022-2023 and 2023-2024 time periods were obtained from independent applications of the survey-weighted hierarchical Bayes (SWHB) methodology; that is, the 2023-2024 models were fit independently of the previously fitted 2022-2023 models. This independent analysis approach was followed because there was no desire to revise the previously published 2022-2023 estimates. The methodology used to conduct statistical tests of significance for comparing 2022-2023 and 2023-2024 state population percentages is described here.

Let $\pi_{sa(1)}$ and $\pi_{sa(2)}$ denote the 2022-2023 and 2023-2024 population percentages, respectively, for state-*s* and age group-*a*. The difference between $\pi_{sa(1)}$ and $\pi_{sa(2)}$ is defined in terms of the log-odds ratio (lor_{sa}) as opposed to the simple difference because the posterior distribution of lor_{sa} is closer to Gaussian than the posterior distribution of the simple difference ($\pi_{sa(2)} - \pi_{sa(1)}$). Let ln denote the natural logarithm, then lor_{sa} is defined as follows:

$$lor_{sa} = \ln\left[\frac{\pi_{sa(2)} / (1 - \pi_{sa(2)})}{\pi_{sa(1)} / (1 - \pi_{sa(1)})}\right].$$

The *p* value given in the above referenced tables is computed to test the null hypothesis of no difference (i.e., $\pi_{sa(2)} = \pi_{sa(1)}$ or equivalently, $lor_{sa} = 0$). An estimate of lor_{sa} is given by

$$l\hat{o}r_{sa} = \ln\left[\frac{\hat{\pi}_{sa(2)} / (1 - \hat{\pi}_{sa(2)})}{\hat{\pi}_{sa(1)} / (1 - \hat{\pi}_{sa(1)})}\right],$$

[1] For details, see Section B in *2023-2024 National Surveys on Drug Use and Health: Guide to State Tables and Summary of Small Area Estimation Methodology* on the NSDUH State Releases web page.

where $\hat{\pi}_{sa(1)}$ and $\hat{\pi}_{sa(2)}$ are small area estimates of $\pi_{sa(1)}$ and $\pi_{sa(2)}$, respectively.

Let $\hat{\theta}_1 = \dfrac{\hat{\pi}_{sa(1)}}{1-\hat{\pi}_{sa(1)}}$ and $\hat{\theta}_2 = \dfrac{\hat{\pi}_{sa(2)}}{1-\hat{\pi}_{sa(2)}}$, noting that subscript *sa* has been dropped from $\hat{\theta}_1$ and $\hat{\theta}_2$ in order to simplify the notation. An estimate of the posterior variance of lor_{sa} is given by the following formula:

$$v(l\hat{o}r_{sa}) = v\left[\ln(\hat{\theta}_1)\right] + v\left[\ln(\hat{\theta}_2)\right] - 2\operatorname{cov}\left[\ln(\hat{\theta}_1), \ln(\hat{\theta}_2)\right],$$

where $\operatorname{cov}\left[\ln(\hat{\theta}_1), \ln(\hat{\theta}_2)\right]$ denotes the covariance between $\ln(\hat{\theta}_1)$ and $\ln(\hat{\theta}_2)$. This covariance is defined in terms of the associated correlation as follows:

$$\operatorname{cov}\left[\ln(\hat{\theta}_1), \ln(\hat{\theta}_2)\right] = \text{correlation}\left[\ln(\hat{\theta}_1), \ln(\hat{\theta}_2)\right] \times \sqrt{v\left[\ln(\hat{\theta}_1)\right] \times v\left[\ln(\hat{\theta}_2)\right]}\,.$$

Note that $v\left[\ln(\hat{\theta}_1)\right]$ and $v\left[\ln(\hat{\theta}_2)\right]$ used here to calculate $v(l\hat{o}r_{sa})$ are the same posterior variances used in calculating 2022-2023 and 2023-2024 Bayesian confidence intervals, respectively.

The correlation between $\ln(\hat{\theta}_1)$ and $\ln(\hat{\theta}_2)$ was obtained by simultaneously modeling the 2022, 2023, and 2024 NSDUH data. This simultaneous modeling approach was adopted based on the results of the validation study[2] conducted for measuring change in the 1999-2000 and 2000-2001 state population percentages. For this simultaneous model, four age groups (12 to 17, 18 to 25, 26 to 34, and 35 or older) by 3 years (2022, 2023, and 2024), that is, 12 subpopulation-specific models, were fitted, each with its own set of fixed and random effects. These models used the same predictors (fixed effects) employed in the 2023-2024 small area estimation models for all 3 years. The general covariance matrices for the state and within-state random effects were 12 × 12 matrices corresponding to the 12 element (age group × year) vectors of random effects. Note that the survey-weighted, Bernoulli-type log likelihood employed in the SWHB methodology was appropriate for this simultaneous model because the 12 (age group × year) subpopulations were nonoverlapping. The correlation $\left[\ln(\hat{\theta}_1), \ln(\hat{\theta}_2)\right]$ was approximated by the correlation calculated using the posterior distributions of $\ln\left[\pi_{sa(1)} / (1-\pi_{sa(1)})\right]$ and $\ln\left[\pi_{sa(2)} / (1-\pi_{sa(2)})\right]$ from the simultaneous model.

[2] See Appendix E, Section E.2, of the following report: Wright, D. (2003). *State estimates of substance use from the 2001 National Household Survey on Drug Abuse: Volume II. Individual state tables and technical appendices* (HHS Publication No. SMA 03-3826, NHSDA Series H-20). Substance Abuse and Mental Health Services Administration, Office of Applied Studies.

Note that for four outcomes,[3] the above-mentioned model did not converge. A different model based on simultaneous modeling of 2022-2023 and 2023-2024 data where 2023 data are repeated twice was used to obtain the correlations between 2022-2023 and 2023-2024 state estimates. This overlapping year model simultaneously fits eight subpopulation-specific models (i.e., four age groups × two overlapping time points [2022-2023 and 2023-2024]) instead of 12 subpopulation-specific models. Based on previous validation studies, this model is shown to underestimate the correlations,[4] resulting in more conservative tests, meaning that fewer significant differences may have been able to be detected for these outcomes.

To calculate the p value for testing the null hypothesis of no difference ($lor_{sa} = 0$), it is assumed that the posterior distribution of lor_{sa} is normal with estimated $mean = l\hat{o}r_{sa}$ and $variance = v(l\hat{o}r_{sa})$. The Bayesian p value or significance level for the null hypothesis of no difference, $lor_{sa} = 0$, is p value $= 2 * P\left[Z \geq abs(z)\right]$, where Z is a standard normal random variate, $z = \frac{l\hat{o}r_{sa}}{\sqrt{v(l\hat{o}r_{sa})}}$, and $abs(z)$ denotes the absolute value of z. This Bayesian significance level (or p value) for the null value of lor_{sa}, say lor_0, is defined following Rubin (1987)[5] as the posterior probability for the collection of the lor_{sa} values that are less likely or have smaller posterior density, $d(lor_{sa})$, than the null (no change) value, lor_0. That is,

$$p \text{ value}(lor_0) = probability\left[d(lor_{sa}) \leq d(lor_0)\right].$$

With the posterior distribution of lor_{sa} approximately normal, p value(lor_0) is given by the above expression.

[3] The outcomes were cocaine use in the past year (Table 6), heroin use in the past year (Table 8), hallucinogen use in the past year (Table 10), and methamphetamine use in the past year (Table 11).

[4] See Appendix E, Section E.1, of the following report: Wright, D. (2003). *State estimates of substance use from the 2001 National Household Survey on Drug Abuse: Volume II. Individual state tables and technical appendices* (HHS Publication No. SMA 03-3826, NHSDA Series H-20). Substance Abuse and Mental Health Services Administration, Office of Applied Studies.

[5] See the following reference: Rubin, D. B. (1987). *Multiple imputation for nonresponse in surveys* (Wiley Series in Probability and Mathematical Statistics: Applied Probability and Statistics). John Wiley & Sons.