

Guidance for Selecting Model Options in the National Cancer Institute Joinpoint Regression Software

Data Evaluation and Methods Research



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

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U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES
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Guidance for Selecting Model Options in the National Cancer Institute Joinpoint Regression Software

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Abstract

Background

The National Center for Health Statistics (NCHS) often evaluates and reports on trends over time based on data from NCHS surveys and the National Vital Statistics System. The National Cancer Institute's (NCI's) Joinpoint software has often been used for performing trend analyses, although the software includes several options for adjusting the default menu options (for example, log transformations, modeling method and constraints, and the various model selection methods), which can lead to differing conclusions about the trend.

Objective

The purpose of this report is to provide guidance to users of NCHS data in the selection of modeling options when using the NCI Joinpoint regression software to analyze trends. This report complements another report, "National Center for Health Statistics Guidelines for Analysis of Trends." Considerations are presented for selecting the modeling options, with examples illustrating the choices. The tradeoffs and consequences of choosing the various modeling options using data from NCHS data systems are discussed.

Keywords: grid search constraints • linear spline regression • model selection methods • trend analysis

Introduction

The National Center for Health Statistics (NCHS) provides data to the public from population health surveys, national vital statistics data, and data from establishment surveys. NCHS surveys and data systems are often used to perform trend analyses; for details see "National Center for Health Statistics Guidelines for Analysis of Trends" (1). National trends in health-related and demographic measures have been reported from a number of data systems, including the National Health Interview Survey, National Health and Nutrition Examination Survey, National Ambulatory Medical Care Survey, National Survey of Family Growth, and National Vital Statistics System (2–7). While many statistical software programs can perform trend analyses, the Joinpoint Regression Software (8) is commonly used at NCHS and among NCHS data users to analyze trends over time for many NCHS data products, including *Data Briefs*, *National Vital Statistics Reports*, and *Health, United States* (2–5,7).

The Joinpoint software was developed by the National Cancer Institute (NCI) and has a graphical user interface for interactive use (9). The software was first established to

evaluate trends in cancer rates, although analysts outside of NCI have used it to assess trends in various outcomes from many different data sources. The Joinpoint software implements a segmented regression model in which segments of the trend are joined by inflection points, or "joinpoints," at which the trend changes. The software package fits the simplest model to the data using a specified model selection method.

In addition to identifying the number of joinpoints in the segmented regression model, the NCI Joinpoint software can be used to identify the location of the joinpoints and estimate the regression parameters of the trend lines. The Joinpoint software has many user-specified options that make it a useful exploratory tool for investigating changes in trends over time.

This report supports the "National Center for Health Statistics Guidelines for Analysis of Trends" report (1) by providing guidance on selecting the Joinpoint software's model options and presenting examples of common issues encountered at NCHS with the use of this software. This report considers the model options that are available in the NCI Joinpoint software, including log transformations,

constraints on the number and location of joinpoints, and model selection methods. Examples of some commonly encountered situations are included in the Appendix. Analysts are cautioned to evaluate each model option carefully to ensure that the information provided is applicable to their data and analysis. Throughout this report, analysts are also referred to the NCHS trends guidance report (1) when making decisions about trend analysis of NCHS data. Note that NCI updates the Joinpoint software regularly, and so, the current version may differ from version 4.9.0.0 used for this report (8). However, most of the guidelines discussed in this report should be applicable in later versions. This report is not intended to serve as an introduction to the Joinpoint software. Users should reference the Joinpoint Help Manual (10) for questions and more information about the software.

Joinpoint Software Modeling Options and Defaults

Overview

The Joinpoint software has several modeling options to specify parameters for identifying the number and locations of joinpoints and for fitting the model. On the Joinpoint software input tabs, the user may adjust the following options:

- Heteroscedastic/correlated errors option (Input File tab)
- Log transformation (Input File tab)
- Modeling method and constraints (Method and Parameters tab)
- Number of joinpoints (minimum and maximum number of joinpoints) (Method and Parameters tab)
- Model selection method (Method and Parameters tab)

Descriptions of these options are provided on the NCI Joinpoint software webpage (<https://surveillance.cancer.gov/joinpoint/>). The defaults for each of the model options in NCI's Joinpoint software version 4.9.0.0 are shown in Table A.

While the Joinpoint software provides default model options, users do not need to use defaults automatically. The Joinpoint regression software includes several options to allow users the flexibility to adjust the trend model. While this enhances the flexibility of analyses, the NCHS trend guidance report recommends fitting a model and then making an informed and justifiable decision whether to adjust the default model selection options. Analysts are advised to carefully consider the analytic implications before adjusting the defaults. In most cases, the defaults are appropriate starting conditions for evaluating the trend.

Variance and Correlated Errors

The Joinpoint software contains options for users to specify the variance for a weighted least-squares analysis and to specify the error model to fit.

There are four options for specifying the variance:

1. Constant Variance (Homoscedasticity): This option can be used if the data consists of subpopulations with similar variance estimates. No standard errors from the data file can be used for input.
2. Standard Error (Provided): This is the default option that should be used when the standard error is provided in the data file. The errors may be homoscedastic or heteroscedastic, based on the variance structure provided in the data file.
3. Poisson Variance: This option can be used for errors that are uncorrelated but heteroscedastic. The nonconstant

Table A. Joinpoint software method and parameters options

Option	Suboption	Default
Correlated errors option	...	Uncorrelated
Log transformation	...	Yes
Modeling method	...	Grid search
Grid search constraints on the locations of joinpoints	Minimum number of observations from a joinpoint to either end of the data (excluding first or last joinpoint if it falls on an observation)	2
	Minimum number of observations between two joinpoints (excluding any joinpoint if it falls on an observation)	2
	Number of points to place between adjacent observed x values in the grid search ¹	0
Number of joinpoints	Minimum	0
	Maximum	Determined based on the number of data points ²
Model selection method	...	Permutation test (overall significance level = 0.05, number of permutations = 4,499) ³

... Category not applicable.

¹x value refers to the independent variable, which is the observation (years).

²The recommended maximum number of joinpoints varies based on the number of data points. The defaults are shown in Table B in this report.

³As of the National Cancer Institute's Joinpoint software version 4.9.0.0, the default model selection method is the permutation test. However, this could change in new releases because the National Cancer Institute has reported considering the Weighted Bayesian Information Criterion as a default in future software releases.

variance is estimated assuming that the dependent variable follows a Poisson distribution.

4. **Variance-Covariance Matrix (Provided):** This option can be used for errors that are correlated following a specified covariance structure, which is provided by the user. It was implemented as an “alpha” feature in version 4.9.0.0 that is still in development.

In general, autocorrelated error models are not recommended for the analysis of NCHS data. For the analysis of trends in survey data that may have correlated estimates, the autocorrelated errors model does not account for the type of correlation related to the survey design and structure. For vital statistics data (birth rates, mortality rates, etc.), the data are assumed to have minimal or no year-to-year correlation (1). For these analyses, the uncorrelated errors model is recommended.

Log Transformation

By default, the Joinpoint regression software uses a log transformation of the dependent variable. The transformation will impact both the fit and the interpretation of the trend model. Selecting a log transformation fits a linear model to the trend on a log scale. When this option is selected, NCI’s Joinpoint software will automatically fit an overall exponential curve to the original dependent data and then follow up with piecewise splines (on the log scale). This option will provide output that allows the user to directly compare relative differences and annual percent changes (APCs) during the period.

Alternatively, changing the default to no log transformation will automatically include a simple linear regression line and then follow up with additional linear splines. The model output allows the user to directly compare overall differences in rates between years (absolute change). Generally, if a user’s interest is in obtaining the relative differences and discussing the APCs, the model with the log transformation should be selected with the understanding that NCI’s Joinpoint software will determine trends on the log scale. Similarly, if the user’s interest is in obtaining the absolute differences, no log transformation should be selected. Additionally, a user may choose whether to use a log transformation based on the type of outcome (rates, counts, or percentages, for example) to improve the interpretability or ease of reporting the results. Examples 1 and 2 in the Appendix demonstrate the use and interpretation of the log transformation in vital statistics data and survey data, respectively.

Modeling Method and Constraints

The grid search method is the modeling approach used to fit trend data with the segmented regression model in the Joinpoint software. The grid search method evaluates the grid of all possible joinpoints based on the locations defined using the specified constraints in the software. For each

possible location, NCI’s Joinpoint software will determine the best fit by calculating and comparing the sum of squared errors for each model.

The grid search method has three constraints that can be adjusted for identifying the locations of joinpoints. The first option is used to specify the minimum number of observations from a joinpoint to either end of the data (excluding first or last joinpoint if it falls on an observation). This option is used to adjust the distance of joinpoints from the end points. The Joinpoint regression software requires this constraint to be between one and nine (default is two), so that joinpoints cannot occur on the end points. If the user believes that a trend deviates near the end points of the data, smaller values of this constraint should be specified. See Example 3 in the Appendix for an example of a case where this grid search constraint is adjusted.

The second option is used to specify the minimum number of observations between two joinpoints (excluding any joinpoint if it falls on an observation). This constraint controls how close joinpoints can be to other joinpoints and ranges from one to nine (default is two). The observation that falls on a joinpoint is not included in this count. In trends where the rate is changing frequently, smaller values may be specified to capture changes that happen in successive years. In trends where the rate is constant or should change only after a certain number of years, a larger value of the constraint can be specified.

The third option is used to specify the number of points to place between adjacent observed values in the grid search. This constraint allows joinpoints to be identified between values or observations of the independent variable (years). Under the default setting (zero), joinpoints will occur exactly at observed time points rather than between observations, but the Joinpoint software allows this option to be increased up to nine. NCHS does not recommend adjusting this grid search constraint for analyzing NCHS data because a joinpoint occurring between two observed time points may be misinterpreted or could result in line segments with slopes and standard errors that cannot be estimated due to few time points between joinpoints. For more information, see issue 11 in “National Center for Health Statistics Guidelines for Analysis of Trends” (1).

The grid search constraints determine the possible locations of the joinpoints and can be changed based on the particular application. Generally, changing constraints to allow for more possible joinpoints, like reducing the number of points allowed between joinpoints, creates a finer grid and will thus check for more possible joinpoints, which increases computation time. Computation time can be decreased by implementing tighter restrictions on the locations of joinpoints.

Note that Hudson’s Method was previously offered as an alternative modeling approach, but it was disabled in version 4.5.0.0 because of an issue with the algorithms for setting

the distance between joinpoints and setting the distance between joinpoints and the end of the data. Although Hudson’s Method may be available in future versions, it is not recommended for the analysis of NCHS data because it estimates the locations of joinpoints on a continuous spectrum and allows joinpoints to be inserted between years, similar to the third grid search constraint (1).

Number of Joinpoints

Constraints on the minimum and maximum number of joinpoints in the segmented regression model can also be specified. The default minimum number of joinpoints is set to zero for all trends. Increasing the minimum number of joinpoints will force the Joinpoint regression software to fit a trend model with at least the specified minimum number of joinpoints. For analyzing NCHS data, it is not recommended to increase the minimum number of joinpoints because this would exclude the evaluation of the linear trend and force the segmented regression model to include joinpoints that may not be appropriate for the trend. NCI’s Joinpoint software documentation (10) recommends a default maximum number of joinpoints based on the number of data points in the trend (Table B).

Table B. Default maximum number of joinpoints

Number of data points	Default maximum number of joinpoints ¹
0–6.....	0
7–11.....	1
12–16.....	2
17–21.....	3
22–26.....	4
27 or more.....	5

¹A maximum of nine joinpoints can be used when specifying the grid search method.

Users may increase the specified maximum number of joinpoints in the model set up if there is evidence of additional joinpoints (for example, a visual inspection of the trend or results of a nonlinearity assessment; see Example 4 in the Appendix) or interest in detecting small to moderate changes in the trend (1). Users may also specify fewer joinpoints than the default maximum number of joinpoints. In cases where there is little variation in the trend and the Joinpoint regression software identifies joinpoints, it could be appropriate to specify fewer joinpoints than recommended even if the differences in slope are statistically significant. Statistically significant changes in trend may also be identified with large data sets and may not reflect meaningful or important differences in the trends. Caution should be used because the significance level for testing the presence of joinpoints can be impacted by the specified maximum for some model selection techniques (that is, permutation test; see Example 4 in the Appendix).

An alternative to specifying fewer joinpoints is to use the Minimum APC Difference Worth Detecting (MADWD) feature, which was implemented in the Joinpoint regression software in version 4.8.0.0. The MADWD feature will remove joinpoints between segments with small differences in APCs, which will produce similar results to a model with fewer specified joinpoints (see Example 5 in the Appendix). In cases where there is little variation in the trend but the Joinpoint software identifies a joinpoint, it may be beneficial to remove the joinpoint to focus on the larger differences for practical importance or to improve interpretability. This option allows users to specify the minimum APC difference needed for reporting. The minimum APC depends on the context of the analysis and should be determined based on subject-matter expertise. More information can be found in the Joinpoint software documentation (10).

Model Selection Methods

The specified model selection method is used to identify the number of significant joinpoints in the trend model. Details about the segmented regression model parameterization can be found in the Joinpoint documentation (10) and in Kim et al. (9).

The most recent release of NCI’s Joinpoint software (version 4.9.0.0) (8) has seven options for model selection methods: the permutation test, Bayesian Information Criterion (BIC), BIC3, modified BIC, data dependent selection, weighted BIC, and weighted BIC alternative. The permutation test is the default model selection method in the Joinpoint software; however, users can select alternative model selection methods based on the features of their data. A brief description and guidelines on the appropriate use for each of the methods is provided in the following sections. A full description of each model selection technique and technical details can be found in the Joinpoint documentation (10). See Example 6 in the Appendix for a comparison of model selection methods.

The permutation test uses a sequence of tests to determine the optimal number of joinpoints. The permutation test compares permutations of the sampled observations and evaluates the likelihood of the observed sample. In most cases, the permutation test can be used for identifying the significant joinpoints in the trend model. However, according to the NCHS guidelines for analysis of trends, alternative model selection methods should be considered over the permutation test when there are fewer than 10 time points and the number of observations in the record level data is sufficiently large to assume normality, the exchangeability assumption of the permutation test may not hold, or it is important to detect small changes in the trend (1). The permutation test has two options that can be adjusted, the overall significance level used for the permutation test and the number of randomly permuted data sets. The overall significance level can be adjusted from the default (0.05) based on the acceptable type I error rate determined by

the user. NCI does not recommend changing the number of permutations from the default (4,499) unless the user has a good understanding of the implications (10).

The BIC approach was described by Kim et al. (11) and finds the model with the best fit by imposing a penalty based on the number of model parameters. This method identifies subtle changes in the trend and should be used in applications where the goal is to detect even slight changes. Additionally, this approach can be considered in analyses where there are fewer than 10 time points.

The BIC3 approach was introduced by Kim and Kim (12) and was added in version 4.6.0.0 of the Joinpoint software. This method is similar to BIC but imposes a harsher penalty on models with more parameters. BIC3 has been shown to produce similar results to the permutation test, although the permutation test has the advantage of being one of the longest available approaches in the Joinpoint software. However, BIC3 has reduced computation time and should be considered for longer trends or when the user wants to produce similar results to the permutation test but is limited by computation time.

The modified BIC selects the model using an asymptotic approximation of the Bayes factor, a likelihood ratio of two hypotheses. This test is not recommended for the analysis of NCHS data because the method facilitates selection of joinpoints between observed time points (1).

The data dependent selection approach selects the optimal method between BIC and BIC3 based on the characteristics of the data, including the number of estimated joinpoints and the mean square error. Typically, the BIC method is recommended when the effect size of the data is small, and the BIC3 method is recommended when the effect size of the data is large. Since the analyst will not know the true effect sizes in practice, this method selects the optimal method based on characteristics of the data. This option was added in Joinpoint software version 4.6.0.0, although it is currently a beta-version feature. It is still undergoing evaluation, so is not recommended for use in final analyses.

The weighted BIC selects the model using a combination of BIC and BIC3, where the weighted penalty term is based on the characteristics of the data, including the number of observations, the sum of squared errors, and a function of the coefficient of determination (R^2). This approach should be considered when the user wants flexibility in the selection method by combining BIC and BIC3 to select the optimal model. This method is easily adaptable, although the permutation test, BIC, and BIC3 may have better performance in specific situations. The weighted BIC was added in Joinpoint software version 4.7.0.0. It is currently a beta-version feature, although it is being considered as a default for future Joinpoint software versions due to its flexibility across a range of situations.

The weighted BIC alternative is calculated similarly to the weighted BIC, although it is less conservative. This

approach was added in Joinpoint version 4.7.0.0. NCI does not generally recommend using this method because it is included for specialized purposes and performs the worst out of the data-driven BIC methods (10).

Note that the Joinpoint software reports the mean squared error (MSE) for each fitted model. The MSE is an indicator of the spread of the data points and the fit of the trend model, although the MSE alone should not be used to select the final model. Generally, adding joinpoints to the model will decrease the MSE. Since the MSE does not penalize models for adding additional joinpoints, it is recommended that users utilize an NCI Joinpoint software model selection method to select the final model.

Summary

The NCI Joinpoint software can be a useful tool for evaluating trend analyses, particularly since the software identifies the locations of the change points in the trend in addition to estimating the slope of the segments. While the software recommends default options, users have the flexibility to specify their own modeling options. This report provides additional information and guidance on selecting the Joinpoint model options, including log transformations, constraints on the number of joinpoints, and the various model selection methods. The Appendix provides several examples from NCHS data systems that demonstrate practical use of specifying model options other than the defaults. The model options provided by Joinpoint software can enhance trend analyses and should be carefully evaluated (see discussion in Appendix examples). For guidance on using the Joinpoint software, see the Joinpoint software documentation (10). For additional guidance on trend analyses and selecting the model options, see “National Center for Health Statistics Guidelines for Analysis of Trends”(1).

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Appendix. Examples of Trend Analyses Using the National Cancer Institute Joinpoint Software

For the examples described in this Appendix, the default Joinpoint software options are used unless otherwise specified (default options are reported in [Table A](#)).

Example 1: Log Transformation on Vital Statistics Data

A National Center for Health Statistics (NCHS) *Data Brief* published in 2018 evaluated suicide mortality in the United States from 1999 to 2017 (3). Mortality data from the National Vital Statistics System (NVSS) were evaluated to describe differences by sex, age group, and urbanization level. Trends in suicide mortality were evaluated using the Joinpoint software. This example evaluates the trend in age-adjusted suicide rates for the total population for 1999–2017 and considers the use of the log transformation for this trend analysis. The default setting was to use a logarithmic transformation of the dependent variable, age-adjusted suicide rate per 100,000 standard population. The trend plot is shown in [Figure I](#).

By specifying the log transformation, the results reflect relative changes in the dependent variable. The Joinpoint regression software computes and displays the annual percent changes (APCs) for the line segments on either side of the joinpoint. These results show that the age-adjusted suicide rate increased between 1999 and 2017 with a joinpoint detected in 2006. The pace of increase was greater from 2006 to 2017 (2.04% per year) than from 1999 to 2006 (0.80% per year). For

the log-transformed model, the mean squared error (MSE) is 2.83, and the Bayesian Information Criterion (BIC) is 1.43 (results not shown).

When the log transformation is not selected, the trend plot shown in [Figure II](#) is generated. The graph looks virtually identical to the graph with the log transformation ([Figure I](#)) and the joinpoint is still detected in 2006. However, in this case the slopes of the line segments (the average annual absolute change in age-adjusted rates) on either side of the joinpoint are presented rather than the APCs. Similar to the log-transformation results, the slopes on either side of the joinpoint are positive, the slopes are significantly different than zero, and the slope for 2006–2017 (0.25) is greater than the slope for 1999–2006 (0.08). Although the results are consistent, these changes are on the scale of the outcome variable (for example, annual differences in the age-adjusted rate), which can make it difficult to compare across subgroups or different outcomes where the rates may be very different (for example, age-specific rates for stroke mortality), and the APCs may be preferred in those cases. For the model without a log transformation, the MSE is 2.99 and the BIC is 1.48.

For most analyses using vital statistics rates, the log transformation is preferred because the interest is in reporting relative changes, and the APCs are more easily compared across subgroups or different outcomes than the absolute slopes. In addition, the model fit statistics (that is, MSE and BIC) are smaller for the log-transformed option in this example,

Figure I. Trend plot from Joinpoint, log-transformed, age-adjusted suicide rates, total population: United States, 1999–2017

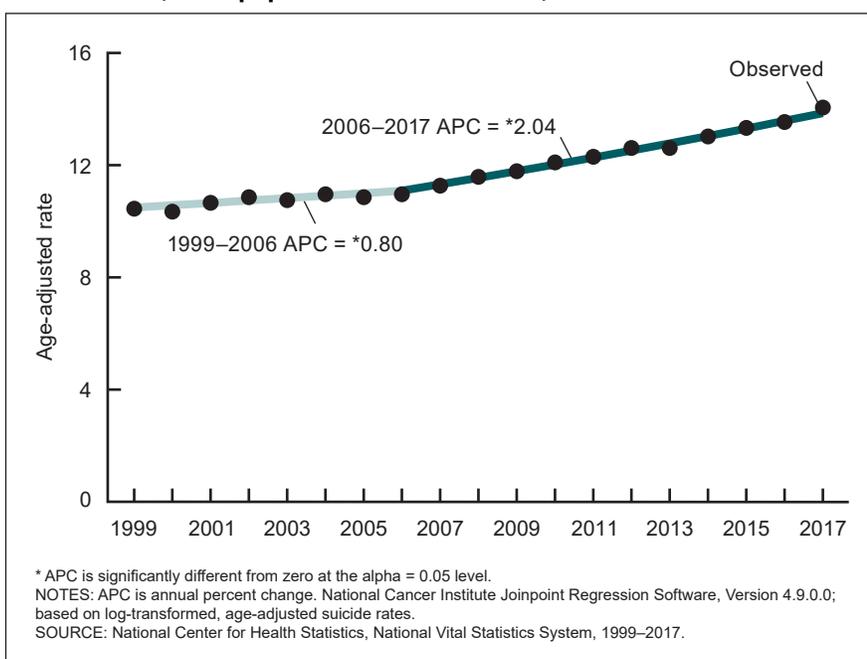


Figure II. Trend plot from Joinpoint, age-adjusted suicide rates, total population: United States, 1999–2017

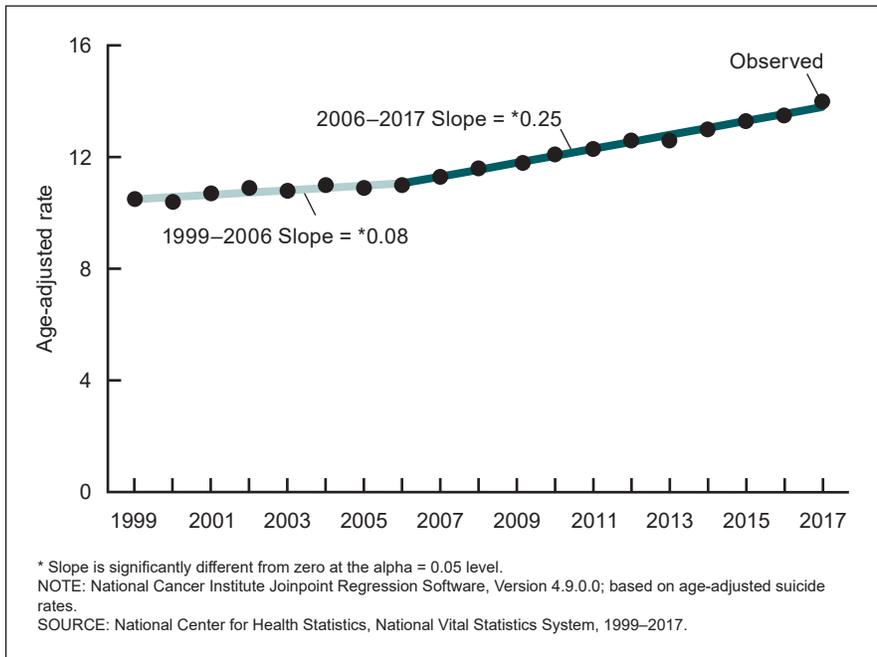
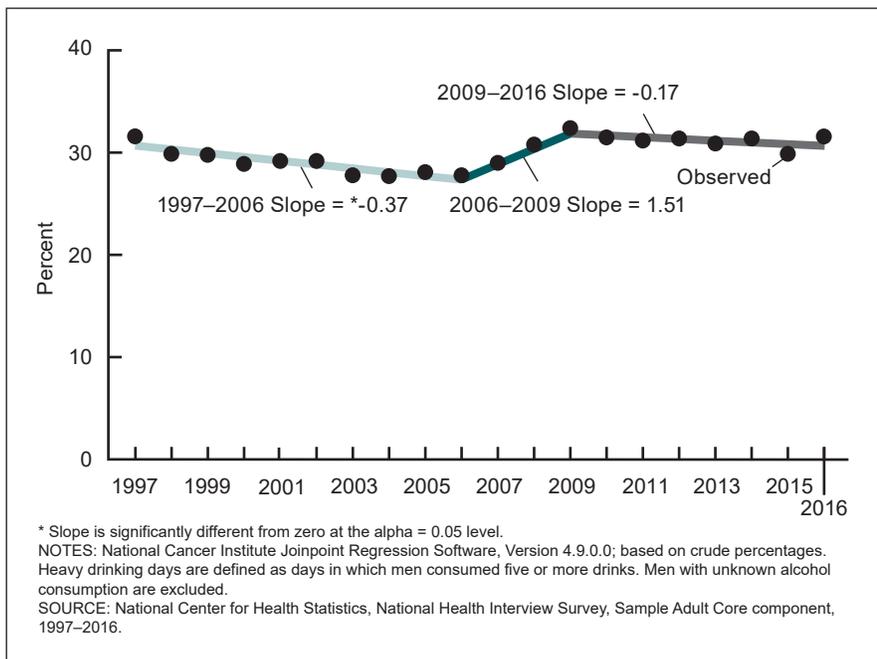


Figure III. Trend plot from Joinpoint, percentages of men aged 18 and over who had at least 1 heavy drinking day in the past year: United States, 1997–2016



which suggests that the log-transformed model is the preferred model. In the example from the *Data Brief*, the log transformation was used and the following language was used to describe the trend using APCs: The annual percent increase in rates accelerated from approximately 1% per year from 1999 through 2006 to 2% per year from 2006 through 2017 (3).

Example 2: Log Transformation on Survey Data

The National Health Interview Survey (NHIS) Early Release Program provides timely estimates of selected health indicators based on reported data from household interviews of a nationally representative sample of the U.S. civilian noninstitutionalized population. An *Early Release* report from the 2016 NHIS included estimates (crude percentages) of adults in the United States aged 18 and over who had five or more drinks in 1 day at least once in the past year, reported by sex (13). The report described the trend in alcohol consumption from 1997 to 2016, excluding adults with unknown alcohol consumption (less than 2.0% per year). This example evaluates alcohol consumption among men over this time period and assesses the use of the log transformation on survey data.

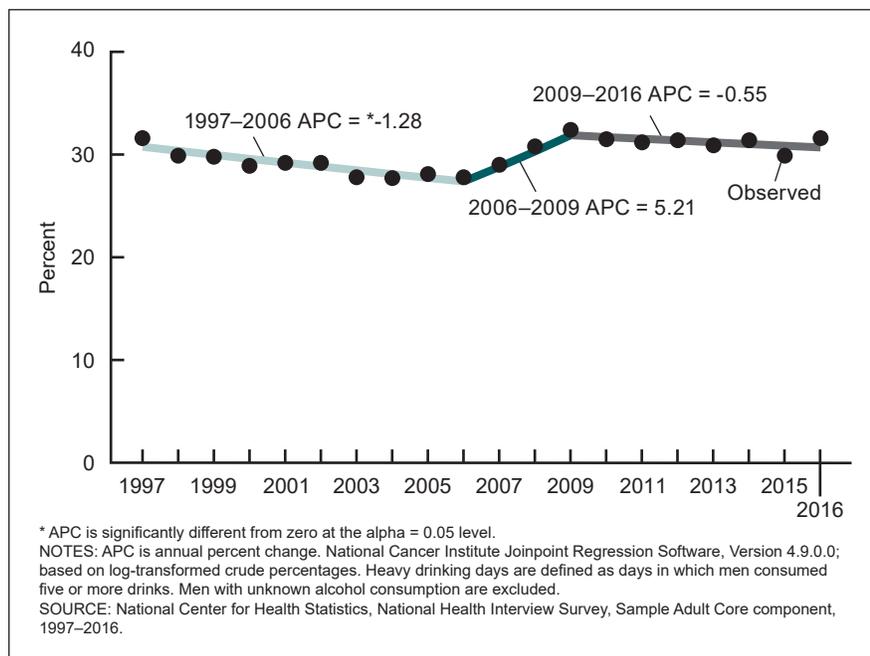
To demonstrate the model fit, the percentages were input into Joinpoint. [Figure III](#) displays the results where no log transformation was specified. For the nonlog-transformed trend, the Joinpoint regression software identified two joinpoints at 2006 and 2009. The software found that the slope of the first segment from 1997 to 2006 was statistically significant, which indicates that the percentage of men who had at least 1 heavy drinking day in the past year decreased significantly from 31.6% in 1997 to 27.8% in 2006 by approximately 0.37 percentage points per year. Interestingly, the absolute magnitude of the slope for the second segment (1.51 from 2006 to 2009) was larger than the first segment (-0.37), but the change over this period was not identified as statistically significant. In this case, since there are few data points in this segment and the Joinpoint software uses a conservative approach for estimating the standard error for the test of zero slope (14), the software did not identify a significantly increasing trend between 2006 and 2009, although the percentages increased from 27.8% in

2006 to 32.4% in 2009. The Joinpoint software found that the percentage of men with at least 1 heavy drinking day in the past year remained stable between 2009 and 2016. This model had an MSE of 1.14.

The analysis was repeated under the same model options but with a log transformation of the data. The graph of the log-transformed trend is shown in Figure IV. Similar to the nonlog-transformed analysis, the log-transformed model identified joinpoints at 2006 and 2009 with a statistically significant decrease between 1997 and 2006. Similarly, the percentages of men who had at least 1 heavy drinking day in the past year for the remaining segments (2006–2009 and 2009–2016) were not found to be significantly increasing or decreasing. However, the Joinpoint software reports APCs in this case rather than the absolute differences. For example, the segment from 1997 to 2006 had an APC of -1.28, which can be interpreted as a 1.28% annual decrease from 1997 to 2006. For the log-transformed model, the MSE was 1.13.

The modeled percentage may differ based on whether or not the data were log transformed. The extent to which they differ is directly dependent on how much the data were transformed. Modeled percentages from data that were highly skewed would have a greater difference when compared with modeled percentages from the corresponding log-transformed data. In this example, the modeled percentages only varied slightly, so no difference was observed in the estimated locations of the joinpoints between the log-transformed models and the nonlog-transformed models. Additionally, the MSE remained consistent between both the log-transformed and nonlog-transformed models. For this example, the user should select the nontransformed approach if they are interested in reporting absolute differences and the log-transformed approach if they are interested in reporting relative differences. For the *Early Release* report, the general trend (increasing, decreasing, remained stable) was reported, but the differences (absolute or relative) were not reported, so either the nontransformed or log-transformed approach would be appropriate for this example.

Figure IV. Trend plot from Joinpoint, log-transformed percentages of men aged 18 and over who had at least 1 heavy drinking day in the past year: United States, 1997–2016



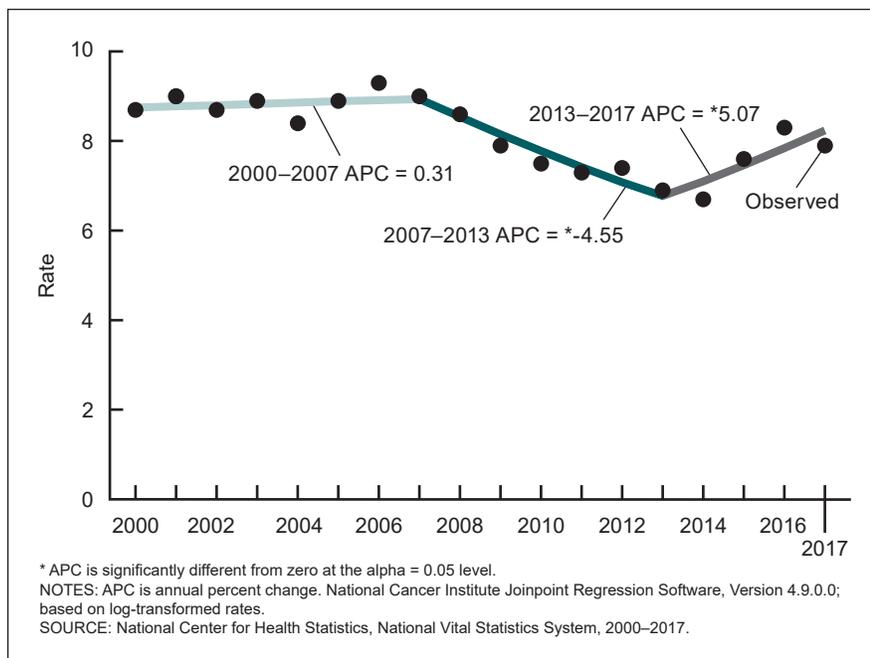
Example 3: Changing the Minimum Number of Points Between Joinpoints and the End Points of the Data

An NCHS *Data Brief* on suicide and homicide deaths among people aged 10–24 years (4) evaluated trends in violent death rates (suicide and homicide) between 2000 and 2017. The report assessed changes in violent death rates for all people aged 10–24 and for the age groups 10–14, 15–19, and 20–24. This example considers the trend in the rate of homicide deaths among all people aged 10–24. The assessment of the trend using all default options results in the plot shown in Figure V.

The trend was stable from 2000 to 2007, significantly decreased from 2007 to 2013, and then significantly increased from 2013 to 2017. Based on the points in the figure, there appears to be a possible joinpoint in 2016 that was not identified (that is, an increase before 2016 and then a decrease between 2016 and 2017). However, with the software defaults, the Joinpoint software is unable to detect this joinpoint because there must be at least two data points between the joinpoint and the end of the data (for example, because annual data are reported from 2000 to 2017, the last possible joinpoint can occur at 2015). However, changing the default to a minimum of one observation from either end of the data (to potentially detect a joinpoint in 2016 under the constraints) still does not detect a joinpoint at the end of the trend.

Although the Joinpoint software did not identify a joinpoint in 2016 after adjusting the defaults, a z test was performed for comparison. For vital statistics, z tests are commonly used for pairwise comparisons because the population variance is assumed to be known; for example, the NCHS report that accompanies the release of the annual death data file (for 2017, “Mortality in the United States, 2017” [15]), where differences between the most recent data year and the previous year are compared. Note that

Figure V. Trend plot from Joinpoint, homicide death rates among people aged 10–24: United States, 2000–2017



the z test can identify changes in the rates between 2 years but cannot be used for identifying changes in the overall trend. For this example, the difference between the rates for 2016 and 2017 was significant using a z test. However, the National Cancer Institute’s (NCI’s) Joinpoint software did not detect a joinpoint in 2016, and the relative magnitude of the difference between 2016 and 2017 (-5%) was small. Additionally, this change could be the result of a year-to-year fluctuation in the data or the beginning of a downward trend. This is an example of a situation where the results of NCI’s Joinpoint software are not definitive because Joinpoint is limited in evaluating joinpoints at the ends of a trend and further evaluation and alternative ways to test significance of apparent changes are not needed.

There have been instances in other analyses where adjusting the default model options have identified a suspected joinpoint near the end of the trend. For example, in another NCHS *Data Brief* evaluating drug overdose deaths among adolescents aged 15–19 (2), the Joinpoint software identified a joinpoint after adjusting the model options, but the APC was not significant. However, since the magnitude of the relative percent change between the last 2 years was large (19%), the z test was included in the findings of the report. These situations illustrate the challenge of detecting changes in a trend at the end of the study period when there are few points in the segment. In these cases, the analysts and subject-matter experts must determine how to present possible differences.

Example 4: Increasing the Maximum Number of Joinpoints

Health, United States is an annual report on trends in health statistics that is published by NCHS. This report includes evaluations of trends over the past 10 years for selected outcomes including health status and determinants, health care utilization, and health care resources. *Health, United States, 2018* (7) included the evaluation of the trend of nonreceipt of needed prescription drugs in the past 12 months due to cost among adults aged 18–64 for 2007–2017. These data were collected using NHIS and reported by poverty level, which is calculated as

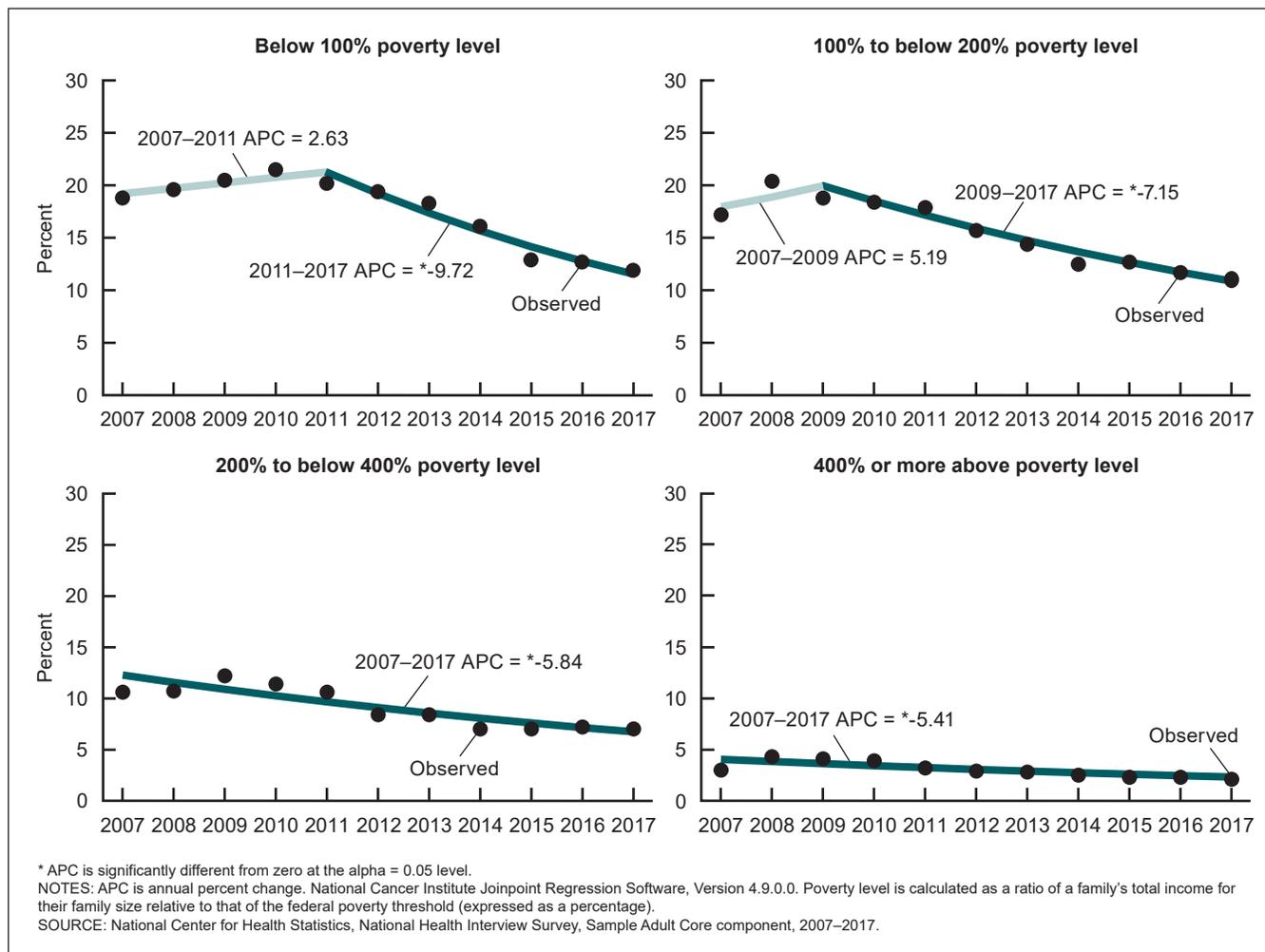
the ratio of a family’s total income for their family size relative to that of the federal poverty threshold.

Based on the Joinpoint’s software-recommended default maximum number of joinpoints, a maximum of one joinpoint would be specified for 11 data points. The results of the trend analyses for each subgroup are shown in [Figure VI](#). In this analysis, one joinpoint is identified in the trends for adults living below the poverty level (in 2011) and for adults living at 100% to 199% of the poverty level (in 2009), and no joinpoints are identified in the remaining two subgroups. However, in the production of *Health, United States*, linear, quadratic, and cubic trends are tested in separate regression models before evaluating the trend in the Joinpoint software. For the evaluation of nonreceipt of needed prescription drugs in the past 12 months due to cost, the preliminary evaluations in SUDAAN suggest significant cubic trends (results not shown), which are not consistent with the results from the Joinpoint software.

Because *Health, United States* evaluates trends over the past 10 years (11 data points), the trend analyses would be limited to identifying a single change in the trend (as shown in [Figure VI](#)) under the default Joinpoint software options. To resolve this issue, the *Health, United States, 2018* (7) technical notes state, “If a cubic trend is statistically significant and the analysis included at least 11 time points, Joinpoint software is used to search for up to two inflection points” (for example, increase the maximum number of joinpoints to two). The results of the trend analysis fit using a maximum of two joinpoints for each of the subgroups are shown in [Figure VII](#).

In this analysis, the trends for adults living below the poverty level and for adults at or above 400% of the poverty level are consistent with the trends identified when specifying a maximum of one joinpoint in the software. As reported in *Health, United States, 2018*, for adults living below the poverty level, the percentage who had

Figure VI. Trend plot from Joinpoint with a maximum of one joinpoint, percentage of adults aged 18–64 who did not get needed prescription drugs due to cost, by poverty level: United States, 2007–2017



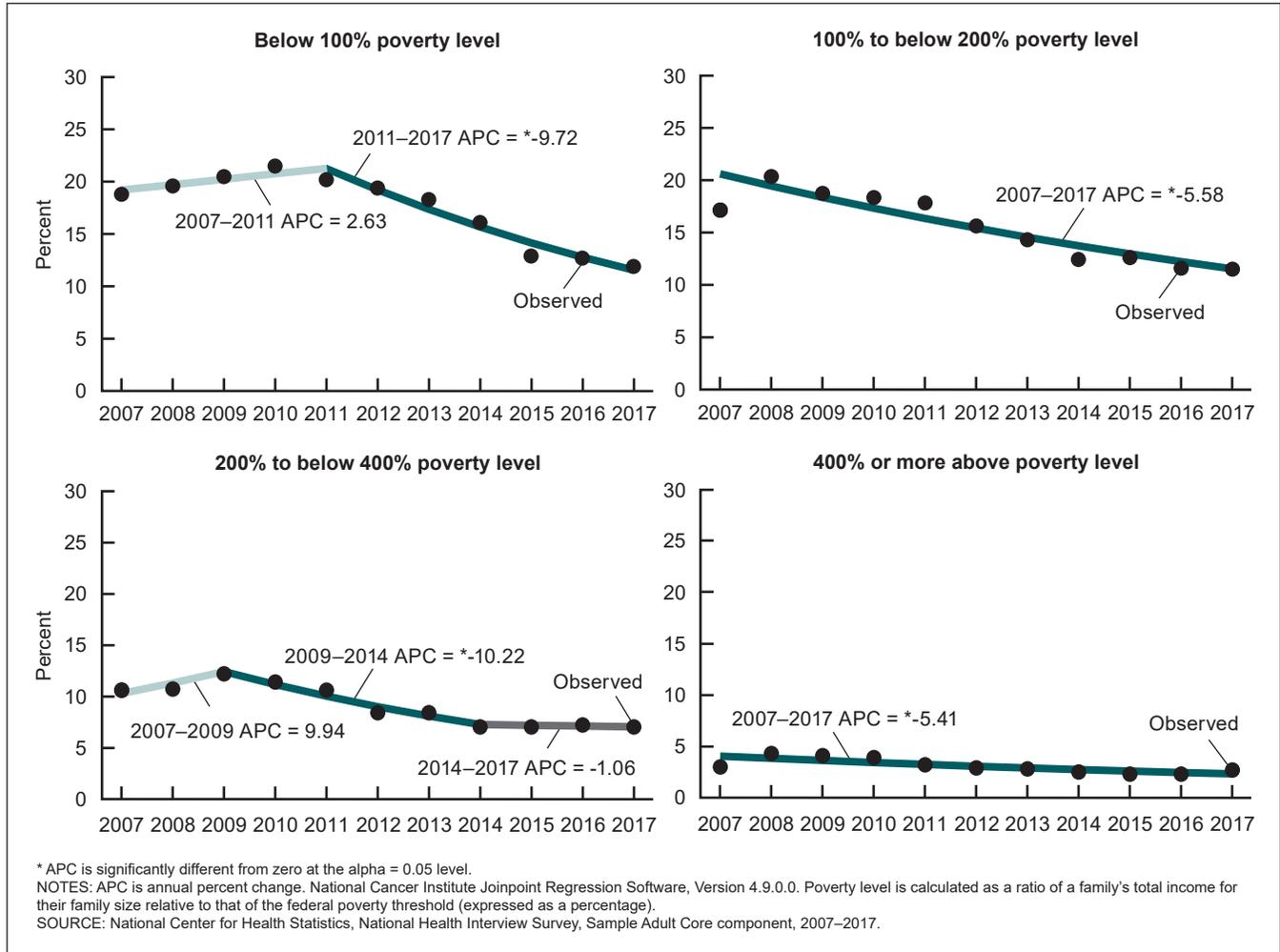
unmet prescription drug need increased from 2007 to 2010, and then decreased through 2017. For adults living at or above 400% of the poverty level, their unmet prescription need in 2017 was similar to the percentage in 2007, although an overall decreasing trend was observed from 2007 to 2017.

After increasing the maximum number of joinpoints to two, the trend for adults living at 200% to less than 400% of the poverty level was found to have two joinpoints in 2009 and 2014 (compared with no joinpoints in the previous analysis). This finding is consistent with the initial evaluation that suggested a significant cubic trend. For this subgroup, the percentage of adults who had an unmet prescription drug need increased from 2007 to 2009, decreased from 2009 to 2014, and then remained stable through 2017.

The trend analysis result for adults living at 100% to 199% of the poverty level appears to be surprising. In the analysis with a maximum of one joinpoint, a joinpoint was identified in 2009. However, under the analysis with a maximum of two joinpoints, no joinpoints are identified over the study period. This is an example of how increasing the specified maximum number of joinpoints can impact the significance testing

result for the permutation test model selection. For the test based on a maximum of one joinpoint, the permutation test is evaluated using a significance level of 0.05 and identifies one joinpoint (p value = 0.03). However, for the test based on a maximum of two joinpoints, the permutation test is evaluated twice with significance levels of 0.025 for each test (the test of zero joinpoints compared with one joinpoint has a p value of 0.028). This conservative approach results in the unexpected finding in this example. In this example, the Joinpoint software default of a maximum of one joinpoint for trend analyses of 11 time points is adjusted to specify a maximum of two joinpoints. In the case where there is evidence of a cubic trend over a period less than 12 time points, a user may choose to increase the specified maximum number of joinpoints.

Figure VII. Trend plot from Joinpoint with a maximum of two joinpoints, percentage of adults aged 18–64 who did not get needed prescription drugs due to cost, by poverty level: United States, 2007–2017



Example 5: Reducing the Maximum Number of Joinpoints Through the Minimum APC Difference Worth Detecting Feature

Trend analyses were used from a *National Vital Statistics Report* (NVSR) to assess changes in cancer and heart disease death rates among people aged 45–64 from 1999 to 2017 (5). In the NVSR, cancer and heart disease death rate trends were analyzed overall and by sex and race and ethnicity. For each evaluation, changes in the death rates over the time period were described and patterns in each trend were compared across groups. In the analysis, the default settings in the NCI Joinpoint software detected two joinpoints for most of the trends. However, there was one trend, cancer death rates for men aged 45–64, where three joinpoints were detected (Figure VIII).

The trend model for cancer death rates among men has an MSE of 1.04. The overall trend for this subgroup was a decrease. However, the period 2012–2015 had an APC coefficient (-0.88) that was not statistically significant.

Although joinpoints were detected in 2006, 2012, and 2015, the segments for 2006–2012 and 2012–2015 were both decreasing and the difference between the two were not of analytic interest. Note that the absolute difference between the APCs for 2006–2012 (-0.39) and 2012–2015 (-0.88) is small for this application (0.49). In this case, it is preferable to use fewer joinpoints to describe the trend. As described previously, the Minimum APC Difference Worth Detecting (MADWD) feature allows the user to use the default number of joinpoints but will remove joinpoints between segments where the change in APCs is relatively small.

Fitting the Joinpoint model with the MADWD option selected (with a minimum percentage point difference of 0.5, predetermined by subject-matter experts) produces the trend plot graph for men aged 45–64 shown in Figure IX. Selecting the MADWD option eliminates the brief period where the APC coefficient was not statistically significant. Given that most of the other trends in the NVSR (5) were already explained with two or fewer joinpoints, using the MADWD option also resulted in more consistency in comparing the trends across subgroups. Note that the

Figure VIII. Trend plot from Joinpoint, log-transformed cancer death rates among men aged 45–64: United States, 1999–2017

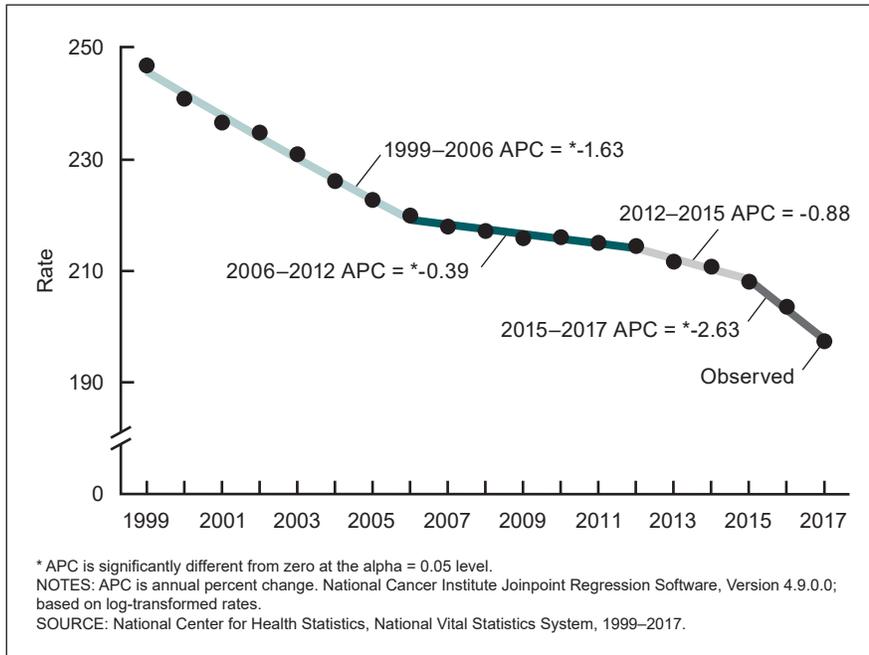
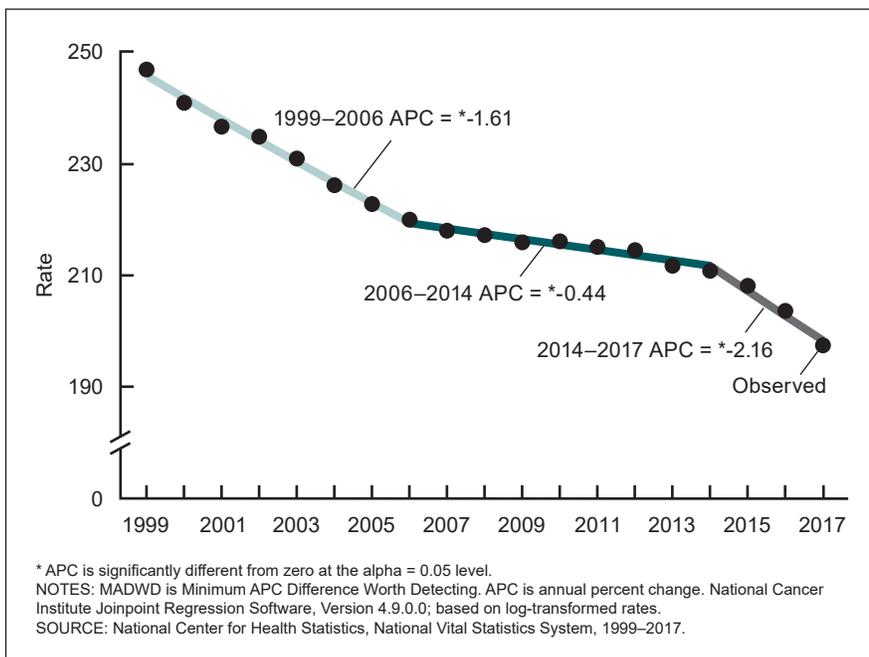


Figure IX. Trend plot from Joinpoint using the MADWD option, log-transformed cancer death rates among men aged 45–64: United States, 1999–2017



model obtained using the MADWD option is the same model obtained when specifying a maximum of two joinpoints (less than the default maximum number of joinpoints). In this case, the model selected (which has two joinpoints) had an MSE of 1.49. Although the model fit statistics indicate that the original model with three joinpoints provides the best fit for this subgroup, two joinpoints are preferred in this case because this improves the interpretability of the results for subgroup

comparisons and removes a joinpoint between two segments with similar APCs.

Example 6: Comparing Permutation Test and BIC Model Selection Methods

The National Ambulatory Medical Care Survey is a nationally representative sample survey of visits to nonfederally employed office-based physicians who are primarily engaged in direct patient care (16). A recent report used data to describe the trend in the percentage of preventive visits between 2005 and 2015 where weight and height were recorded for youth aged 2–11 years (6). Preventive visits include any visit reported for general medical examinations and routine periodic examinations to family practice physicians or pediatricians. Visits that did not record height and weight data were considered missing, which ranged from 2.9% to 13.1% over the time period. This example considers the choice of the model selection technique in the evaluation of this trend.

Because there are 11 time points in the data, the trend is evaluated using the permutation test (the default option and NCI’s recommended approach based on the number of data points). The resulting trend model is shown in Figure X. In this case, the Joinpoint software did not identify any joinpoints (linear trend), and the resulting model has an MSE of 2.74. The results of the segmented regression suggest that the percentage of preventive visits where weight and height were recorded for youth aged 2–11 is slightly increasing between 2005 and 2015, although it is not statistically significant. However, from the plot, the trend line does not appear to fit the data well, which could be in part due to the small number of time points being evaluated and the relatively small sample sizes for each year of data. An initial evaluation of linear, quadratic, and cubic trends in SUDAAN found a significant quadratic trend ($p = 0.004$, results not shown),

Figure X. Trend plot from Joinpoint using the permutation test, log-transformed percentage of visits where weight and height were recorded among preventive visits made by youth aged 2–11 years: United States, 2005–2015

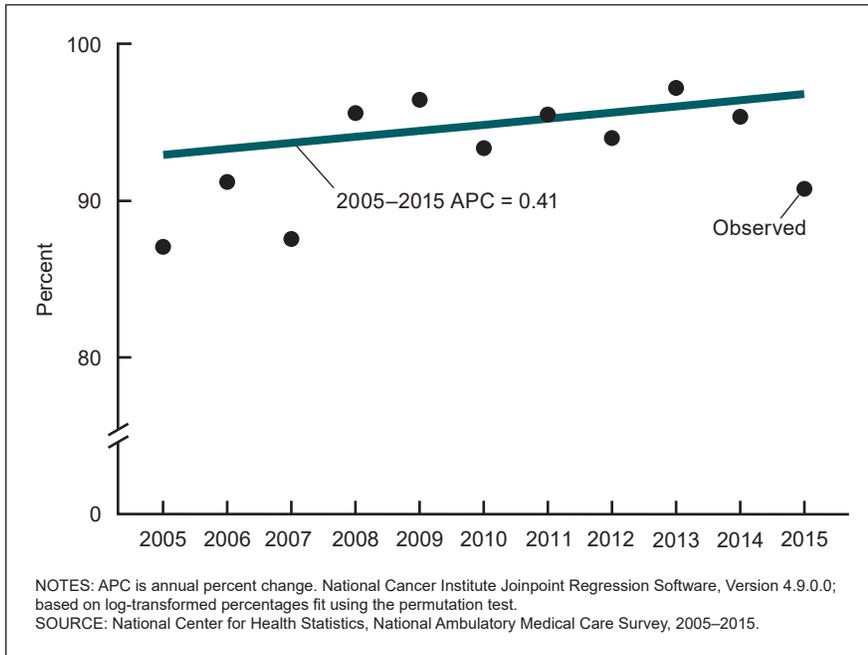
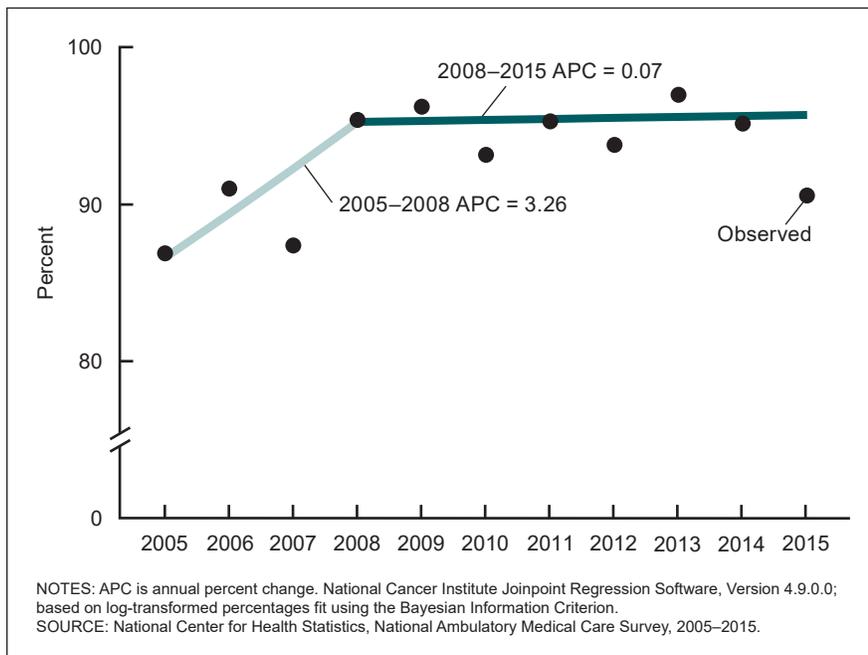


Figure XI. Trend plot from Joinpoint using the Bayesian Information Criterion, log-transformed percentage of visits where weight and height were recorded among preventive visits made by youth aged 2–11 years: United States, 2005–2015



which supports a trend model with one joinpoint.

In order to assess changes over the trend, even with small effect sizes, BIC is considered as an alternative model selection method. The resulting trend plot using the BIC approach is shown in Figure XI. In this case, the model has an MSE of 2.21 and identifies one joinpoint in 2008. Visual inspection of the plot and the model fit statistic (that is, MSE) suggest that this model has an improved fit. Additionally, the identification of one joinpoint is supported by the prior test of quadratic trends, which accounted for the survey design.

In this example, the default model selection method, the permutation test, is compared with BIC in a step-by-step procedure. However, note that the data dependent selection method selects the optimal method between BIC and BIC3 (which performs similarly to the permutation test) based on the estimated effect sizes. This option can be useful to users for determining the optimal model selection method using a data-driven approach. For this particular data set, the data dependent selection method selects the BIC approach, which agrees with the conclusions reached through the step-by-step procedure described previously.

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