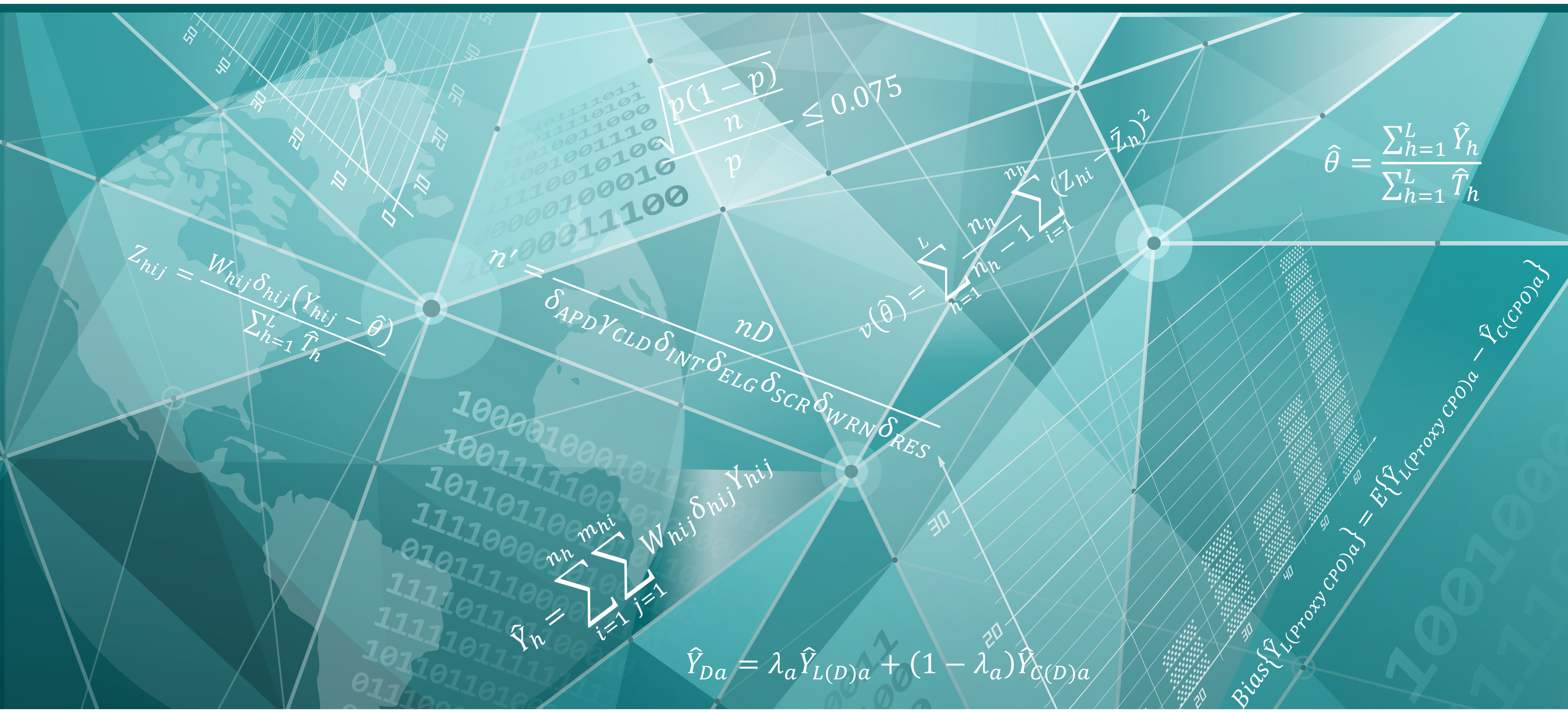
NATIONAL CENTER FOR HEALTH STATISTICS

Vital and Health Statistics

Series 2, Number 209 September 2024



Technical Guidance for Using the Modified Kalman Filter in Small-domain Estimation at the National Center for Health Statistics

Data Evaluation and Methods Research

U.S. CENTERS FOR DISEASE CONTROL AND PREVENTION

NCHS reports can be downloaded from: https://www.cdc.gov/nchs/products/index.htm.

Suggested citation

Talih M, Rossen LM, Patel P, Earp M, Parker JD. Technical guidance for using the modified Kalman filter in small-domain estimation at the National Center for Health Statistics. National Center for Health Statistics. Vital Health Stat 2(209). 2024. DOI: https://dx.doi.org/10.15620/cdc/157496.

For sale by the U.S. Government Publishing Office
Superintendent of Documents
Mail Stop: SSOP
Washington, DC 20401–0001
Printed on acid-free paper.

NATIONAL CENTER FOR HEALTH STATISTICS

Vital and Health Statistics

Series 2, Number 209 September 2024

Technical Guidance for Using the Modified Kalman Filter in Small-domain Estimation at the National Center for Health Statistics

Data Evaluation and Methods Research

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

Hyattsville, Maryland
September 2024

National Center for Health Statistics

Brian C. Moyer, Ph.D., *Director*

Amy M. Branum, Ph.D., *Associate Director for Science*

Division of Research and Methodology

Jennifer D. Parker, Ph.D., *Director*

John R. Pleis, Ph.D., *Associate Director for Science*

Contents

Text Figures

Detailed Table

Contents—Con.

Appendix Figures

Appendix Table

Acknowledgments

The first author completed this work under a contract with Windsor Group, LLC, a Centers for Disease Control and Prevention, National Center for Health Statistics contract holder. The authors would like to thank Claude Setodji and colleagues at the RAND Corporation who developed the original modified Kalman filter approach.

Technical Guidance for Using the Modified Kalman Filter in Small-domain Estimation at the National Center for Health Statistics

by Makram Talih, Ph.D., Lauren M. Rossen, Ph.D., Priyam Patel, M.S.P.H., Morgan Earp, Ph.D., and Jennifer D. Parker, Ph.D.

Abstract

Background

The modified Kalman filter (MKF) produces model-based estimates for small populations by borrowing strength across groups, over time, and between health outcomes, consequently improving the reliability of estimates and the measurement of disparities. An earlier implementation of the MKF procedure featured linear time-trend models, equally spaced data points, and fixed sampling variances. While those features were appealing in proof-of-concept studies, they hindered adoption in data that exhibited nonlinear trends, were irregularly spaced, and included random sampling variances. The National Center for Health Statistics recently evaluated the earlier MKF procedure to broaden its scope and allow for its use in producing model-based estimates for small populations.

Objective

This report documents differences between the earlier and enhanced MKF procedures and provides technical guidance for use of the latter in small-domain estimation at the National Center for Health Statistics.

Results

The enhanced MKF procedure accommodates nonlinear time trends, irregularly spaced data points, and random sampling variances for the underlying population subgroup estimates. Bayesian estimation is implemented adaptably and transparently in a macro that uses PROC MCMC and related SAS 9.4 procedures instead of relying on an associated executable file that could not be modified or inspected by end users. Bayesian model averaging, which renders MKF predictions more robust to trend model misspecification, uses a mixture prior approach instead of relying on values of the Bayesian information criterion. Various other enhancements improve functionality and usability relative to the earlier macro.

Conclusions

The enhanced MKF procedure enables production of model-based estimates for small populations where direct estimates may lack precision, improving the availability of data for assessing and monitoring health disparities. Methodological improvements relative to the earlier procedure allow for more transparency in the underlying models and more flexibility in generating estimates under different scenarios, such as nonlinear trends, irregularly spaced data points, and random sampling variances.

Keywords: mixed-effects model • state-space model • Bayes factor • complex health survey • vital statistics • statistical reliability

Introduction

The National Center for Health Statistics (NCHS) is the nation's principal health statistics agency, conducting and supporting statistical and epidemiological activities to improve the effectiveness, efficiency, and quality of health services in the United States. NCHS collects and analyzes population data from birth and death records, medical records, health interview surveys, and health examinations, resulting in dissemination of critical public health information, for example, on health status and determinants, health care access and use, and health disparities.

NCHS uses thorough and transparent data presentation standards to inform users of its products on whether published estimates are considered statistically reliable (1,2). Many factors contribute to statistical reliability, including but not limited to, sample size, precision, and, for survey-based estimates, design effects. As a result, statistically reliable estimates for small population subgroups or rare health outcomes are scarce and typically require the aggregation of multiple time points, potentially jeopardizing their timeliness and public health relevance.

Model-based methods can improve the precision of estimates for small population subgroups and rare health outcomes by borrowing strength over time, across groups, and between related health outcomes (3–7). The earlier modified Kalman filter (MKF) procedure and accompanying SAS macro were developed in 2009–2012 to generate improved estimates for small racial and ethnic populations for which direct estimates were statistically unreliable, as defined at the time using a relative standard error (RSE) criterion of RSE ≥ 30% (8–11). The papers describing the development and evaluation of the earlier MKF relied on previous years of cross-sectional National Health Interview Survey (NHIS) data to generate improved prevalence estimates for the most current year of NHIS data for small population groups. The approach used a model-based prediction technique called the Kalman filter, which assumed a linear time trend in the true health state of each population subgroup—borrowing strength over time to recursively project past data forward to the most recent data year. Shared random effects that flexibly captured deviations from each group's linear trend were also featured in the earlier MKF—borrowing strength across groups to improve variance estimation. Additionally, when two correlated health outcomes were considered, the earlier MKF procedure and macro allowed for model-based estimates from one outcome to inform the estimation of the other outcome—borrowing strength across health outcomes (8–11).

The earlier MKF procedure featured linear time trends, equally spaced data points, and fixed sampling variances for the underlying population subgroup means, rates, or proportions. The earlier MKF macro also relied on an associated executable file with precompiled C code for Bayesian estimation. While those features were appealing in proof-of-concept studies (8,9), they hindered wider adoption in the context of data that exhibited nonlinear trends, were irregularly spaced, and included random sampling variances.

NCHS recently implemented several enhancements to the earlier MKF procedure and macro to broaden their scope and allow for their use in producing model-based estimates for small populations. This report documents methodological and operational differences between the earlier MKF and the enhanced MKF procedures and macros and provides technical guidance for the use of the latter in small-domain estimation at NCHS.

Earlier MKF Procedure

The statistical model underlying the earlier MKF procedure was a **mixed-effects model** (8–11):

$$y_{gt} = \mu_{gt} + \gamma_{gt} + \varepsilon_{gt}.$$

- **Population subgroup means, rates, or proportions** y_{gt} for group *g* at time *t* were direct estimates obtained from complex health survey data (using appropriate weighting) or from vital statistics.
- **Fixed effects** μ_{gt} for group *g* at time *t* were assumed to be linear in time, of the form:

$$\mu_{gt} = \beta_{0g} + \beta_{1g}t.$$

- **Random effects** γ_{gt} followed a first-order autoregressive—AR(1)—process with an autocorrelation coefficient $\rho, |\rho| < 1$, and a so-called "innovation" variance τ^2 that were common parameters across groups. In other words, for equally spaced time points, it was assumed that the random effect γ_{gt+1} for group *g* at time $t+1$ was a function of its value γ_{gt} at time *t* plus an independent random "innovation" or exogenous shock ξ_{gt}, that is

$$\gamma_{gt+1} = \rho\gamma_{gt} + \xi_{gt}$$

  where the innovations ξ_{gt} were normally distributed with mean zero and variance τ^2 and were independent of the γ_{gt}. The AR(1) process was assumed to be stationary, having started at time $t = 0$ with γ_{gt} drawn according to a normal distribution with mean zero and variance $\tau^2/(1-\rho^2)$ and remained distributed accordingly at later times.
- **Sampling errors** ε_{gt} were assumed to be normally distributed with mean zero and known variances σ^2_{gt}. The variances σ^2_{gt} were replaced with their sample versions S^2_{gt}, but neither estimation nor sampling errors in variance estimation were otherwise accounted for.
- To guard against model uncertainty in the maximum likelihood-based estimation of trend coefficients, the earlier MKF macro enabled users to conduct **model averaging** over linear trend models with varying restrictions on the coefficients, to include:
  - A **group-specific linear** trend $\mu_{gt} = \beta_{0g} + \beta_{1g}t$ for each group *g* (with independent slopes and intercepts across groups)
  - A **common linear** trend $\mu_{gt} = \beta_{0g} + \beta_1 t$ (with independent intercepts across groups)
  - An **intercepts-only** model $\mu_{gt} = \beta_{0g}$ where all group-specific trends were dropped
- A **Bayesian hierarchical model** was also available in the earlier MKF macro, referred to as a "fully Bayesian" linear trend model, allowing group-specific regression coefficients β_{kg}, $k = 0,1$, to arise as independent draws from an underlying normal distribution with mean θ_k and variance ν^2_k. As a result, the group-specific coefficients β_{kg} could be "shrunk" toward their common means, $E(\beta_{kg}) = \theta_k$, further borrowing strength; see Appendix I.
- Users of the earlier MKF macro could request that health disparities among population subgroups be estimated in the Bayesian setting. All **pairwise differences** and their standard errors were estimated, and users could specify one of the population groups to use as the reference for tabulation purposes (10,11).

The scope of the earlier MKF procedure and macro limited their applicability to NCHS data systems in the following ways:

- Some of the trend data published by NCHS exhibit nonlinearities, for example, quadratic, or even cubic trends (12–17). With nonlinear trends, the lack of model fit when a linear trend is used for the fixed effects would inflate variance for the random effects, negating any advantages of borrowing strength from past time points (9).
- The earlier MKF macro was restricted to equally spaced time points (10,11), yet NCHS data are sometimes irregularly spaced, for example, due to survey redesign, changes in sponsored supplements, or breaks in periodicity of selected questionnaire items or tests.
- Variance estimates are subject to stochastic variability (in the case of vital statistics data) or sampling variability (in the case of survey data) that should be accounted for (2,5–7), yet the earlier MKF procedure assumed known variances (8–11).
- Model averaging in the earlier MKF macro relied on each model's Bayesian information criterion (BIC) value—a widely used criterion for comparing statistical models by rating their goodness-of-fit relative to their complexity—to obtain an approximation to the natural logarithm of the Bayes factor relative to the null, intercepts-only model (9). Bayes factors measure the evidence in support of each model relative to the null, and are used as weights for averaging predictions and prediction errors across models for the true health states $\eta_{gt} = \mu_{gt} + \gamma_{gt}$ at time point t. However, even when the number of data points is very large, the relative error in approximating the Bayes factor remains bounded away from zero, producing possibly inaccurate estimates (18).
- Because Bayesian estimation in the earlier MKF macro was incorporated into an associated external executable file (10,11), it was only available for the trend models that were specified in the earlier MKF procedure. Modifying model specifications or the sampling algorithms used in Bayesian estimation was not possible.
- Random effects were assumed to be independent draws from a common distribution with shared AR(1) parameters ρ and τ^2 across groups. With sufficient data, more accurate estimates may be obtained with group-specific parameters ρ_g and τ_g^2 (8).

Enhanced MKF Procedure

The enhanced MKF procedure and macro accommodate nonlinear time trends, irregularly spaced data points, and random sampling variances for the underlying population subgroup means, rates, or proportions. Bayesian estimation is implemented adaptably and transparently using PROC MCMC (Markov Chain Monte Carlo) and related SAS 9.4 procedures instead of relying on code that was neither modifiable nor inspectable by end users. Bayesian model averaging, which renders predictions more robust to the misspecification of the polynomial trend, uses a mixture prior approach to obtain relative model weights for averaging predictions across models. In the earlier MKF macro, BIC was used instead because it was more readily available from standard statistical software—as mentioned before, BIC balances goodness-of-fit with model complexity and reflects a preference for more parsimonious (simpler) models—and offered a reasonable approximation to the correct model averaging weights. Various other features in the enhanced MKF macro also improve its functionality and usability relative to the earlier macro. An overview of the enhanced MKF procedure and macro is provided in the following section, and full technical details are provided in Appendixes I and II.

The statistical model underlying the enhanced MKF procedure remains a mixed-effects model:

$$y_{gt} = \mu_{gt} + \gamma_{gt} + \varepsilon_{gt}.$$

- Population subgroup means, rates, or proportions y_{gt} for group g at time t are direct estimates obtained from complex health survey (appropriately weighted) or vital statistics data.
- Fixed effects μ_{gt} follow a possibly **nonlinear (polynomial) time trend**, which, in the enhanced MKF macro, takes the form:

  $$\mu_{gt} = \beta_{0g} + \beta_{1g}t + \beta_{2g}t^2 + \beta_{3g}t^3.$$

  As a result, by imposing a series of constraints on the regression coefficients, the following trend models are available in the enhanced MKF macro:

  1. A **group-specific cubic** trend for each group g, with unconstrained cubic (β_{3g}), quadratic (β_{2g}), and linear terms (β_{1g}) that are independent across groups
  2. A **group-specific quadratic** trend for each group g, with $\beta_{3g} \equiv 0$ and independent quadratic (β_{2g}) and linear terms (β_{1g}) across groups
  3. A **group-specific linear** trend for each group g, with $\beta_{3g} \equiv 0$, $\beta_{2g} \equiv 0$, and independent linear terms (β_{1g}) across groups
  4. A **common cubic** trend across groups, with $\beta_{3g} \equiv \beta_3$, $\beta_{2g} \equiv \beta_2$, and $\beta_{1g} \equiv \beta_1$
  5. A **common quadratic** trend across groups, with $\beta_{3g} \equiv 0$, $\beta_{2g} \equiv \beta_2$, and $\beta_{1g} \equiv \beta_1$
  6. A **common linear** trend across groups, with $\beta_{3g} \equiv 0$, $\beta_{2g} \equiv 0$, and $\beta_{1g} \equiv \beta_1$
  7. An **intercepts-only** model for each group, with $\beta_{3g} \equiv 0$, $\beta_{2g} \equiv 0$, and $\beta_{1g} \equiv 0$, dropping all group-specific trends

- Collinearities among linear, quadratic, and cubic terms may lead to unstable estimates. For this reason, and to retain comparability between coefficients in different dimensions, the enhanced MKF macro uses **orthogonal polynomials**; see Appendix I.
- Random effects γ_{gt} still follow a stationary AR(1) process in the enhanced MKF procedure, but due to the possibly

irregularly spaced time points $t_1 < t_2 < \ldots < t_n$, the autoregression is written for any two time points s and t with $|t-s|>0$ as

$$\gamma_{gt} = \rho^{|t-s|}\gamma_{gs} + \xi_{gs},$$

where the "innovations" ξ_{gs} are normally distributed with mean zero and variance

$$\tau^2\left(1-\rho^{2|t-s|}\right)\Big/\left(1-\rho^2\right)$$

and are independent of the γ_{gs}. The stationary variance remains $\tau^2/(1-\rho^2)$, as in the earlier MKF procedure.

- Sampling errors ε_{gt} remain normally distributed with mean zero and variances S_{gt}^2. However, conditional on group-specific variance parameters σ_g^2, the **sample variances** S_{gt}^2 in the enhanced MKF procedure are modeled as **scaled chi-squared** variables with $n_{gt} - 1$ degrees of freedom, where n_{gt} is the (effective) sample size for group g at time t. In other words, conditional on σ_g^2, the ratios $(n_{gt}-1)S_{gt}^2/\sigma_g^2$ follow a $\chi^2(n_{gt}-1)$ distribution. The unknown **variance parameters** σ_g^2 are assumed to arise from an **inverse-gamma distribution**, which, being conjugate to the chi-squared distribution, gives a convenient closed-form analytic expression to use in Bayesian estimation (5–7); see Appendix I.
- In the enhanced MKF macro, **Bayesian model averaging** is conducted entirely within the Bayesian paradigm, and Bayes factors are estimated from the marginal distribution of the y_{gt} instead of approximated using BIC. A **mixture prior** distribution is assumed for the regression coefficients (for example, with equal prior weights given to each of the seven sets of constraints in the cubic trend model described previously), resulting in a mixture posterior distribution that is equivalent to model averaging (19); see Appendix I.
- **Bayesian estimation** in the enhanced MKF macro is implemented adaptably and transparently using PROC MCMC and related SAS 9.4 procedures (such as PROC FCMP) instead of relying on an associated external executable file, with precompiled C code, that was neither modifiable nor inspectable by end users. As a result, it is possible for experienced end users to modify model specifications or the Bayesian sampling algorithms in the enhanced MKF macro to suit their needs. The enhanced MKF macro parameter settings, default values, and functionality are described in detail in Appendix II. The full SAS code of the enhanced MKF macro is available from: https://github.com/CDCgov/eMKF.
- As in the earlier MKF macro, users of the enhanced MKF macro can request that health disparities be estimated in the Bayesian setting. In addition to all pairwise differences, the enhanced MKF macro calculates all **pairwise ratios** and their standard errors from the posterior samples. The enhanced MKF macro also allows users to request that disparities (differences and ratios) be displayed relative to the group with the most favorable (or least adverse) health outcome—instead of specifying one of the population groups as the reference group—and compute **overall measures of disparity**, such as the maximal rate difference, maximal rate ratio, and summary rate ratio (20,21). Interested users can further calculate other health disparities measures directly from the posterior samples; users can save all posterior draws to a data set for later analysis.
- To allow for the possibility that more accurate estimates may be obtained if **group-specific AR(1) parameters** ρ_g and τ_g^2 were allowed (8), while preserving the borrowing of strength across groups, the ρ_g and τ_g^2 in the enhanced MKF macro can be drawn from a common distribution and shrunk toward their means $\rho = E(\rho_g)$ and $\tau^2 = E(\tau_g^2)$, respectively; see Appendix I.

Guided Example

This section describes a typical application of the enhanced MKF macro to NCHS data, including the use of nonlinear time trends, unequally spaced time points, and random sampling variances. Although the example in this section uses data from the National Health and Nutrition Examination Survey, the enhanced MKF macro can potentially be used with any other population- or household-based survey data, vital statistics data, or other types of data (for example, administrative data, web-panel data, or electronic health record data). A case study of the enhanced MKF macro with state-level mortality data by age group, race, and Hispanic origin is available from: https://github.com/CDCgov/eMKF. Additional public-use examples may be available in the future through that GitHub location for users to explore.

Bayesian model averaging over the available trend models is the default specification in the enhanced MKF macro because it protects against misspecification of the trend form and accounts for the uncertainty in model selection through the model-averaged predictions. However, it is possible to select other specifications (for example, maximum likelihood-based estimation of a common linear trend model across groups) in certain analyses where subject-matter, statistical, or computational considerations preclude the default specification; see Appendix II for a detailed description of the enhanced MKF macro parameter settings and default values. Alternatives to the default macro specification are presented in "Alternatives to Bayesian Trend Model Averaging" and illustrated in Appendix III; they should be discussed with a mathematical statistician or clearance official.

Input Data Set

Data input to the enhanced MKF macro are required to be in long (stacked) format, with each row representing a time- and group-specific estimate. Additional columns required include time point and population group identifiers, standard errors, and (effective) sample sizes. The Table shows input public-use data on obesity prevalence among U.S. adults from the National Health and Nutrition Examination Survey, a nationally representative cross-sectional survey of the U.S. civilian noninstitutionalized population. The survey captures both self-reported health data through in-person interviews and measured health status assessed through in-person examinations by health professionals (see: https://www.cdc.gov/nchs/nhanes/index.htm).

While the time point variable ("Year" in the Table) must be numeric, a label variable may be included to designate the period that each time point refers to ("Year" is the midpoint of a given survey cycle identified in the Table). A stratification variable can also be included, for example, age group, as shown in the "Age group" column. As in the earlier MKF, while missing estimates are not accepted, some (but not all) estimates and standard errors may be zero; cells with zero standard errors are subsequently imputed using an average over the nonzero standard errors for that group and stratum (10,11) or, at worst, an average across strata for that group and time point. These built-in imputation strategies should not prevent users from carefully considering whehter to combine groups or time points to reduce substantial missingness.

For the data shown in the Table, body mass index was calculated from measured height and weight and was defined as weight (kilograms) / [height (meters)]^2. For both men and women, obesity was indicated by a body mass index of 30.0 or higher. The population group variable used was race and Hispanic origin, consisting of the categories Black non-Hispanic (subsequently, Black); White non-Hispanic; other race non-Hispanic, which also includes non-Hispanic people identifying as more than one race; Mexican American; and other Hispanic. The stratification variable used was age group (18–24, 25–44, 45–64, and 65 and older).

Unequally Spaced Data Points

Unlike the earlier macro, the enhanced MKF macro accommodates irregularly spaced data. In the Table, data are biennial starting in 1999–2000, except for the last data point, which consists of data from the 2017–March 2020 prepandemic file (22).

Random Sampling Variances

The Table includes an effective sample size column, which is required for modeling the sample variances as scaled chi-squared random variables (the default option in the enhanced MKF macro). Unless impractical, users should account for the uncertainty in estimating the sample variances; to do so, the (effective) sample sizes must be provided as part of the input data. In the case of survey data where estimates are proportions (percentages divided by 100), users may calculate the effective sample sizes from the ratios $n_{gt}^{(\text{eff})} = y_{gt}\left(1 - y_{gt}\right) / \text{SE}_{gt}^2$, where y_{gt} is the sample proportion for group g at time t and SE_{gt} is the corresponding standard error.

Bayesian Trend Model Averaging

A description of the full set of enhanced MKF macro parameters is included in Appendix II. To provide the reader with a snapshot of the macro's functionality, the following SAS code snippet shows a typical call to the enhanced MKF macro from within an active SAS session:

```
%mkf(data        = NHANESobesity,
     group       = Population,
     time        = Year,
     by          = Age,
     outcome     = Obesity,
     se          = SE_obesity,
     neff        = NEFF_obesity,
     Bayesmodel  = bma_cubic,
     comparedto  = MIN,
     out         = bmac);
```

The full SAS program for this example, as well as additional examples using other NCHS health surveys or vital statistics, are available from: https://github.com/CDCgov/eMKF.

The data set name (`data`) and the names of the columns indicating the population group (`group`) and time points (`time`) are required. The optional `by` variable allows users to indicate a stratification variable—here, age group—although users may also create composite population groups (for example, by age and race and ethnicity) to borrow strength across groups defined using multiple dimensions. The `outcome` and `se` macro variables are required and indicate the names of the columns in the input SAS data set containing the desired outcome variable (rate, proportion, or mean) and its (design-based) standard error. The (effective) sample size variable (`neff`) must be specified to run a Bayesian model with random sampling variances, which is the default setting in the enhanced MKF macro. In the maximum likelihood-based estimation setting (Appendix III), or if option `randomVars = NO` is specified in the Bayesian setting to override the default (perhaps due to the unavailability of effective sample sizes), the enhanced MKF macro treats variances as known, as in the earlier MKF macro, and `neff` is ignored.

As in the earlier MKF macro, Bayesian estimation is the default method in the enhanced MKF macro when only one outcome is specified. In the enhanced MKF macro, the macro variable `Bayesmodel` can be any one the following options, corresponding to the trend models listed previously, respectively: 1) `indep_cubic`, 2) `indep_quad`, 3) `indep_linear`, 4) `common_cubic`, 5) `common_quad`, 6) `common_linear`, and 7) `dropped` (intercept only). Unless subject-matter or statistical considerations are such that only one of the trend models 1–7 is deemed appropriate, model averaging should be used to guard against misspecification of the trend form and better account for the uncertainty in model selection.

Bayesian model averaging is specified using one of the following options for the `Bayesmodel` variable: a) `bma_` cubic, b) bma_quad, or c) bma_linear.

- Option a) Bayesmodel = bma_cubic is equivalent to listing all seven models to be averaged—namely, Bayesmodel = indep_cubic indep_quad indep_linear common_cubic common_quad common_linear dropped.
- Option b) Bayesmodel = bma_quad is equivalent to listing all five trend models up to quadratic: Bayesmodel = indep_quad indep_linear common_quad common_linear dropped.
- Option c) Bayesmodel = bma_linear is equivalent to Bayesmodel = indep_linear common_linear dropped.

The comparedto macro variable in the example SAS code snippet shown previously allows for the estimation of health disparities; see "Estimating Health Disparities." The out macro variable specifies the prefix to use for SAS data sets that are created when the macro run is completed. As in the earlier MKF macro, output data sets contain parameter estimates, predictions, and other information useful to end users who want to go beyond the tabulated and formatted results shown in the SAS output text or HTML file.

Figure 1 displays the first portion of formatted output resulting from running the example SAS code. For the last time point, which corresponds to the midpoint of the National Health and Nutrition Examination Survey 2017–March 2020 cycle, the direct and MKF-based estimates are shown for each combination of age group and race and ethnicity. As a trade-off with slight increases in bias (as measured by the standardized differences between MKF and direct estimates; "Std. Diff" in Figure 1), all MKF estimates show reductions in the root mean squared error (RMSE), with relative RMSEs (relative to the unbiased direct estimates; "Rel. RMSE" in Figure 1) ranging from 0.4720 for Mexican-American adults ages 18–24 to 0.9617 for Black adults ages 25–44. The standardized difference is the difference between the model-based and direct estimates, divided by the RMSE of the latter. The relative RMSE is the ratio of the model-based RMSE to the direct RMSE. In other words, at worst, MKF-based estimation is equivalent to a 4.0% increase in effective sample size (1.040 = 1/0.9617), whereas at best, it is equivalent to a twofold increase (2.119 = 1 / 0.4720). Those improvements are also reflected in narrower Wald 95% confidence intervals (Figure 1). For direct estimates, RMSE = SE, because the survey-weighted sample proportion is assumed to be an unbiased estimator of the population proportion. Wald 95% confidence intervals are constructed for both direct and model-based estimates using the formula: (point estimate) ± 1.96 • RMSE.

Estimating Health Disparities

In the Bayesian setting, the enhanced MKF macro can calculate disparities (differences and ratios) relative to the minimum, maximum, or any one of the population subgroups listed in the group column in the input data set. This must be explicitly specified by the user, because by default, estimation of disparities is omitted due to the higher computational burden. In the example SAS code, disparities are requested relative to the minimum or lowest group proportion (the most favorable outcome in this example), and this is specified using comparedto = MIN. Disparities are not calculated in the maximum likelihood-based estimation setting; see Appendix III.

Figure 2 displays the disparities portion of the formatted output from the example SAS code. For the last time point (the midpoint of the National Health and Nutrition Examination Survey 2017–March 2020 cycle) and each combination of age group and race and ethnicity, both absolute disparities (differences) and relative disparities (ratios) are estimated from the posterior sample, together with their RMSEs. Wald and log-normal 95% confidence intervals are also calculated for the differences and ratios, respectively. Each block of output displays: 1) a maximal (or range) measure, which compares the maximum with the minimum proportion across groups; 2) a summary measure, which compares the reference proportion (minimum, here) with the average proportion across the groups that did not achieve the minimum; and 3) pairwise comparisons between each of the race and ethnicity groups and the reference proportion.

Number of Data Points

Consistent with "National Center for Health Statistics Guidelines for Analysis of Trends" (17), fitting a degree k polynomial trend (k = 0, 1, 2, 3) generally requires k + 2 available data points for each of the population subgroups included in the analysis within each stratum. As a general rule, at least two additional data points should be available for each group to account for estimating the AR(1) parameters ρ_g and τ_g^2, for a minimum total of k + 4 data points generally required per group (and stratum) to fit a degree k polynomial trend. By default, the enhanced MKF macro returns an error if the required number of time points is not met. Users are advised to consult with a mathematical statistician or their clearance official if an exception to the previously stated rule is deemed necessary, in which case the macro parameter checkSampleSize should be set to NO; see Appendix II. Note that in all cases, the enhanced MKF macro will return an error if there is only one data point per group.

Figure 1. Part 1 output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter Bayesian model average up to the unconstrained cubic trend, with random sampling variances and common autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity

Age	Population	Year	Estimation type	Point estimate	RMSE	Wald 95% CI	Std. diff	Rel. RMSE
18-24	Black, non-Hispanic	2018.6	Sample	0.3387	0.0370	[0.2662, 0.4112]	~~	~~
			MKF estimate	0.3230	0.0268	[0.2705, 0.3755]	-0.4241	0.7237
25-44	Black, non-Hispanic	2018.6	Sample	0.4911	0.0218	[0.4484, 0.5338]	~~	~~
			MKF estimate	0.4972	0.0210	[0.4561, 0.5382]	0.2780	0.9617
45-64	Black, non-Hispanic	2018.6	Sample	0.5724	0.0154	[0.5423, 0.6025]	~~	~~
			MKF estimate	0.5607	0.0132	[0.5348, 0.5867]	-0.7566	0.8618
65+	Black, non-Hispanic	2018.6	Sample	0.4897	0.0222	[0.4461, 0.5334]	~~	~~
			MKF estimate	0.4857	0.0204	[0.4456, 0.5258]	-0.1830	0.9190
18-24	White, non-Hispanic	2018.6	Sample	0.3079	0.0520	[0.2060, 0.4099]	~~	~~
			MKF estimate	0.2585	0.0318	[0.1962, 0.3208]	-0.9500	0.6109
25-44	White, non-Hispanic	2018.6	Sample	0.4221	0.0210	[0.3809, 0.4633]	~~	~~
			MKF estimate	0.4121	0.0189	[0.3751, 0.4490]	-0.4763	0.8972
45-64	White, non-Hispanic	2018.6	Sample	0.4232	0.0296	[0.3651, 0.4813]	~~	~~
			MKF estimate	0.4354	0.0213	[0.3936, 0.4771]	0.4124	0.7184
65+	White, non-Hispanic	2018.6	Sample	0.4233	0.0229	[0.3784, 0.4681]	~~	~~
			MKF estimate	0.4099	0.0210	[0.3686, 0.4511]	-0.5855	0.9194
18-24	Other race, non-Hispanic	2018.6	Sample	0.2918	0.0491	[0.1955, 0.3881]	~~	~~
			MKF estimate	0.2176	0.0352	[0.1486, 0.2867]	-1.5099	0.7170
25-44	Other race, non-Hispanic	2018.6	Sample	0.3087	0.0259	[0.2579, 0.3595]	~~	~~
			MKF estimate	0.2991	0.0226	[0.2547, 0.3434]	-0.3716	0.8732
45-64	Other race, non-Hispanic	2018.6	Sample	0.3246	0.0428	[0.2407, 0.4084]	~~	~~
			MKF estimate	0.2655	0.0253	[0.2160, 0.3150]	-1.3809	0.5904
65+	Other race, non-Hispanic	2018.6	Sample	0.2333	0.0455	[0.1441, 0.3226]	~~	~~
			MKF estimate	0.2351	0.0349	[0.1668, 0.3035]	0.0392	0.7660

See footnotes at end of figure.

Figure 1. Part 1 output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter Bayesian model average up to the unconstrained cubic trend, with random sampling variances and common autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity—Con.

Age	Population	Year	Estimation type	Point estimate	RMSE	Wald 95% CI	Std. diff	Rel. RMSE
25-44	Mexican American	2018.6	Sample	0.5265	0.0231	[0.4812, 0.5717]	~~	~~
			MKF estimate	0.5111	0.0205	[0.4708, 0.5513]	-0.6679	0.8893
45-64	Mexican American	2018.6	Sample	0.5060	0.0355	[0.4365, 0.5756]	~~	~~
			MKF estimate	0.5201	0.0225	[0.4759, 0.5642]	0.3951	0.6346
65+	Mexican American	2018.6	Sample	0.4976	0.0545	[0.3907, 0.6044]	~~	~~
			MKF estimate	0.4441	0.0389	[0.3678, 0.5204]	-0.9813	0.7143
18-24	Other Hispanic	2018.6	Sample	0.3566	0.0512	[0.2563, 0.4570]	~~	~~
			MKF estimate	0.3085	0.0335	[0.2428, 0.3743]	-0.9393	0.6552
25-44	Other Hispanic	2018.6	Sample	0.3845	0.0273	[0.3311, 0.4379]	~~	~~
			MKF estimate	0.3892	0.0239	[0.3423, 0.4361]	0.1721	0.8783
45-64	Other Hispanic	2018.6	Sample	0.4464	0.0375	[0.3729, 0.5199]	~~	~~
			MKF estimate	0.4485	0.0235	[0.4024, 0.4947]	0.0573	0.6277
65+	Other Hispanic	2018.6	Sample	0.4642	0.0413	[0.3833, 0.5452]	~~	~~
			MKF estimate	0.4196	0.0330	[0.3548, 0.4843]	-1.0810	0.7997

NOTES: Obesity is indicated by a body mass index of 30.0 or higher. Body mass index is calculated from measured height and weight and defined as weight (kilograms) / [height (meters)]^2. The category "Other race, non-Hispanic" includes non-Hispanic people identifying as more than one race. The category "Other Hispanic" includes Hispanic or Latino people from origins other than Mexican American. The symbol ~~ indicates that the output is not applicable. Year = 2018.6 is the midpoint of the 2017–March 2020 cycle, which, due to the suspension of field operations for the National Health and Nutrition Examination Survey in March 2020, combines the full 2017–2018 cycle with partial data from 2019 through March 2020; see "National Health and Nutrition Examination Survey, 2017–March 2020 Prepandemic File: Sample Design, Estimation, and Analytic Guidelines" (https://www.cdc.gov/nchs/data/series/sr_02/sr02-190.pdf). Direct estimates of the proportion of adults with obesity are indicated in the rows labeled "Sample," whereas estimates based on the selected modified Kalman filter (MKF) model are indicated in the rows labeled "MKF estimate." Selected MKF models include a common set of autoregression parameters across population groups. RMSE is the root mean squared error; for direct estimates, RMSE is equal to the standard error because the survey-weighted sample proportion is assumed to be an unbiased estimator of the population proportion. The Wald 95% confidence interval (CI) is constructed for both direct and model-based estimates using the formula (point estimate) ± 1.96 • RMSE. The standardized difference (Std. diff) is the difference between the model-based and direct estimates, divided by RMSE (= standard error) of the direct estimate. The relative RMSE (Rel. RMSE) is the ratio of the model-based RMSE to the direct RMSE.

SOURCE: National Center for Health Statistics, National Health and Nutrition Examination Surveys, 1999–March 2020.

Figure 2. Part 2 output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter Bayesian model average up to the unconstrained cubic trend, with random sampling variances and common autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity

```
---------------------------------------------------------------------------------------------------------------------------------------
                         Differences between MKF point estimates by population
   Age          Disparity measure                               Estimate       RMSE           95% CI
   18-24    MAX                        - MIN                     0.1267        0.0341    [ 0.0598,  0.1935]
            AVGEXCLMIN                 - MIN                     0.0867        0.0283    [ 0.0312,  0.1421]
            Black, non-Hispanic        - MIN                     0.1099        0.0389    [ 0.0336,  0.1862]
            White, non-Hispanic        - MIN                     0.0454        0.0350    [-0.0233,  0.1141]
            Other race, non-Hispanic  - MIN                     0.0045        0.0134    [-0.0218,  0.0308]
            Mexican American           - MIN                     0.0914        0.0412    [ 0.0106,  0.1722]
            Other Hispanic             - MIN                     0.0954        0.0401    [ 0.0167,  0.1741]
---------------------------------------------------------------------------------------------------------------------------------------
                         Differences between MKF point estimates by population
   Age          Disparity measure                               Estimate       RMSE           95% CI
   25-44    MAX                        - MIN                     0.2182        0.0280    [ 0.1633,  0.2731]
            AVGEXCLMIN                 - MIN                     0.1533        0.0242    [ 0.1060,  0.2007]
            Black, non-Hispanic        - MIN                     0.1981        0.0296    [ 0.1402,  0.2561]
            White, non-Hispanic        - MIN                     0.1130        0.0288    [ 0.0566,  0.1695]
            Other race, non-Hispanic  - MIN                     0.0000        0.0008    [-0.0014,  0.0015]
            Mexican American           - MIN                     0.2120        0.0304    [ 0.1525,  0.2715]
            Other Hispanic             - MIN                     0.0902        0.0318    [ 0.0279,  0.1524]
---------------------------------------------------------------------------------------------------------------------------------------
                         Differences between MKF point estimates by population
   Age          Disparity measure                               Estimate       RMSE           95% CI
   45-64    MAX                        - MIN                     0.2955        0.0260    [ 0.2446,  0.3464]
            AVGEXCLMIN                 - MIN                     0.2257        0.0275    [ 0.1717,  0.2796]
            Black, non-Hispanic        - MIN                     0.2952        0.0261    [ 0.2441,  0.3464]
            White, non-Hispanic        - MIN                     0.1699        0.0332    [ 0.1048,  0.2350]
            Other race, non-Hispanic  - MIN                     0.0000        0.0002    [-0.0003,  0.0003]
            Mexican American           - MIN                     0.2546        0.0337    [ 0.1884,  0.3207]
            Other Hispanic             - MIN                     0.1830        0.0341    [ 0.1162,  0.2498]
---------------------------------------------------------------------------------------------------------------------------------------
                         Differences between MKF point estimates by population
   Age          Disparity measure                               Estimate       RMSE           95% CI
   65+      MAX                        - MIN                     0.2552        0.0397    [ 0.1773,  0.3331]
            AVGEXCLMIN                 - MIN                     0.2047        0.0373    [ 0.1315,  0.2778]
            Black, non-Hispanic        - MIN                     0.2505        0.0399    [ 0.1724,  0.3287]
            White, non-Hispanic        - MIN                     0.1747        0.0402    [ 0.0960,  0.2535]
            Other race, non-Hispanic  - MIN                     0.0000        0.0001    [-0.0002,  0.0002]
            Mexican American           - MIN                     0.2089        0.0510    [ 0.1090,  0.3089]
            Other Hispanic             - MIN                     0.1845        0.0471    [ 0.0921,  0.2768]
---------------------------------------------------------------------------------------------------------------------------------------
                         Ratios between MKF point estimates by population
   Age          Disparity measure                               Estimate       RMSE           95% CI
   18-24    MAX                        / MIN                     1.6246        0.2466    [ 1.2065,  2.1876]
            AVGEXCLMIN                 / MIN                     1.4318        0.2008    [ 1.0877,  1.8848]
            Black, non-Hispanic        / MIN                     1.5477        0.2597    [ 1.1140,  2.1503]
            White, non-Hispanic        / MIN                     1.2322        0.2023    [ 0.8931,  1.6999]
            Other race, non-Hispanic  / MIN                     1.0204        0.0629    [ 0.9042,  1.1515]
            Mexican American           / MIN                     1.4524        0.2444    [ 1.0443,  2.0199]
            Other Hispanic             / MIN                     1.4747        0.2489    [ 1.0594,  2.0528]
```

See footnotes at end of figure.

Figure 2. Part 2 output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter Bayesian model average up to the unconstrained cubic trend, with random sampling variances and common autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity—Con.

```
-----------------------------------------------------------------------------------------------------------------------------------------
                         Ratios between MKF point estimates by population
   Age         Disparity measure                              Estimate       RMSE          95% CI
   25-44    MAX                       / MIN                   1.7395       0.1445    [ 1.4781,  2.0470]
            AVGEXCLMIN                / MIN                   1.5213       0.1195    [ 1.3042,  1.7746]
            Black, non-Hispanic       / MIN                   1.6717       0.1415    [ 1.4161,  1.9735]
            White, non-Hispanic       / MIN                   1.3858       0.1222    [ 1.1659,  1.6473]
            Other race, non-Hispanic  / MIN                   1.0001       0.0023    [ 0.9955,  1.0047]
            Mexican American          / MIN                   1.7189       0.1492    [ 1.4501,  2.0376]
            Other Hispanic            / MIN                   1.3086       0.1247    [ 1.0857,  1.5773]
-----------------------------------------------------------------------------------------------------------------------------------------
                         Ratios between MKF point estimates by population
   Age         Disparity measure                              Estimate       RMSE          95% CI
   45-64    MAX                       / MIN                   2.1309       0.1980    [ 1.7761,  2.5566]
            AVGEXCLMIN                / MIN                   1.8662       0.1781    [ 1.5478,  2.2501]
            Black, non-Hispanic       / MIN                   2.1299       0.1982    [ 1.7748,  2.5561]
            White, non-Hispanic       / MIN                   1.6544       0.1740    [ 1.3463,  2.0331]
            Other race, non-Hispanic  / MIN                   1.0000       0.0004    [ 0.9991,  1.0009]
            Mexican American          / MIN                   1.9761       0.2023    [ 1.6168,  2.4152]
            Other Hispanic            / MIN                   1.7042       0.1803    [ 1.3851,  2.0968]
-----------------------------------------------------------------------------------------------------------------------------------------
                         Ratios between MKF point estimates by population
   Age         Disparity measure                              Estimate       RMSE          95% CI
   65+      MAX                       / MIN                   2.1341       0.3502    [ 1.5471,  2.9437]
            AVGEXCLMIN                / MIN                   1.9140       0.3106    [ 1.3925,  2.6307]
            Black, non-Hispanic       / MIN                   2.1139       0.3476    [ 1.5316,  2.9177]
            White, non-Hispanic       / MIN                   1.7839       0.2982    [ 1.2856,  2.4755]
            Other race, non-Hispanic  / MIN                   1.0000       0.0004    [ 0.9993,  1.0007]
            Mexican American          / MIN                   1.9321       0.3480    [ 1.3574,  2.7502]
            Other Hispanic            / MIN                   1.8259       0.3230    [ 1.2909,  2.5827]
-----------------------------------------------------------------------------------------------------------------------------------------
```

NOTES: Obesity is indicated by a body mass index of 30.0 or higher. Body mass index is calculated from measured height and weight and defined as weight (kilograms) / [height (meters)]^2. The category "Other race, non-Hispanic" includes non-Hispanic people identifying as more than one race. The category "Other Hispanic" includes Hispanic or Latino people from origins other than Mexican American. Selected modified Kalman filter (MKF) models include a common set of autoregression parameters across population groups. MAX is the estimate of the highest obesity rate across the five population categories based on the selected MKF model, MIN is the lowest rate, and AVGEXCLMIN is the average obesity rate for all but the lowest rate. Because lower obesity rates are more favorable, the lowest rate is used as the reference for evaluating disparities. The disparity measures "MAX – MIN" and "MAX / MIN" are the so-called maximal difference and ratio, respectively, whereas the measures "AVGEXCLMIN – MIN" and "AVGEXCLMIN / MIN" are the summary difference and ratio, respectively; see "Examining Progress Toward Elimination of Racial and Ethnic Health Disparities for Healthy People 2020 Objectives Using Three Measures of Overall Disparity" (https://www.cdc.gov/nchs/data/series/sr_02/sr02-195.pdf). Posterior estimates, standard errors, and 95% confidence interval (CI) limits for the lowest (MIN) and highest (MAX) obesity rates differ from the posterior estimates, standard errors, and 95% CIs for the rates of the groups that achieved the lowest and highest rates, respectively. RMSE is the root mean squared error. For the difference between two rates 1 and 2, RMSE is given by RMSE^2 of Difference = RMSE^2 of Rate 1 + RMSE^2 of Rate 2, and the 95% CI is constructed using the formula Difference ± 1.96 • RMSE of Difference. For the ratio between rates 1 and 2, RMSE is obtained by reverse-transformation from the natural logarithm (ln) of the ratio, with RMSE^2 of ln(Ratio) = [RMSE^2 of Rate 1]/[Rate 1] + [RMSE^2 of Rate 2]/[Rate 2], and the corresponding 95% CI is constructed using the formula exp[ln(Ratio) ± 1.96 • RMSE of ln(Ratio)].

SOURCE: National Center for Health Statistics, National Health and Nutrition Examination Surveys, 1999–March 2020.

Convergence of Bayesian Estimation Algorithms

Many of the default settings in the call to SAS PROC MCMC in the enhanced MKF macro were retained to ensure adequate convergence and mixing of the MCMC algorithm for sampling from the posterior distribution of model parameters in a wide range of applications. Additionally, by default, the enhanced MKF macro combines posterior samples from four chains with randomly selected starting points (23); as in the earlier MKF macro, each chain uses 10,000 burn-in steps (which are discarded) and 50,000 sampling steps.

Parameters for which a Gibbs sampler is not available use the random walk Metropolis–Hastings sampler, whose proposal distribution is specified and tuned within PROC MCMC (24). This requires the program to find a good approximation to the covariance matrix of model parameters, and is done in the "tuning phase" of the MCMC algorithm, before the burn-in steps. In the enhanced MKF macro, the number of iterations per tuning loop is set to 1,000 instead of the PROC MCMC default of 500, and the maximum number of tuning loops is set to 50 instead of the PROC MCMC default of 24. Input parameters for the random walk Metropolis–Hastings sampler are set in the enhanced MKF macro to match PROC MCMC defaults (24), but those can be modified by experienced end users; see Appendix II and the code annotations in the enhanced MKF SAS macro, available from: https://github.com/CDCgov/eMKF.

Mixing of each of the four chains may be assessed using various PROC MCMC diagnostic tools. The enhanced MKF macro defers to PROC MCMC for issuing any warnings about effective sample sizes or serial autocorrelations that may indicate poor mixing (24). Additionally, the Gelman–Rubin diagnostic, not directly available from PROC MCMC, is calculated to flag any potential issues with the convergence of the posterior samples from the four chains (23). If mixing or convergence issues are encountered, model predictions may be unreliable, and users should consider investigating the detailed diagnostic statistics and plots for each chain; those are requested using options `modelprint = YES` and `mcmcplot = YES`, respectively. Mixing and convergence issues are often resolved by increasing the number of sampling steps and by thinning, which, for example, retains every second (`thin = 2`) or fifth (`thin = 5`) iteration—by default, `thin = 1`. For example, one strategy could be to double the number of sampling steps while retaining every other iteration or to increase the number of sampling steps fivefold while retaining every fifth iteration. If MCMC mixing or convergence problems cannot be resolved using those simple strategies, users are advised to consult with a mathematical statistician or their clearance official before modifying any of the other macro parameters described in Appendix II.

Alternatives to Bayesian Trend Model Averaging

As mentioned previously, Bayesian model averaging over the available trend models is the default specification in the enhanced MKF macro. However, in certain analyses where subject-matter, statistical, or computational considerations preclude the default specification, it is possible to select other specifications after discussion with a mathematical statistician or clearance official. The enhanced MKF macro allows for three alternative specifications to Bayesian model averaging.

1. **Model averaging based on maximum likelihood estimation**—As in the earlier MKF macro, selected trend model(s) can be fit using maximum likelihood (via SAS PROC NLMIXED), assuming sampling variances are known instead of random, as explained in Appendix I, "State-space Model Formulation and Maximum Likelihood-based Estimation." When more than one trend model is specified, model averaging is implemented using the BIC values to approximate the Bayes factors when calculating model averaging weights; see Appendix III for an example specification.
2. **"Fully Bayesian" models**—As in the earlier MKF macro, so-called fully Bayesian trend models can be fit by adding a level to the underlying Bayesian hierarchical model to account for the uncertainty in specifying prior means and variances for the regression coefficients and, as a result, offer a compromise between the "independent" and "common" trend cases; see Appendix I, "Bayesian Estimation of Regression Hyperparameters." Setting the `Bayesmodel` macro variable in the enhanced MKF macro to one of the keywords 1) `full_cubic`, 2) `full_quad`, or 3) `full_linear` implements those fully Bayesian hierarchical models, which offer viable alternatives to cubic, quadratic, and linear Bayesian model averaging, respectively. For example, if quadratic or cubic trends are known to be inappropriate based on previous analyses or subject-matter expertise, limiting the macro to the fully Bayesian linear trend model would reduce computational burden. See Appendix III for a specification using the fully cubic Bayesian model with random sampling variances.
3. **Group-specific AR(1) coefficients**—By default, the enhanced MKF macro assumes shared values of the AR(1) parameters ρ_g and τ_g^2 across groups, with $\rho_g \equiv \rho$ and $\tau_g^2 \equiv \tau^2$ (macro option `ARmodel = common_ar`), as in the earlier MKF macro. However, subject-matter or statistical considerations may suggest substantial structural differences across groups, justifying the need for independent AR(1) parameters across groups. This would be specified in the enhanced MKF macro using option `ARmodel = indep_ar`; see Appendix III for an example. Yet, to preserve the borrowing of strength across groups, the ρ_g and τ_g^2 would be drawn from a

common distribution and shrunk toward their means $\rho = E(\rho_g)$ and $\tau^2 = E\left(\tau_g^2\right)$; see Appendix I.

Experienced end users may modify additional model specifications or the Bayesian sampling algorithms in the enhanced MKF macro to suit their needs, after discussion with a mathematical statistician or clearance official. All enhanced MKF macro parameter settings, default values, and functionalities are described in detail in Appendix II.

Discussion

The enhanced MKF procedure and macro broaden the scope of their earlier versions to improve their applicability to NCHS data under a wide set of analytic scenarios, allowing users to account for nonlinear time trends, irregularly spaced data points, and random sampling variances. Model averaging is conducted entirely within the Bayesian paradigm, and Bayes factors are estimated from the marginal distribution of the data instead of approximated using BIC values.

Bayesian estimation in the enhanced MKF macro is implemented adaptably using PROC MCMC and related SAS 9.4 procedures instead of relying on an associated executable file that included code inaccessible to end users. As a result, it is possible for experienced end users to modify the model specifications or the Bayesian sampling algorithms in the enhanced MKF macro to suit their needs. However, to hedge against model uncertainty, Bayesian model averaging over all available trend models is recommended, unless subject-matter, statistical, or computational considerations require the selection of a specific model instead. Generally, to account for the AR(1) parameters in the random effects, at least $k + 4$ data points are required for each population subgroup (and stratum) to fit a trend model using a degree k polynomial, $k = 0, 1, 2, 3$.

When data from two related health outcomes were available, the earlier MKF procedure allowed users to leverage the correlation between the two outcomes to further borrow strength and improve model estimates. This feature is useful in the context of rare health outcomes that may be correlated with more common outcomes, for example. Perhaps due to the added complexity in deriving appropriate Gibbs samplers for Bayesian estimation in the bivariate case, only maximum likelihood-based estimation was available in the earlier MKF macro (10,11). The enhanced MKF macro preserves the earlier settings when two outcomes are specified. Future work may consider extending the enhanced MKF macro to more than two related outcomes, where outcome selection may be informed by subject-matter expertise and include clusters of inter-related health outcomes or conditions, like mental health (25), musculoskeletal conditions (26), respiratory diseases (27), or cardiovascular conditions (28).

Conclusion

The enhanced MKF macro enables the production of model-based estimates for small populations where direct estimates may lack precision, improving assessment and monitoring of health disparities. Methodological improvements relative to the earlier MKF procedure and macro allow for more transparency in the underlying models and more flexibility in generating estimates under different scenarios, such as nonlinear trends, irregularly spaced data points, and random sampling variances.

References

1. Parker JD, Talih M, Malec DJ, Beresovsky V, Carroll M, Gonzalez JF Jr, et al. National Center for Health Statistics data presentation standards for proportions. National Center for Health Statistics. Vital Health Stat 2(175). 2017.
2. Parker JD, Talih M, Irimata KE, Zhang G, Branum AM, Davis D, et al. National Center for Health Statistics data presentation standards for rates and counts. National Center for Health Statistics. Vital Health Stat 2(200). 2023. DOI: https://dx.doi.org/10.15620/cdc:124368.
3. Franco C, Bell WR. Using American Community Survey data to improve estimates from smaller U.S. surveys through bivariate small area estimation models. J Surv Stat Methodol 10(1):225–47. 2022.
4. Sugasawa S, Kubokawa T. Small area estimation with mixed models: A review. Jpn J Stat Data Sci 3:693–720. 2020.
5. Polettini S. A generalised semiparametric Bayesian Fay–Herriot model for small area estimation shrinking both means and variances. Bayesian Anal 12(3):729–52. 2016.
6. Ha NS, Lahiri P, Parsons V. Methods and results for small area estimation using smoking data from the 2008 National Health Interview Survey. Stat Med 33(22):3932–45. 2014.
7. Dass SC, Maiti T, Ren H, Sinha S. Confidence interval estimation of small area parameters shrinking both means and variances. Surv Methodol 38(2):173–87. 2012.
8. Elliott MN, McCaffrey DF, Finch BK, Klein DJ, Orr N, Beckett MN, Lurie N. Improving disparity estimates for rare racial/ethnic groups with trend estimation and Kalman filtering: An application to the National Health Interview Survey. Health Serv Res 44(5 Pt 1):1622–39. 2009.
9. Lockwood JR, McCaffrey DF, Setodji CM, Elliott MN. Smoothing across time in repeated cross-sectional data. Stat Med 30(5):584–94. 2011.

10. Setodji CM, Lockwood JR, McCaffrey DF, Elliott MN, Adams JL. The modified Kalman filter macro: User's guide. RAND Technical Report No. TR-997-DHHS. 2011. Available from: https://www.rand.org/pubs/technical_reports/TR997.html.

11. Setodji CM, Lockwood JR, McCaffrey DF, Elliott MN, Adams JL. The modified Kalman filter macro: User's guide. RAND Health Q 2(1):18. 2012.

12. Aoki Y, Earl S, Clarke J, Servais J, Karthikeyan S. Trends in blood lead, cadmium, and mercury: United States, 1999–2000 through 2017–2018 and Canada, 2007–2009 through 2016–2017. National Center for Health Statistics. Vital Health Stat 3(49). 2023. DOI: https://dx.doi.org/10.15620/cdc:123891.

13. Fryar CD, Kruszon-Moran D, Gu Q, Carroll M, Ogden CL. Mean body weight, height, waist circumference, and body mass index among children and adolescents: United States, 1999–2018. National Health Statistics Reports; no 160. Hyattsville, MD: National Center for Health Statistics. 2021. DOI: https://dx.doi.org/10.15620/cdc:107559.

14. Cha AE, Cohen RA. Problems paying medical bills, 2018. NCHS Data Brief, no 357. Hyattsville, MD: National Center for Health Statistics. 2020.

15. Rui P, Santo L, Ashman JJ. Trends in opioids prescribed at discharge from emergency departments among adults: United States, 2006–2017. National Health Statistics Reports; no 135. Hyattsville, MD: National Center for Health Statistics. 2020.

16. Carroll MD, Kruszon-Moran D, Tolliver E. Trends in apolipoprotein B, non-high-density lipoprotein cholesterol, and low-density lipoprotein cholesterol for adults aged 20 and over, 2005–2016. National Health Statistics Reports; no 127. Hyattsville, MD: National Center for Health Statistics. 2019.

17. Ingram DD, Malec DJ, Makuc DM, Kruszon-Moran D, Gindi RM, Albert M, et al. National Center for Health Statistics guidelines for analysis of trends. National Center for Health Statistics. Vital Health Stat 2(179). 2018.

18. Kass RE, Raftery AE. Bayes factors. J Am Stat Assoc 90(430):773–95. 1995.

19. Campbell H, Gustafson P. Bayes factors and posterior estimation: Two sides of the very same coin. Am Stat 77(3):248–58. 2022.

20. Huang DT, Bassig BA, Hubbard K, Klein RJ, Talih M. Examining progress toward elimination of racial and ethnic health disparities for Healthy People 2020 objectives using three measures of overall disparity. National Center for Health Statistics. Vital Health Stat 2(195). 2022. DOI: https://dx.doi.org/10.15620/cdc:121266.

21. Talih M, Huang DT. Measuring progress toward target attainment and the elimination of health disparities in Healthy People 2020. Healthy People Statistical Notes, no 27. Hyattsville, MD: National Center for Health Statistics. 2016. Available from: https://www.cdc.gov/nchs/data/statnt/statnt27.pdf.

22. Akinbami LJ, Chen TC, Davy O, Ogden CL, Fink S, Clark J, et al. National Health and Nutrition Examination Survey, 2017–March 2020 prepandemic file: Sample design, estimation, and analytic guidelines. National Center for Health Statistics. Vital Health Stat 2(190). 2022. DOI: https://dx.doi.org/10.15620/cdc:115434.

23. Vehtari A, Gelman A, Simpson D, Carpenter B, Bürkner PC. Rank-normalization, folding, and localization: An improved $\hat{R}$ for assessing convergence of MCMC (with discussion). Bayesian Anal 16(2):667–718. 2021.

24. SAS Institute Inc. Chapter 74: The MCMC procedure. In: SAS/STAT 14.2 user's guide. Cary, NC: SAS Institute Inc. 2016.

25. Zablotsky B, Weeks JD, Terlizzi EP, Madans JH, Blumberg SJ. Assessing anxiety and depression: A comparison of National Health Interview Survey measures. National Health Statistics Reports; no 172. Hyattsville, MD: National Center for Health Statistics. 2022. DOI: https://dx.doi.org/10.15620/cdc:117491.

26. Lucas JW, Connor EM, Bose J. Back, lower limb, and upper limb pain among U.S. adults, 2019. NCHS Data Brief, no 415. Hyattsville, MD: National Center for Health Statistics. 2021. DOI: https://dx.doi.org/10.15620/cdc:107894.

27. Office of Disease Prevention and Health Promotion, U.S. Department of Health and Human Services. Healthy People 2030 respiratory diseases workgroup. Available from: https://health.gov/healthypeople/about/workgroups/respiratory-diseases-workgroup.

28. Moore JX, Chaudhary N, Akinyemiju T. Metabolic syndrome prevalence by race/ethnicity and sex in the United States, National Health and Nutrition Examination Survey, 1988–2012. Prev Chronic Dis 14:E24. 2017. DOI: https://dx.doi.org/10.5888/pcd14.160287.

29. Montgomery DC, Peck EA, Vining GG. Chapter 7: Polynomial regression models. In: Introduction to linear regression analysis. 6th ed. Hoboken, NJ: John Wiley & Sons, Inc. 2021.

30. Mallick BK. Bayesian curve estimation by polynomial of random order. J Stat Plan Inference 70(1):91–109. 1998.

31. Keller M, Kamary K. Bayesian model averaging via mixture model estimation. arXiv:1711.10016v2 [stat.ME]. 2018.

32. Lodewyckx T, Kim W, Lee MD, Tuerlinckx F, Kuppens P, Wagenmakers EJ. A tutorial on Bayes factor estimation with the product space method. J Math Psych 55(5):331–47. 2011.

Table. Example of public-use data set in stacked format used as input to the enhanced modified Kalman filter macro: Proportion of U.S. adults with obesity, by survey cycle, race and ethnicity, and age group

Year	Cycle	Population	Age group	Obesity	SE_ obesity	NEFF_ obesity	LL_ obesity	UL_ obesity	Rel_ obesity
1999.5	1999–2000	Black, non-Hispanic	18–24	0.2656	0.0414	113.6	0.1871	0.3566	Yes
1999.5	1999–2000	Black, non-Hispanic	25–44	0.4274	0.0269	338.2	0.3740	0.4820	Yes
1999.5	1999–2000	Black, non-Hispanic	45–64	0.4267	0.0250	392.1	0.3677	0.4872	Yes
1999.5	1999–2000	Black, non-Hispanic	65+	0.4175	0.0349	199.3	0.3483	0.4893	Yes
1999.5	1999–2000	White, non-Hispanic	18–24	0.1777	0.0308	153.7	0.1208	0.2474	Yes
1999.5	1999–2000	White, non-Hispanic	25–44	0.2527	0.0204	452.7	0.2133	0.2954	Yes
1999.5	1999–2000	White, non-Hispanic	45–64	0.3550	0.0344	194.0	0.2878	0.4267	Yes
1999.5	1999–2000	White, non-Hispanic	65+	0.3183	0.0222	440.8	0.2750	0.3640	Yes
1999.5	1999–2000	Other race, non-Hispanic	18–24	0.1707	0.0651	33.4	0.0632	0.3404	No
1999.5	1999–2000	Other race, non-Hispanic	25–44	0.4469	0.0712	48.7	0.3043	0.5962	Yes
1999.5	1999–2000	Other race, non-Hispanic	45–64	0.2727	0.0717	38.6	0.1422	0.4398	Yes
1999.5	1999–2000	Other race, non-Hispanic	65+	0.1961	0.0865	21.1	0.0578	0.4249	No
1999.5	1999–2000	Mexican American	18–24	0.2665	0.0268	271.8	0.2149	0.3232	Yes
1999.5	1999–2000	Mexican American	25–44	0.3339	0.0296	254.7	0.2763	0.3955	Yes
1999.5	1999–2000	Mexican American	45–64	0.3736	0.0387	155.9	0.2976	0.4546	Yes
1999.5	1999–2000	Mexican American	65+	0.3615	0.0481	99.7	0.2676	0.4639	Yes
1999.5	1999–2000	Other Hispanic	18–24	0.1811	0.0439	76.8	0.0953	0.2984	Yes
1999.5	1999–2000	Other Hispanic	25–44	0.2760	0.0200	500.9	0.1970	0.3667	Yes
1999.5	1999–2000	Other Hispanic	45–64	0.3891	0.0631	59.7	0.2656	0.5241	Yes
1999.5	1999–2000	Other Hispanic	65+	0.2666	0.0413	114.8	0.1666	0.3878	Yes
2001.5	2001–2002	Black, non-Hispanic	18–24	0.2864	0.0317	202.8	0.2253	0.3539	Yes
2001.5	2001–2002	Black, non-Hispanic	25–44	0.3947	0.0266	338.8	0.3423	0.4490	Yes
2001.5	2001–2002	Black, non-Hispanic	45–64	0.4452	0.0266	349.2	0.3902	0.5011	Yes
2001.5	2001–2002	Black, non-Hispanic	65+	0.4834	0.0369	183.4	0.4091	0.5582	Yes
2001.5	2001–2002	White, non-Hispanic	18–24	0.2446	0.0289	220.9	0.1894	0.3067	Yes
2001.5	2001–2002	White, non-Hispanic	25–44	0.3020	0.0146	991.2	0.2715	0.3338	Yes
2001.5	2001–2002	White, non-Hispanic	45–64	0.3722	0.0159	929.4	0.3386	0.4067	Yes
2001.5	2001–2002	White, non-Hispanic	65+	0.3634	0.0269	319.9	0.3106	0.4187	Yes
2001.5	2001–2002	Other race, non-Hispanic	18–24	0.1034	0.0349	76.0	0.0353	0.2224	No
2001.5	2001–2002	Other race, non-Hispanic	25–44	0.2150	0.0369	123.7	0.1319	0.3196	Yes
2001.5	2001–2002	Other race, non-Hispanic	45–64	0.2003	0.0712	31.6	0.0799	0.3802	No
2001.5	2001–2002	Other race, non-Hispanic	65+	0.2473	0.1817	5.6	0.0156	0.7256	No
2001.5	2001–2002	Mexican American	18–24	0.2270	0.0230	332.4	0.1831	0.2759	Yes
2001.5	2001–2002	Mexican American	25–44	0.2925	0.0204	497.1	0.2519	0.3358	Yes
2001.5	2001–2002	Mexican American	45–64	0.4585	0.0337	219.2	0.3912	0.5269	Yes
2001.5	2001–2002	Mexican American	65+	0.3218	0.0400	136.6	0.2445	0.4070	Yes
2001.5	2001–2002	Other Hispanic	18–24	0.4450	0.1196	17.3	0.2114	0.6980	No
2001.5	2001–2002	Other Hispanic	25–44	0.3743	0.0525	85.1	0.2717	0.4859	Yes
2001.5	2001–2002	Other Hispanic	45–64	0.3138	0.0675	47.3	0.1868	0.4652	Yes
2001.5	2001–2002	Other Hispanic	65+	0.4453	0.0728	46.6	0.2997	0.5981	Yes
2003.5	2003–2004	Black, non-Hispanic	18–24	0.3265	0.0318	217.0	0.2646	0.3933	Yes
2003.5	2003–2004	Black, non-Hispanic	25–44	0.4960	0.0339	218.0	0.4278	0.5643	Yes
2003.5	2003–2004	Black, non-Hispanic	45–64	0.4697	0.0293	290.1	0.4111	0.5289	Yes
2003.5	2003–2004	Black, non-Hispanic	65+	0.4501	0.0382	169.6	0.3737	0.5282	Yes
2003.5	2003–2004	White, non-Hispanic	18–24	0.2351	0.0281	227.0	0.1816	0.2958	Yes
2003.5	2003–2004	White, non-Hispanic	25–44	0.3035	0.0161	820.5	0.2721	0.3365	Yes
2003.5	2003–2004	White, non-Hispanic	45–64	0.3635	0.0268	322.1	0.3109	0.4186	Yes
2003.5	2003–2004	White, non-Hispanic	65+	0.3009	0.0170	726.5	0.2677	0.3357	Yes
2003.5	2003–2004	Other race, non-Hispanic	18–24	0.1588	0.0612	35.7	0.0585	0.3197	No
2003.5	2003–2004	Other race, non-Hispanic	25–44	0.2547	0.0889	24.0	0.1009	0.4719	No
2003.5	2003–2004	Other race, non-Hispanic	45–64	0.1320	0.0429	62.2	0.0595	0.2419	No
2003.5	2003–2004	Other race, non-Hispanic	65+	0.2213	0.0790	27.6	0.0868	0.4190	No
2003.5	2003–2004	Mexican American	18–24	0.2403	0.0422	102.3	0.1614	0.3349	Yes
2003.5	2003–2004	Mexican American	25–44	0.3819	0.0323	225.6	0.3182	0.4487	Yes
2003.5	2003–2004	Mexican American	45–64	0.4424	0.0353	198.5	0.3721	0.5144	Yes
2003.5	2003–2004	Mexican American	65+	0.3574	0.0188	649.9	0.3002	0.4177	Yes
2003.5	2003–2004	Other Hispanic	18–24	0.4199	0.1146	18.5	0.1991	0.6670	No
2003.5	2003–2004	Other Hispanic	25–44	0.2460	0.0830	26.9	0.1019	0.4488	No
2003.5	2003–2004	Other Hispanic	45–64	0.3125	0.0692	44.8	0.1689	0.4883	No
2003.5	2003–2004	Other Hispanic	65+	0.3513	0.1011	22.3	0.1639	0.5797	No

See footnotes at end of table.

Table. Example of public-use data set in stacked format used as input to the enhanced modified Kalman filter macro: Proportion of U.S. adults with obesity, by survey cycle, race and ethnicity, and age group—Con.

Year	Cycle	Population	Age group	Obesity	SE_ obesity	NEFF_ obesity	LL_ obesity	UL_ obesity	Rel_ obesity
2005.5	2005–2006	Black, non-Hispanic	18–24	0.3877	0.0471	107.2	0.2952	0.4867	Yes
2005.5	2005–2006	Black, non-Hispanic	25–44	0.4478	0.0201	612.8	0.3989	0.4975	Yes
2005.5	2005–2006	Black, non-Hispanic	45–64	0.4692	0.0273	333.5	0.4146	0.5243	Yes
2005.5	2005–2006	Black, non-Hispanic	65+	0.5269	0.0264	358.1	0.4586	0.5946	Yes
2005.5	2005–2006	White, non-Hispanic	18–24	0.2276	0.0349	144.0	0.1619	0.3048	Yes
2005.5	2005–2006	White, non-Hispanic	25–44	0.3178	0.0287	262.5	0.2619	0.3778	Yes
2005.5	2005–2006	White, non-Hispanic	45–64	0.3971	0.0255	368.1	0.3467	0.4491	Yes
2005.5	2005–2006	White, non-Hispanic	65+	0.3155	0.0197	555.3	0.2770	0.3559	Yes
2005.5	2005–2006	Other race, non-Hispanic	18–24	0.1986	0.0820	23.7	0.0648	0.4124	No
2005.5	2005–2006	Other race, non-Hispanic	25–44	0.2172	0.0505	66.7	0.1255	0.3351	Yes
2005.5	2005–2006	Other race, non-Hispanic	45–64	0.4689	0.0709	49.5	0.3257	0.6160	Yes
2005.5	2005–2006	Other race, non-Hispanic	65+	0.1484	0.0775	21.0	0.0331	0.3697	No
2005.5	2005–2006	Mexican American	18–24	0.2170	0.0318	167.8	0.1572	0.2871	Yes
2005.5	2005–2006	Mexican American	25–44	0.3333	0.0210	506.2	0.2904	0.3784	Yes
2005.5	2005–2006	Mexican American	45–64	0.4313	0.0301	270.6	0.3702	0.4939	Yes
2005.5	2005–2006	Mexican American	65+	0.3301	0.0311	228.0	0.2519	0.4158	Yes
2005.5	2005–2006	Other Hispanic	18–24	0.1960	0.0885	20.1	0.0554	0.4314	No
2005.5	2005–2006	Other Hispanic	25–44	0.4472	0.0449	122.6	0.3385	0.5597	Yes
2005.5	2005–2006	Other Hispanic	45–64	0.2866	0.0954	22.5	0.1181	0.5139	No
2005.5	2005–2006	Other Hispanic	65+	0.0602	0.0527	20.4	0.0019	0.2795	No
2007.5	2007–2008	Black, non-Hispanic	18–24	0.3233	0.0295	251.0	0.2551	0.3976	Yes
2007.5	2007–2008	Black, non-Hispanic	25–44	0.4296	0.0240	423.7	0.3803	0.4799	Yes
2007.5	2007–2008	Black, non-Hispanic	45–64	0.4815	0.0313	255.2	0.4188	0.5447	Yes
2007.5	2007–2008	Black, non-Hispanic	65+	0.4854	0.0288	301.8	0.4244	0.5467	Yes
2007.5	2007–2008	White, non-Hispanic	18–24	0.2248	0.0393	113.0	0.1516	0.3129	Yes
2007.5	2007–2008	White, non-Hispanic	25–44	0.3233	0.0261	320.6	0.2724	0.3775	Yes
2007.5	2007–2008	White, non-Hispanic	45–64	0.3690	0.0223	466.3	0.3251	0.4146	Yes
2007.5	2007–2008	White, non-Hispanic	65+	0.3260	0.0175	713.6	0.2917	0.3618	Yes
2007.5	2007–2008	Other race, non-Hispanic	18–24	0.1950	0.0812	23.8	0.0629	0.4076	No
2007.5	2007–2008	Other race, non-Hispanic	25–44	0.1579	0.0433	70.8	0.0821	0.2639	Yes
2007.5	2007–2008	Other race, non-Hispanic	45–64	0.2682	0.0958	21.4	0.1024	0.5011	No
2007.5	2007–2008	Other race, non-Hispanic	65+	0.1744	0.0809	22.0	0.0479	0.3942	No
2007.5	2007–2008	Mexican American	18–24	0.2817	0.0449	100.5	0.1965	0.3802	Yes
2007.5	2007–2008	Mexican American	25–44	0.4055	0.0430	130.7	0.3205	0.4948	Yes
2007.5	2007–2008	Mexican American	45–64	0.4424	0.0356	194.9	0.3714	0.5151	Yes
2007.5	2007–2008	Mexican American	65+	0.4054	0.0354	192.7	0.3266	0.4880	Yes
2007.5	2007–2008	Other Hispanic	18–24	0.3074	0.0654	49.8	0.1845	0.4541	Yes
2007.5	2007–2008	Other Hispanic	25–44	0.2794	0.0271	273.7	0.2198	0.3453	Yes
2007.5	2007–2008	Other Hispanic	45–64	0.4583	0.0378	173.8	0.3827	0.5355	Yes
2007.5	2007–2008	Other Hispanic	65+	0.3637	0.0473	103.3	0.2713	0.4641	Yes
2009.5	2009–2010	Black, non-Hispanic	18–24	0.3519	0.0371	165.6	0.2794	0.4298	Yes
2009.5	2009–2010	Black, non-Hispanic	25–44	0.5132	0.0461	117.7	0.4193	0.6063	Yes
2009.5	2009–2010	Black, non-Hispanic	45–64	0.5385	0.0248	404.4	0.4886	0.5879	Yes
2009.5	2009–2010	Black, non-Hispanic	65+	0.4816	0.0497	101.1	0.3812	0.5832	Yes
2009.5	2009–2010	White, non-Hispanic	18–24	0.2290	0.0363	134.0	0.1608	0.3094	Yes
2009.5	2009–2010	White, non-Hispanic	25–44	0.3269	0.0169	769.8	0.2938	0.3613	Yes
2009.5	2009–2010	White, non-Hispanic	45–64	0.3838	0.0201	583.9	0.3442	0.4246	Yes
2009.5	2009–2010	White, non-Hispanic	65+	0.3872	0.0177	754.1	0.3522	0.4230	Yes
2009.5	2009–2010	Other race, non-Hispanic	18–24	0.1299	0.0722	21.7	0.0258	0.3432	No
2009.5	2009–2010	Other race, non-Hispanic	25–44	0.2549	0.0459	90.0	0.1689	0.3577	Yes
2009.5	2009–2010	Other race, non-Hispanic	45–64	0.1304	0.0270	155.7	0.0703	0.2145	Yes
2009.5	2009–2010	Other race, non-Hispanic	65+	0.1990	0.0597	44.7	0.0948	0.3453	Yes
2009.5	2009–2010	Mexican American	18–24	0.2281	0.0328	163.4	0.1662	0.3002	Yes
2009.5	2009–2010	Mexican American	25–44	0.4077	0.0189	674.8	0.3603	0.4564	Yes
2009.5	2009–2010	Mexican American	45–64	0.4885	0.0255	384.7	0.4375	0.5397	Yes
2009.5	2009–2010	Mexican American	65+	0.3654	0.0502	92.2	0.2675	0.4722	Yes
2009.5	2009–2010	Other Hispanic	18–24	0.2181	0.0363	129.6	0.1345	0.3230	Yes
2009.5	2009–2010	Other Hispanic	25–44	0.3209	0.0327	203.7	0.2574	0.3897	Yes
2009.5	2009–2010	Other Hispanic	45–64	0.4396	0.0662	56.2	0.3074	0.5784	Yes
2009.5	2009–2010	Other Hispanic	65+	0.4395	0.0351	200.2	0.3432	0.5392	Yes

See footnotes at end of table.

Table. Example of public-use data set in stacked format used as input to the enhanced modified Kalman filter macro: Proportion of U.S. adults with obesity, by survey cycle, race and ethnicity, and age group—Con.

Year	Cycle	Population	Age group	Obesity	SE_ obesity	NEFF_ obesity	LL_ obesity	UL_ obesity	Rel_ obesity
2011.5	2011–2012	Black, non-Hispanic	18–24	0.3177	0.0274	288.4	0.2620	0.3776	Yes
2011.5	2011–2012	Black, non-Hispanic	25–44	0.5293	0.0353	200.2	0.4577	0.6001	Yes
2011.5	2011–2012	Black, non-Hispanic	45–64	0.5020	0.0154	1,055.5	0.4605	0.5435	Yes
2011.5	2011–2012	Black, non-Hispanic	65+	0.4451	0.0377	173.5	0.3698	0.5224	Yes
2011.5	2011–2012	White, non-Hispanic	18–24	0.2094	0.0477	72.7	0.1228	0.3208	Yes
2011.5	2011–2012	White, non-Hispanic	25–44	0.3083	0.0245	353.9	0.2606	0.3593	Yes
2011.5	2011–2012	White, non-Hispanic	45–64	0.3818	0.0324	224.8	0.3180	0.4487	Yes
2011.5	2011–2012	White, non-Hispanic	65+	0.3313	0.0245	369.1	0.2834	0.3818	Yes
2011.5	2011–2012	Other race, non-Hispanic	18–24	0.1285	0.0359	86.8	0.0663	0.2176	Yes
2011.5	2011–2012	Other race, non-Hispanic	25–44	0.1886	0.0363	116.3	0.1220	0.2716	Yes
2011.5	2011–2012	Other race, non-Hispanic	45–64	0.2011	0.0466	74.1	0.1169	0.3103	Yes
2011.5	2011–2012	Other race, non-Hispanic	65+	0.2647	0.0387	129.8	0.1912	0.3493	Yes
2011.5	2011–2012	Mexican American	18–24	0.3432	0.0501	89.8	0.2462	0.4509	Yes
2011.5	2011–2012	Mexican American	25–44	0.4208	0.0338	213.1	0.3537	0.4902	Yes
2011.5	2011–2012	Mexican American	45–64	0.5404	0.0398	157.0	0.4591	0.6201	Yes
2011.5	2011–2012	Mexican American	65+	0.5196	0.0887	31.7	0.3358	0.6995	No
2011.5	2011–2012	Other Hispanic	18–24	0.3227	0.0504	86.0	0.2258	0.4322	Yes
2011.5	2011–2012	Other Hispanic	25–44	0.3557	0.0400	143.3	0.2775	0.4399	Yes
2011.5	2011–2012	Other Hispanic	45–64	0.4128	0.0457	116.3	0.3222	0.5078	Yes
2011.5	2011–2012	Other Hispanic	65+	0.3942	0.0296	272.4	0.3115	0.4816	Yes
2013.5	2013–2014	Black, non-Hispanic	18–24	0.2968	0.0338	183.2	0.2317	0.3686	Yes
2013.5	2013–2014	Black, non-Hispanic	25–44	0.4828	0.0322	241.0	0.4182	0.5478	Yes
2013.5	2013–2014	Black, non-Hispanic	45–64	0.5398	0.0350	202.9	0.4686	0.6098	Yes
2013.5	2013–2014	Black, non-Hispanic	65+	0.4516	0.0345	208.2	0.3828	0.5219	Yes
2013.5	2013–2014	White, non-Hispanic	18–24	0.2209	0.0332	156.5	0.1586	0.2941	Yes
2013.5	2013–2014	White, non-Hispanic	25–44	0.3717	0.0181	710.1	0.3361	0.4085	Yes
2013.5	2013–2014	White, non-Hispanic	45–64	0.4110	0.0267	338.3	0.3580	0.4655	Yes
2013.5	2013–2014	White, non-Hispanic	65+	0.3694	0.0229	444.3	0.3244	0.4162	Yes
2013.5	2013–2014	Other race, non-Hispanic	18–24	0.2180	0.0620	44.3	0.1082	0.3675	Yes
2013.5	2013–2014	Other race, non-Hispanic	25–44	0.2296	0.0274	235.2	0.1775	0.2887	Yes
2013.5	2013–2014	Other race, non-Hispanic	45–64	0.1681	0.0412	82.3	0.0947	0.2667	Yes
2013.5	2013–2014	Other race, non-Hispanic	65+	0.2016	0.0411	95.3	0.1264	0.2962	Yes
2013.5	2013–2014	Mexican American	18–24	0.3121	0.0381	147.6	0.2384	0.3934	Yes
2013.5	2013–2014	Mexican American	25–44	0.5096	0.0154	1,055.2	0.4505	0.5685	Yes
2013.5	2013–2014	Mexican American	45–64	0.4795	0.0293	289.9	0.4185	0.5410	Yes
2013.5	2013–2014	Mexican American	65+	0.4471	0.0478	108.1	0.3514	0.5457	Yes
2013.5	2013–2014	Other Hispanic	18–24	0.3334	0.0628	56.4	0.2135	0.4715	Yes
2013.5	2013–2014	Other Hispanic	25–44	0.3624	0.0364	174.4	0.2911	0.4385	Yes
2013.5	2013–2014	Other Hispanic	45–64	0.3801	0.0328	218.6	0.3103	0.4538	Yes
2013.5	2013–2014	Other Hispanic	65+	0.3327	0.0457	106.5	0.2388	0.4374	Yes
2015.5	2015–2016	Black, non-Hispanic	18–24	0.2576	0.0359	148.7	0.1894	0.3357	Yes
2015.5	2015–2016	Black, non-Hispanic	25–44	0.4998	0.0279	321.1	0.4438	0.5558	Yes
2015.5	2015–2016	Black, non-Hispanic	45–64	0.5106	0.0287	303.8	0.4528	0.5681	Yes
2015.5	2015–2016	Black, non-Hispanic	65+	0.4453	0.0342	210.6	0.3770	0.5152	Yes
2015.5	2015–2016	White, non-Hispanic	18–24	0.2806	0.0392	131.4	0.2058	0.3657	Yes
2015.5	2015–2016	White, non-Hispanic	25–44	0.3718	0.0299	261.4	0.3130	0.4335	Yes
2015.5	2015–2016	White, non-Hispanic	45–64	0.4156	0.0308	256.1	0.3546	0.4786	Yes
2015.5	2015–2016	White, non-Hispanic	65+	0.3893	0.0222	482.8	0.3455	0.4344	Yes
2015.5	2015–2016	Other race, non-Hispanic	18–24	0.3014	0.0631	52.9	0.1829	0.4430	Yes
2015.5	2015–2016	Other race, non-Hispanic	25–44	0.2519	0.0381	129.7	0.1798	0.3356	Yes
2015.5	2015–2016	Other race, non-Hispanic	45–64	0.2831	0.0503	80.2	0.1881	0.3948	Yes
2015.5	2015–2016	Other race, non-Hispanic	65+	0.3472	0.0656	52.6	0.2213	0.4910	Yes
2015.5	2015–2016	Mexican American	18–24	0.3699	0.0342	199.3	0.2910	0.4543	Yes
2015.5	2015–2016	Mexican American	25–44	0.4863	0.0241	431.3	0.4350	0.5379	Yes
2015.5	2015–2016	Mexican American	45–64	0.5533	0.0282	309.8	0.4960	0.6095	Yes
2015.5	2015–2016	Mexican American	65+	0.4593	0.0391	162.7	0.3810	0.5391	Yes
2015.5	2015–2016	Other Hispanic	18–24	0.3502	0.0700	46.4	0.2161	0.5041	Yes
2015.5	2015–2016	Other Hispanic	25–44	0.4351	0.0376	174.2	0.3603	0.5122	Yes
2015.5	2015–2016	Other Hispanic	45–64	0.4633	0.0432	133.2	0.3765	0.5517	Yes
2015.5	2015–2016	Other Hispanic	65+	0.4269	0.0425	135.6	0.3424	0.5147	Yes

See footnotes at end of table.

Table. Example of public-use data set in stacked format used as input to the enhanced modified Kalman filter macro: Proportion of U.S. adults with obesity, by survey cycle, race and ethnicity, and age group—Con.

Year	Cycle	Population	Age group	Obesity	SE_ obesity	NEFF_ obesity	LL_ obesity	UL_ obesity	Rel_ obesity
2018.6	2017–March 2020	Black, non-Hispanic	18–24	0.3387	0.0370	163.7	0.2667	0.4167	Yes
2018.6	2017–March 2020	Black, non-Hispanic	25–44	0.4911	0.0218	526.6	0.4476	0.5347	Yes
2018.6	2017–March 2020	Black, non-Hispanic	45–64	0.5724	0.0154	1,037.8	0.5404	0.6039	Yes
2018.6	2017–March 2020	Black, non-Hispanic	65+	0.4897	0.0222	504.9	0.4453	0.5343	Yes
2018.6	2017–March 2020	White, non-Hispanic	18–24	0.3079	0.0520	78.7	0.2087	0.4221	Yes
2018.6	2017–March 2020	White, non-Hispanic	25–44	0.4221	0.0210	552.5	0.3805	0.4645	Yes
2018.6	2017–March 2020	White, non-Hispanic	45–64	0.4232	0.0296	277.8	0.3644	0.4836	Yes
2018.6	2017–March 2020	White, non-Hispanic	65+	0.4233	0.0229	466.1	0.3779	0.4696	Yes
2018.6	2017–March 2020	Other race, non-Hispanic	18–24	0.2918	0.0491	85.6	0.1985	0.4000	Yes
2018.6	2017–March 2020	Other race, non-Hispanic	25–44	0.3087	0.0259	318.0	0.2583	0.3627	Yes
2018.6	2017–March 2020	Other race, non-Hispanic	45–64	0.3246	0.0428	119.8	0.2419	0.4162	Yes
2018.6	2017–March 2020	Other race, non-Hispanic	65+	0.2333	0.0455	86.3	0.1490	0.3367	Yes
2018.6	2017–March 2020	Mexican American	18–24	0.3937	0.0814	36.0	0.2355	0.5701	No
2018.6	2017–March 2020	Mexican American	25–44	0.5265	0.0231	467.8	0.4761	0.5764	Yes
2018.6	2017–March 2020	Mexican American	45–64	0.5060	0.0355	198.6	0.4344	0.5775	Yes
2018.6	2017–March 2020	Mexican American	65+	0.4976	0.0545	84.1	0.3866	0.6087	Yes
2018.6	2017–March 2020	Other Hispanic	18–24	0.3566	0.0512	87.5	0.2570	0.4662	Yes
2018.6	2017–March 2020	Other Hispanic	25–44	0.3845	0.0273	318.6	0.3281	0.4433	Yes
2018.6	2017–March 2020	Other Hispanic	45–64	0.4464	0.0375	175.6	0.3715	0.5231	Yes
2018.6	2017–March 2020	Other Hispanic	65+	0.4642	0.0413	145.8	0.3813	0.5486	Yes

NOTES: Obesity is indicated by a body mass index of 30.0 or higher. Body mass index is calculated from measured height and weight and defined as weight (kilograms) / [height (meters)]^2. The variable “Year” is the midpoint of each survey cycle. Due to the suspension of field operations for the National Health and Nutrition Examination Survey in March 2020, the survey cycle 2017–March 2020 combines the full 2017–2018 cycle with partial data from 2019 through March 2020; see “National Health and Nutrition Examination Survey, 2017–March 2020 Prepandemic File: Sample Design, Estimation, and Analytic Guidelines” (https://www.cdc.gov/nchs/data/series/sr_02/sr02-190.pdf). The category “Other race, non-Hispanic” includes non-Hispanic people identifying as more than one race. The category “Other Hispanic” includes Hispanic or Latino people from origins other than Mexican American. The variable “Obesity” is the survey-weighted proportion of adults with obesity; SE_obesity is the standard error; NEFF_obesity is the effective sample size; LL_obesity and UL_obesity are the lower and upper limits, respectively, of the 95% Korn–Graubard confidence interval; and Rel_obesity indicates whether the proportion meets National Center for Health Statistics data presentation standards; see “National Center for Health Statistics Data Presentation Standards for Proportions” (https://www.cdc.gov/nchs/data/series/sr_02/sr02_175.pdf).

SOURCE: National Center for Health Statistics, National Health and Nutrition Examination Surveys, 1999–March 2020.

Appendix I. Statistical Modeling and Estimation Details

Orthogonal Polynomial Regression

Because collinearities among the linear, quadratic, and cubic terms for the fixed effects

$$\mu_{gt} = \beta_{0g} + \beta_{1g}t + \beta_{2g}t^2 + \beta_{3g}t^3$$

may lead to unstable estimates, the enhanced modified Kalman filter (MKF) macro uses orthogonal polynomials by default (29). Orthogonal polynomials are also useful to retain comparability between regression coefficients in different dimensions (30), which is relevant in model averaging. To facilitate interpretation, the design matrix

$$\mathbf{X} = \begin{bmatrix} 1 & t_1 & t_1^2 & t_1^3 \\ 1 & t_2 & t_2^2 & t_2^3 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & t_n & t_n^2 & t_n^3 \end{bmatrix},$$

where $t_1 < t_2 < \ldots < t_n$ are the n time points, is right-multiplied by a scalar matrix $\boldsymbol{\Gamma}$ to convert the raw predictors $\mathbf{X}$ into the orthogonal predictors $\mathbf{Z} = \mathbf{X}\boldsymbol{\Gamma}$. As a result, the estimated coefficients

$$\hat{\boldsymbol{\beta}}_{\mathbf{g}} = \begin{bmatrix} \hat{\beta}_{0g} \\ \hat{\beta}_{1g} \\ \hat{\beta}_{2g} \\ \hat{\beta}_{3g} \end{bmatrix}$$

are mapped from the orthogonal polynomial regression back to "raw" coefficients using $\boldsymbol{\Gamma}\hat{\boldsymbol{\beta}}_{\mathbf{g}}$, preserving interpretability for end-users. This reverse-transformation is also applied to the coefficients' standard errors, rendering the background orthogonal polynomial transformation (from the SAS IML orpol function) inconsequential to end-users.

State-space Model Formulation and Maximum Likelihood-based Estimation

Unlike in the earlier MKF procedure and macro where time points were equally spaced (8–11), the derivations in this section apply for any two time points t and s, with $|t-s|>0$.

Define z_{gt} as $z_{gt} = y_{gt} - \mu_{gt}$, representing the detrended estimate for group g at time t. The mixed-effects model underlying the MKF procedure can be conceptualized using an "observation" equation

$$z_{gt} = \gamma_{gt} + \varepsilon_{gt},$$

where the observation error ε_{gt} is normally distributed with mean zero and variance σ_{gt}^2, and a "state" equation that, for $|t-s|>0$, specifies the transition from state γ_{gs} at time s to state γ_{gt} at time t as a step of length $|t-s|$ in a first-order autoregressive AR(1) process with autocorrelation coefficient ρ, $|\rho| < 1$, and a so-called "innovation" variance τ^2:

$$\gamma_{gt} = \rho^{|t-s|}\gamma_{gs} + \xi_{gs}.$$

The innovation ξ_{gs} (sometimes referred to as an exogenous shock) in the transition from time s to time t is normally distributed with mean zero and variance

$$\tau^2\left(1-\rho^{2|t-s|}\right)\Big/\left(1-\rho^2\right)$$

and is independent of the state γ_{gs} at time s. As in the earlier MKF procedure, the AR(1) process is assumed to be stationary, which means that the γ_{gt} are drawn according to a normal distribution with mean 0 and variance $\tau^2\big/\left(1-\rho^2\right)$ at time t = 0 and all later times t.

If the observation variance σ_{gt}^2, time trend μ_{gt}, autocorrelation parameter ρ, and innovation variance τ^2 were known, and if the process had been observed up to time s with $|t-s|>0$, then the best linear unbiased predictor (8,9) of the true underlying health state $\eta_{gt} = \mu_{gt} + \gamma_{gt}$ for group g at time t would be given by $\hat{\eta}_{gt} = \mu_{gt} + \hat{\gamma}_{gt}$, where

$$\hat{\gamma}_{gt} = \lambda_{gt}^{(s)} z_{gt} + \left(1-\lambda_{gt}^{(s)}\right)\rho^{|t-s|}\hat{\gamma}_{gs}.$$

This convex linear combination is based on combining the observed deviation $z_{gt} = y_{gt} - \mu_{gt}$ from the fitted trend at time t and the prediction from the state equation of that deviation, namely $\rho^{|t-s|}\hat{\gamma}_{gs}$. The optimal value (minimizing mean squared error) for the "shrinkage" factor $\lambda_{gt}^{(s)}$ is given by

$$\lambda_{gt}^{(s)} = \frac{\delta_{gt}^{(s)}}{\delta_{gt}^{(s)} + \sigma_{gt}^2},$$

where

$$\sigma_{gt}^2 = E\left[\left(z_{gt} - \gamma_{gt}\right)^2\right]$$

is the observation error variance, that is, the variance of $z_{gt} = y_{gt} - \mu_{gt}$ as a predictor of γ_{gt}, and

$$\delta_{gt}^{(s)} = E\left[\left(\rho^{|t-s|}\hat{\gamma}_{gs} - \gamma_{gt}\right)^2\right],$$

the variance of $\rho^{|t-s|}\hat{\gamma}_{gs}$ as a predictor of γ_{gt} (8,9).

By adding and subtracting the term

$$\rho^{|t-s|}\gamma_{gs}$$

and expanding the square in the expression of $\delta_{gt}^{(s)}$, it can be shown that $\delta_{gt}^{(s)}$ satisfies the relation

$$\delta_{gt}^{(s)} = \rho^{2|t-s|}\omega_{gs} + \tau^2\left(\frac{1-\rho^{2|t-s|}}{1-\rho^2}\right),$$

where ω_{gs} is given by

$$\omega_{gs} = E\left[\left(\hat{\gamma}_{gs} - \gamma_{gs}\right)^2\right]$$

and, in turn, ω_{gt} satisfies the recurrence relation

$$\omega_{gt} = \left(1-\lambda_{gt}^{(s)}\right)\delta_{gt}^{(s)}.$$

In general, the observation variances σ_{gt}^2, trends μ_{gt}, autocorrelation coefficient ρ, and innovation variance τ^2 are unknown. The observation variances are replaced by their sample versions S_{gt}^2 but otherwise assumed fixed. The trends μ_{gt}, autocorrelation coefficient ρ, and innovation variance τ^2 are estimated using SAS PROC NLMIXED, after having transformed ρ to

$$\psi = \ln\left(\frac{1-\rho}{1+\rho}\right)$$

and τ^2 to $\iota = 2\ln\tau$ (10,11).

Bayesian Hierarchical Modeling and Estimation

Let $t_1 < t_2 < \ldots < t_n$ denote the n time points. Using matrix notation, with

$$\mathbf{y_{g\cdot}} = \left(y_{gt_1}, y_{gt_2}, \ldots, y_{gt_n}\right)^{\mathsf{T}},$$
$$\boldsymbol{\eta}_{\mathbf{g\cdot}} = \left(\eta_{gt_1}, \eta_{gt_2}, \ldots, \eta_{gt_n}\right)^{\mathsf{T}},$$
$$\boldsymbol{\beta}_{\mathbf{g}} = \left(\beta_{0g}, \beta_{1g}, \beta_{2g}, \beta_{3g}\right)^{\mathsf{T}},$$
$$\boldsymbol{\theta} = \left(\theta_0, \theta_1, \theta_2, \theta_3\right)^{\mathsf{T}}$$

and

$$\mathbf{X} = \begin{bmatrix} 1 & t_1 & t_1^2 & t_1^3 \\ 1 & t_2 & t_2^2 & t_2^3 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & t_n & t_n^2 & t_n^3 \end{bmatrix},$$

the top three levels of the hierarchical model are given by multivariate normal (MVN) distributions:

1. The MVN$_n$($\boldsymbol{\eta}_{\mathbf{g\cdot}}$, $\boldsymbol{\Delta}_{\mathbf{g}}$) distribution for $\mathbf{y_{g\cdot}}|\boldsymbol{\eta}_{\mathbf{g\cdot}}, \boldsymbol{\Delta}_{\mathbf{g}}$, where
$$\boldsymbol{\Delta}_{\mathbf{g}} = \text{diag}\left(S_{gt_1}^2, S_{gt_2}^2, \cdots, S_{gt_n}^2\right);$$
2. The MVN$_n$($\mathbf{X}\boldsymbol{\beta}_{\mathbf{g}}$, $\mathbf{A}$) distribution for $\boldsymbol{\eta}_{\mathbf{g\cdot}}|\boldsymbol{\beta}_{\mathbf{g}}, \rho, \tau^2$, where
$$\mathbf{A} = \left(A_{ij}\right)_{i,j=1}^{n} \text{ and } A_{ij} = \frac{\tau^2}{1-\rho^2}\rho^{|t_i - t_j|};$$
3. And the MVN$_4$($\boldsymbol{\theta}$, $\boldsymbol{\Lambda}$) distribution for $\boldsymbol{\beta}_{\mathbf{g}}|\,\boldsymbol{\theta}, \boldsymbol{\Lambda}$, where
$$\boldsymbol{\Lambda} = \text{diag}\left(\nu_0^2, \nu_1^2, \nu_2^2, \nu_3^2\right).$$

Bayesian estimation of regression coefficients

In the "**independent**" **trends case**, regression coefficients $\boldsymbol{\beta}_{\mathbf{g}}$ are specific to each group. Combining the top two levels of the previous hierarchical model, the likelihood function for $\boldsymbol{\beta}_{\mathbf{g}}$ is

$$f\left(\mathbf{y_{g\cdot}} \mid \boldsymbol{\beta}_{\mathbf{g}}, \mathbf{V_g}\right) \propto \left|\mathbf{V_g^{-1}}\right|^{1/2} \exp\left\{-\frac{1}{2}\left(\mathbf{y_{g\cdot}} - \mathbf{X}\boldsymbol{\beta}_{\mathbf{g}}\right)^{\mathsf{T}} \mathbf{V_g^{-1}}\left(\mathbf{y_{g\cdot}} - \mathbf{X}\boldsymbol{\beta}_{\mathbf{g}}\right)\right\},$$

where $\mathbf{V_g} = \mathbf{A} + \boldsymbol{\Delta}_{\mathbf{g}}$ and $\left|\mathbf{V_g^{-1}}\right|$ denotes the determinant of $\mathbf{V_g^{-1}}$, given by $\left|\mathbf{V_g^{-1}}\right| = \left|\mathbf{V_g}\right|^{-1}$. Expanding the quadratic form

$$\left(\mathbf{y_{g\cdot}} - \mathbf{X}\boldsymbol{\beta}_{\mathbf{g}}\right)^{\mathsf{T}} \mathbf{V_g^{-1}}\left(\mathbf{y_{g\cdot}} - \mathbf{X}\boldsymbol{\beta}_{\mathbf{g}}\right)$$

around $\mathbf{X}\hat{\boldsymbol{\beta}}_{\mathbf{g}}$, where $\hat{\boldsymbol{\beta}}_{\mathbf{g}}$ is the weighted least-squares estimator

$$\hat{\boldsymbol{\beta}}_{\mathbf{g}} = \left(\mathbf{X}^{\mathsf{T}}\mathbf{V_g^{-1}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathsf{T}}\mathbf{V_g^{-1}}\mathbf{y_{g\cdot}},$$

combining with the prior density function (from level 3 of the hierarchy), and collecting terms in $\boldsymbol{\beta}_{\mathbf{g}}$, the joint posterior density function of $\mathbf{y_{g\cdot}}$ and $\boldsymbol{\beta}_{\mathbf{g}}$ given the remaining parameters is proportional to:

$$\left|\mathbf{V_g^{-1}}\right|^{1/2}\left|\boldsymbol{\Lambda}^{-1}\right|^{1/2}\exp\left\{-\frac{1}{2}\mathbf{y_{g\cdot}^{\mathsf{T}}}\mathbf{V_g^{-1}}\mathbf{y_{g\cdot}} + \frac{1}{2}\mathbf{m_g^{\mathsf{T}}}\boldsymbol{\Phi}_{\mathbf{g}}^{-1}\mathbf{m_g} - \frac{1}{2}\boldsymbol{\theta}^{\mathsf{T}}\boldsymbol{\Lambda}^{-1}\boldsymbol{\theta} - \frac{1}{2}\left(\boldsymbol{\beta}_{\mathbf{g}} - \mathbf{m_g}\right)^{\mathsf{T}}\boldsymbol{\Phi}_{\mathbf{g}}^{-1}\left(\boldsymbol{\beta}_{\mathbf{g}} - \mathbf{m_g}\right)\right\},$$

where

$$\boldsymbol{\Phi}_{\mathbf{g}}^{-1} = \mathbf{X}^{\mathsf{T}}\mathbf{V_g^{-1}}\mathbf{X} + \boldsymbol{\Lambda}^{-1} \text{ and } \mathbf{m_g} = \boldsymbol{\Phi}_{\mathbf{g}}\left(\boldsymbol{\Lambda}^{-1}\boldsymbol{\theta} + \mathbf{X}^{\mathsf{T}}\mathbf{V_g^{-1}}\mathbf{y_{g\cdot}}\right).$$

It follows that the conditional posterior distribution for $\boldsymbol{\beta}_{\mathbf{g}}$ is MVN with mean vector $\mathbf{m_g}$ and variance-covariance matrix $\boldsymbol{\Phi}_{\mathbf{g}}$, which is used in Gibbs sampling. Additionally, the marginal density function of $\mathbf{y_{g\cdot}}$ is proportional to:

$$\left|\boldsymbol{\Phi}_{\mathbf{g}}\right|^{1/2}\left|\mathbf{V_g^{-1}}\right|^{1/2}\left|\boldsymbol{\Lambda}^{-1}\right|^{1/2}\exp\left\{-\frac{1}{2}\mathbf{y_{g\cdot}^{\mathsf{T}}}\mathbf{V_g^{-1}}\mathbf{y_{g\cdot}} + \frac{1}{2}\mathbf{m_g^{\mathsf{T}}}\boldsymbol{\Phi}_{\mathbf{g}}^{-1}\mathbf{m_g} - \frac{1}{2}\boldsymbol{\theta}^{\mathsf{T}}\boldsymbol{\Lambda}^{-1}\boldsymbol{\theta}\right\}$$

The latter is required to calculate Bayes factors and will be used in Bayesian model averaging; see "Bayesian model averaging via mixture prior on regression coefficients."

In the **"common" trends case**, trends are assumed parallel across groups, with $\beta_{kg} \equiv \beta_k$ for k = 1,2,3. Posterior inference for the intercepts proceeds as in the independent trends case. However, conditional on the intercepts, all groups contribute to posterior estimation of the common regression coefficients. To derive the conditional posterior distribution, let $z_{gt} = y_{gt} - \beta_{0g}$ and define

$$\vec{\boldsymbol{\beta}} = \left(\beta_1, \beta_2, \beta_3\right)^{\mathsf{T}}, \vec{\mathbf{X}} = \begin{bmatrix} t_1 & t_1^2 & t_1^3 \\ t_2 & t_2^2 & t_2^3 \\ \vdots & \vdots & \vdots \\ t_n & t_n^2 & t_n^3 \end{bmatrix}, \vec{\boldsymbol{\theta}} = \left(\theta_1, \theta_2, \theta_3\right)^{\mathsf{T}}, \text{ and } \vec{\boldsymbol{\Lambda}} = \text{diag}\left(\nu_1^2, \nu_2^2, \nu_3^2\right).$$

Arrow notation $\vec{\boldsymbol{\beta}}$ is used here to distinguish the three-dimensional vector $\vec{\boldsymbol{\beta}} = (\beta_1, \beta_2, \beta_3)^{\mathsf{T}}$ of common linear, quadratic, and cubic terms across groups from the four-dimensional vector $\boldsymbol{\beta}_\mathbf{g} = (\beta_{0g}, \beta_{1g}, \beta_{2g}, \beta_{3g})^{\mathsf{T}}$, which includes the group-specific intercepts. Following similar steps as before, the conditional posterior distribution for the vector $\vec{\boldsymbol{\beta}}$ of common regression coefficients is MVN with mean vector $\vec{\mathbf{m}}$ and covariance matrix $\vec{\boldsymbol{\Phi}}$, where

$$\vec{\boldsymbol{\Phi}}^{-1} = \vec{\mathbf{X}}^{\mathsf{T}} \left[\sum_{\mathbf{g}} \mathbf{V}_\mathbf{g}^{-1} \right] \vec{\mathbf{X}} + \vec{\boldsymbol{\Lambda}}^{-1} \text{ and}$$

$$\vec{\mathbf{m}} = \vec{\boldsymbol{\Phi}} \left(\vec{\boldsymbol{\Lambda}}^{-1} \vec{\boldsymbol{\theta}} + \vec{\mathbf{X}}^{\mathsf{T}} \left[\sum_{\mathbf{g}} \mathbf{V}_\mathbf{g}^{-1} \mathbf{z}_{\mathbf{g}\cdot} \right] \right).$$

Bayesian estimation of regression hyperparameters

As in the earlier macro, the enhanced MKF macro allows for three classes of models for the regression coefficients $\boldsymbol{\beta}_\mathbf{g} = (\beta_{0g}, \beta_{1g}, \beta_{2g}, \beta_{3g})^{\mathsf{T}}$:

1. In the independent trends case, the prior distribution for $\boldsymbol{\beta}_\mathbf{g}$ is MVN with mean vector $\boldsymbol{\theta}$ and a diagonal variance-covariance matrix $\boldsymbol{\Lambda}$. The hyperparameters $\boldsymbol{\theta}$ and $\boldsymbol{\Lambda}$ are specified by the user, with default values of $\theta_k = 0$ for k = 1, 2, 3, to reflect an *a priori* model with no time trend; default values for θ_0 and the ν_k are loosely determined from the range (r = max − min) of the y_{gt} over both g and t, as in the earlier MKF. The default value for θ_0 is $\theta_0 = r/2$ (roughly the median), whereas the default for ν_0^2 and ν_1^2 is 1,000,000 × r^2, which are large prior variances relative to the range of the data that practically will not impact posterior estimation. Prior variances for the quadratic and cubic coefficients are such that the coefficients tend to be smaller as polynomial degree increases, with $\nu_2^2 = \nu_1^2/2$ and $\nu_3^2 = \nu_1^2/4$ by default, reflecting a prior preference for simpler trends (30).
2. In the common trends case, all group-specific trends are assumed parallel, with $\beta_{kg} \equiv \beta_k$ for k = 1,2,3. Otherwise, the vector $\boldsymbol{\beta}_\mathbf{g} = (\beta_{0g}, \beta_1, \beta_2, \beta_3)^{\mathsf{T}}$ remains distributed according to an MVN with means $\boldsymbol{\theta} = (\theta_0, \theta_1, \theta_2, \theta_3)^{\mathsf{T}}$ and variances
$$\boldsymbol{\Lambda} = \text{diag}\left(\nu_0^2, \nu_1^2, \nu_2^2, \nu_3^2\right);,$$
where those hyperparameters take on the values specified in the independent case.
3. In the fully Bayesian trend case, an additional level is added to the Bayesian hierarchical model to account for the uncertainty in specifying prior means and variances for the regression coefficients, but also to reinforce borrowing strength across groups and offer a compromise between the independent and common trend cases (10,11). Under the fully Bayesian trend model in the enhanced MKF macro, hyperparameters θ_0 and ν_0^2 for the intercepts remain as in the independent and common trend cases, but hyperparameters for the linear, quadratic, and cubic terms, namely θ_k and ν_k^2, with k = 1,2,3, are themselves modeled using adequately selected hyperprior distributions. The θ_k are assumed to be *a priori* normally distributed with means $\vartheta_k = 0$ and variances $\varsigma_k^2 = 0.1 \times r^2 / 2^{k-1}$, k = 1,2,3. The standard deviations ν_k are assumed to be uniformly distributed between 0 and 0.5 × r × (k + 1)/2, k = 1,2,3. As before, the enhanced MKF macro matches the prior specification in the earlier MKF macro for the linear term (k = 1), but selects priors for the quadratic (k = 2) and cubic (k = 3) terms in such a way that the coefficients will be smaller in magnitude as the degree k increases, although with decreasing precision.

In the fully Bayesian case, because both the prior for $\vec{\boldsymbol{\beta}}_\mathbf{g} = (\beta_{1g}, \beta_{2g}, \beta_{3g})^{\mathsf{T}}$ and hyperprior for $\vec{\boldsymbol{\theta}} = (\theta_1, \theta_2, \theta_3)^{\mathsf{T}}$ are MVNs with respective mean vectors $\vec{\boldsymbol{\theta}} = (\theta_1, \theta_2, \theta_3)^{\mathsf{T}}$ and $\vec{\boldsymbol{\vartheta}} = (\vartheta_1, \vartheta_2, \vartheta_3)^{\mathsf{T}}$, and covariance matrices

$$\vec{\boldsymbol{\Lambda}} = \text{diag}\left(\nu_1^2, \nu_2^2, \nu_3^2\right) \text{ and } \vec{\boldsymbol{\Xi}} = \text{diag}\left(\varsigma_1^2, \varsigma_2^2, \varsigma_3^2\right),$$

the conditional posterior distribution for $\vec{\boldsymbol{\theta}}$ given the remaining model parameters is also MVN, with mean vector $\vec{\boldsymbol{\Omega}}\left(\vec{\boldsymbol{\Lambda}}^{-1}\vec{\boldsymbol{\beta}}_\mathrm{g} + \vec{\boldsymbol{\Xi}}^{-1}\vec{\boldsymbol{\vartheta}}\right)$ and covariance matrix $\vec{\boldsymbol{\Omega}} = \left(\vec{\boldsymbol{\Lambda}}^{-1} + \vec{\boldsymbol{\Xi}}^{-1}\right)^{-1}$, which is used in Gibbs sampling.

For the standard deviation parameters ν_k in the fully Bayesian case, closed-form expressions for the conditional posterior distributions are not readily available. As a result, Gibbs sampling is not available for the ν_k, and the random walk Metropolis–Hastings sampler is used instead.

Bayesian estimation of true health states

From the top two levels of the Bayesian hierarchical model, the joint posterior density function of $\mathbf{y}_{\mathbf{g}\cdot}$ and $\boldsymbol{\eta}_{\mathbf{g}\cdot}$ given the remaining parameters is proportional to:

$$\left|\mathbf{A}^{-1}\right|^{1/2} \left|\boldsymbol{\Delta}_\mathbf{g}^{-1}\right|^{1/2} \exp\left\{-\frac{1}{2}\left(\mathbf{y}_{\mathbf{g}\cdot} - \boldsymbol{\eta}_{\mathbf{g}\cdot}\right)^{\mathsf{T}} \boldsymbol{\Delta}_\mathbf{g}^{-1} \left(\mathbf{y}_{\mathbf{g}\cdot} - \boldsymbol{\eta}_{\mathbf{g}\cdot}\right) - \frac{1}{2}\left(\boldsymbol{\eta}_{\mathbf{g}\cdot} - \mathbf{X}\boldsymbol{\beta}_\mathbf{g}\right)^{\mathsf{T}} \mathbf{A}^{-1} \left(\boldsymbol{\eta}_{\mathbf{g}\cdot} - \mathbf{X}\boldsymbol{\beta}_\mathbf{g}\right)\right\}.$$

Expanding and completing the quadratic form in $\boldsymbol{\eta}_{\mathbf{g}\cdot}$ the conditional posterior density function for $\boldsymbol{\eta}_{\mathbf{g}\cdot}$ is recognized as MVN with mean vector

$$\mathbf{W}_\mathbf{g}\left(\boldsymbol{\Delta}_\mathbf{g}^{-1}\mathbf{y}_{\mathbf{g}\cdot} + \mathbf{A}^{-1}\mathbf{X}\boldsymbol{\beta}_\mathbf{g}\right)$$

and variance-covariance matrix

$$\mathbf{W}_\mathbf{g} = \left(\boldsymbol{\Delta}_\mathbf{g}^{-1} + \mathbf{A}^{-1}\right)^{-1},$$

which is used in Gibbs sampling.

Algebraic expressions for inverse and determinant of AR(1) correlation matrix

The AR(1) covariance matrix $\mathbf{A}$ is defined as:

$$\mathbf{A} = \left(A_{ij}\right)_{i,j=1}^{n} \text{ and } A_{ij} = \frac{\tau^2}{1-\rho^2}\rho^{\left|t_i - t_j\right|}.$$

Let $\mathbf{A(\rho)}$ denote the AR(1) *correlation* matrix, with entries $\rho^{\left|t_i - t_j\right|}$. It can be shown that the determinant of $\mathbf{A(\rho)}$ is given by:

$$\left|\mathbf{A(\rho)}\right| = \prod_{j=1}^{n-1}\left[1-\rho^{2\left|t_{j+1}-t_j\right|}\right].$$

It can also be shown that the inverse $\mathbf{B(\rho)}$ of $\mathbf{A(\rho)}$ is a tridiagonal matrix, with diagonal entries

$$[\mathbf{B(\rho)}]_{ii} = \begin{cases} \dfrac{1}{1-\rho^{2\left|t_2-t_1\right|}}, & \text{for } i = 1, \\ \dfrac{1-\rho^{2\left|t_{i+1}-t_{i-1}\right|}}{\left[1-\rho^{2\left|t_{i+1}-t_i\right|}\right]\left[1-\rho^{2\left|t_i-t_{i-1}\right|}\right]}, & \text{for } i = 2,\cdots,n-1, \\ \dfrac{1}{1-\rho^{2\left|t_n-t_{n-1}\right|}}, & \text{for } i = n, \end{cases}$$

and off-diagonal entries

$$[\mathbf{B(\rho)}]_{i,i+1} = \frac{-\rho^{\left|t_{i+1}-t_i\right|}}{1-\rho^{2\left|t_{i+1}-t_i\right|}},$$

$$[\mathbf{B(\rho)}]_{j+1,j} = \frac{-\rho^{\left|t_{j+1}-t_j\right|}}{1-\rho^{2\left|t_{j+1}-t_j\right|}}, \text{ and}$$

$[\mathbf{B(\rho)}]_{ij} = 0$ for $\left|i-j\right| > 1$. Those expressions are used in the enhanced MKF macro to speed up computations of the determinant and matrix inverse, which are needed in the Gibbs sampler for the true health states $\boldsymbol{\eta}_{\mathbf{g}\cdot}$, and can be costly to compute (for example, via the Cholesky decomposition).

Bayesian estimation of AR(1) model parameters

Closed-form expressions for the conditional posterior distributions of the AR(1) parameters ρ and τ^2 are not readily available. As a result, the random walk Metropolis–Hastings sampler is used instead of the Gibbs sampler for those parameters. The mean and variance for the prior normal distribution of the transformed autocorrelation parameter ρ, namely

$$\psi = \ln\left(\frac{1-\rho}{1+\rho}\right),$$

are user-specified, with default values of 0 and 1, respectively, as in the earlier MKF macro. The lower and upper limits of the uniform prior for the innovation standard deviation τ are also user-specified, with default values of 0.0001 and 0.1 × r, respectively, as in the earlier macro (10,11).

Unlike the earlier macro, the enhanced MKF macro allows fitting group-specific AR(1) parameters ρ_g and τ_g^2. Yet, as a compromise between separate and shared values per group, and to maximize the amount of borrowed strength, the parameters

$$\psi_g = \ln\left(\frac{1-\rho_g}{1+\rho_g}\right)$$

are drawn from an underlying normal $\mathrm{N}\left(\vartheta_\psi, \varsigma_\psi^2\right)$ prior and "shrunk" toward their mean ϑ_ψ. The latter has a normal hyperprior distribution that can be specified by the user, with default values of 0 for its mean and the constant $c = 1$ for its variance, respectively. The standard deviation ς_ψ is drawn from a user-specified uniform distribution, with default values of 0.0001 for the lower and $\sqrt{c} = 1$ for the upper limit. Finally, the innovation standard deviations τ_g are independent draws from the same uniform as before, with default values of 0.0001 and 0.1 × r for the lower and upper limits, respectively.

Bayesian estimation of variance parameters

Conditional on group-specific variance parameters σ_g^2, the sampling variances $S_{gt_i}^2, i = 1, 2, \cdots, n$ are modeled as scaled chi-squared random variables with $n_{gt_i} - 1$ degrees of freedom (5–7), where n_{gt_i} is the (effective) sample size for group g at time t_i:

$$\left.\frac{\left(n_{gt_i}-1\right)S_{gt_i}^2}{\sigma_g^2}\right| \sigma_g^2 \text{ distributed as } \chi^2\left(n_{gt_i}-1\right)$$

The unknown variance parameters σ_g^2 are assumed to arise from the conjugate inverse-gamma prior distribution with shape parameter a and scale parameter b, resulting in an inverse-gamma posterior distribution with shape parameter

$$a + \tfrac{1}{2}\sum_{i=1}^{n}\left(n_{gt_i}-1\right)$$

and scale parameter

$$b + \tfrac{1}{2}\sum_{i=1}^{n}\left(n_{gt_i}-1\right)S_{gt_i}^2,$$

which is used in the Gibbs sampler for the σ_g^2. Default values for the hyperparameters a and b, with $a > 2$ and $b > 0$, are loosely informed by the data, using the median of the sampling variances $S_{gt_i}^2, i = 1, 2, \cdots, n$ instead of the prior mean

$$\frac{b}{(a-1)}$$

and 10 times their interquartile range instead of the prior standard deviation

$$\frac{b}{(a-1)\sqrt{a-2}}.$$

Bayesian model averaging via mixture prior on regression coefficients

In the enhanced MKF macro, a mixture prior approach is used, resulting in posterior inference that is equivalent to Bayesian model averaging (19,31,32).

Let $L = \ell$ indicate the specific set of constraints from 1 through 7 on the overarching cubic trend model, with 1 = independent cubic, 2 = independent quadratic, 3 = independent linear, 4 = common cubic, 5 = common quadratic, 6 = common linear, and 7 = dropped trend models. By default, all seven sets of constraints are given equal prior probability of 1/7. Posterior probabilities for the indicator variable $L = \ell$ are calculated conditional on the intercepts, so it is enough to work with $z_{gt} = y_{gt} - \beta_{0g}$.

Define $\vec{\boldsymbol{\beta}}_{\mathbf{g}}^{(\ell)} = \left(\beta_{1g}, \beta_{2g}, \beta_{3g}\right)^{\mathsf{T}}$ and

$$\vec{\mathbf{X}}^{(\ell)} = \begin{bmatrix} t_1 & t_1^2 & t_1^3 \\ t_2 & t_2^2 & t_2^3 \\ \vdots & \vdots & \vdots \\ t_n & t_n^2 & t_n^3 \end{bmatrix}$$

for $\ell = 1$ or $\ell = 4$;

$\vec{\boldsymbol{\beta}}_{\mathbf{g}}^{(\ell)} = \left(\beta_{1g}, \beta_{2g}\right)^{\mathsf{T}}$ and

$$\vec{\mathbf{X}}^{(\ell)} = \begin{bmatrix} t_1 & t_1^2 \\ t_2 & t_2^2 \\ \vdots & \vdots \\ t_n & t_n^2 \end{bmatrix}$$

for $\ell = 2$ or $\ell = 5$; and

$\vec{\boldsymbol{\beta}}_{\mathbf{g}}^{(\ell)} = \left(\beta_{1g}\right)$ and

$$\vec{\mathbf{X}}^{(\ell)} = \begin{bmatrix} t_1 \\ t_2 \\ \vdots \\ t_n \end{bmatrix}$$

for $\ell = 3$ or $\ell = 6$, again using arrow notation $\vec{\boldsymbol{\beta}}_{\mathbf{g}}^{(\ell)}$ to highlight the intercept-less vectors of regression coefficients.

Also define

$$\vec{\boldsymbol{\theta}}^{(\ell)} = \left(\theta_1, \theta_2, \theta_3\right)^{\mathsf{T}} \text{ and } \vec{\boldsymbol{\Lambda}}^{(\ell)} = \text{diag}\left(\nu_1^2, \nu_2^2, \nu_3^2\right)$$

for $\ell = 1$ or $\ell = 4$;

$$\vec{\boldsymbol{\theta}}^{(\ell)} = \left(\theta_1, \theta_2\right)^{\mathsf{T}} \text{ and } \vec{\boldsymbol{\Lambda}}^{(\ell)} = \text{diag}\left(\nu_1^2, \nu_2^2\right)$$

for $\ell = 2$ or $\ell = 5$; and

$$\vec{\boldsymbol{\theta}}^{(\ell)} = \left(\theta_1\right) \text{ and } \vec{\boldsymbol{\Lambda}}^{(\ell)} = \text{diag}\left(\nu_1^2\right)$$

for $\ell = 3$ or $\ell = 6$.

Conditional on a value of $L = \ell$ from 1 through 3, corresponding to the independent trend models, the posterior variance-covariance matrix and mean vector for the regression coefficients other than the intercepts are given by

$$\vec{\boldsymbol{\Phi}}_{\mathbf{g}}^{(\ell)^{-1}} = \vec{\mathbf{X}}^{(\ell)^{\mathsf{T}}} \mathbf{V}_{\mathbf{g}}^{-1} \vec{\mathbf{X}}^{(\ell)} + \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \text{ and } \vec{\mathbf{m}}_{\mathbf{g}}^{(\ell)} = \vec{\boldsymbol{\Phi}}_{\mathbf{g}}^{(\ell)} \left(\vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \vec{\boldsymbol{\theta}}^{(\ell)} + \vec{\mathbf{X}}^{(\ell)^{\mathsf{T}}} \mathbf{V}_{\mathbf{g}}^{-1} \mathbf{z}_{\mathbf{g\cdot}} \right),$$

as seen earlier. As a result, posterior probabilities for the indicator variable $L = \ell$ will be proportional to the product of marginal densities of the $\mathbf{z}_{\mathbf{g\cdot}}$:

$$\prod_g \left\{ \left| \vec{\boldsymbol{\Phi}}_{\mathbf{g}}^{(\ell)} \right|^{1/2} \left| \mathbf{V}_{\mathbf{g}}^{-1} \right|^{1/2} \left| \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \right|^{1/2} \exp\left[-\frac{1}{2} \mathbf{z}_{\mathbf{g}}^{\mathsf{T}} \mathbf{V}_{\mathbf{g}}^{-1} \mathbf{z}_{\mathbf{g}} + \frac{1}{2} \vec{\mathbf{m}}_{\mathbf{g}}^{(\ell)^{\mathsf{T}}} \vec{\boldsymbol{\Phi}}_{\mathbf{g}}^{(\ell)^{-1}} \vec{\mathbf{m}}_{\mathbf{g}}^{(\ell)} - \frac{1}{2} \vec{\boldsymbol{\theta}}^{(\ell)^{\mathsf{T}}} \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \vec{\boldsymbol{\theta}}^{(\ell)} \right] \right\}.$$

Terms in $\mathbf{z}_{\mathbf{g\cdot}}$ cancel out upon standardization (that is, so that probabilities sum to one), and those posterior probabilities are proportional to a product of ratios of prior to posterior MVN densities:

$$\prod_g \left\{ \frac{\left| \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \right|^{1/2} \exp\left[-\frac{1}{2} \vec{\boldsymbol{\theta}}^{(\ell)^{\mathsf{T}}} \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \vec{\boldsymbol{\theta}}^{(\ell)} \right]}{\left| \vec{\boldsymbol{\Phi}}_{\mathbf{g}}^{(\ell)^{-1}} \right|^{1/2} \exp\left[-\frac{1}{2} \vec{\mathbf{m}}_{\mathbf{g}}^{(\ell)^{\mathsf{T}}} \vec{\boldsymbol{\Phi}}_{\mathbf{g}}^{(\ell)^{-1}} \vec{\mathbf{m}}_{\mathbf{g}}^{(\ell)} \right]} \right\},$$

For $L = \ell$ from 4 through 6, the common trend models, posterior probabilities are proportional to:

$$\frac{\left| \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \right|^{1/2} \exp\left[-\frac{1}{2} \vec{\boldsymbol{\theta}}^{(\ell)^{\mathsf{T}}} \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \vec{\boldsymbol{\theta}}^{(\ell)} \right]}{\left| \vec{\boldsymbol{\Phi}}^{(\ell)^{-1}} \right|^{1/2} \exp\left[-\frac{1}{2} \vec{\mathbf{m}}^{(\ell)^{\mathsf{T}}} \vec{\boldsymbol{\Phi}}^{(\ell)^{-1}} \vec{\mathbf{m}}^{(\ell)} \right]},$$

where $\vec{\boldsymbol{\Phi}}^{(\ell)^{-1}} = \vec{\mathbf{X}}^{(\ell)^{\mathsf{T}}} \left[\sum_{\mathbf{g}} \mathbf{V}_{\mathbf{g}}^{-1} \right] \vec{\mathbf{X}}^{(\ell)} + \vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}}$ and $\vec{\mathbf{m}}^{(\ell)} = \vec{\boldsymbol{\Phi}}^{(\ell)} \left(\vec{\boldsymbol{\Lambda}}^{(\ell)^{-1}} \vec{\boldsymbol{\theta}}^{(\ell)} + \vec{\mathbf{X}}^{(\ell)^{\mathsf{T}}} \left[\sum_{\mathbf{g}} \mathbf{V}_{\mathbf{g}}^{-1} \mathbf{z}_{\mathbf{g\cdot}} \right] \right)$.

Finally, for $L = \ell = 7$, the intercept-only model, the posterior probability is proportional to 1.

Gibbs sampling uses these posterior probabilities to directly sample from the posterior distribution of $L = \ell$ with ℓ taking values from 1 through 7.

The previous derivations were for $L = \ell$, with ℓ taking values from 1 through 7, where all seven sets of constraints were given equal prior probability of 1/7 (enhanced MKF macro option `Bayesmodel = bma_cubic`). Similar derivations (not shown) apply when an overarching quadratic model is used instead (option `Bayesmodel = bma_quad`), where $L = \ell$ with ℓ taking values from 1 through 5, with 1 = independent quadratic, 2 = independent linear, 3 = common quadratic, 4 = common linear, and 5 = dropped trend models. In this case, by default, all five sets of constraints are given equal prior probability of 1/5. Similarly, when an overarching linear model is used (`Bayesmodel = bma_linear`), $L = \ell$ with ℓ taking values from 1 through 3, with 1 = independent linear, 2 = common linear, and

3 = dropped trend models, and the three sets of constraints are given prior probability of 1/3.

As an alternative to using equal prior weights across each set of constraints, a Dirichlet distribution may be used to generate prior model weights (24). As of the present release of the enhanced MKF macro (version 1.4 2024-08-10), lines of source code related to the implementation of the Dirichlet prior for model weights have been commented out; advanced end-users may modify the SAS source code to experiment with this potential extension to the enhanced MKF macro.

Appendix II. Parameter Settings, Defaults, and Functionality in the Enhanced Modified Kalman Filter Macro

Table. Enhanced modified Kalman filter macro parameters settings, default values, and functionality

Macro parameter	Default value	Description	Notes
data =	<no default>	SAS data set name	A valid SAS data set name. Data should be in stacked (long) format. Groups should have the same number of time points.
outcome =	<no default>	Variable name of outcome	Must be numeric. Missing values are not allowed.
se =	<no default>	Variable name of standard error	Must be numeric. Missing values are not allowed. Zeros will be imputed using the average of nonzero standard errors within the group. Cannot have only zero standard errors within the group, unless a stratified analysis is requested, in which case imputation is attempted across strata for each group and time point.
neff =	<no default>	Variable name of (effective) sample size	Must be numeric. Missing values are not allowed. Zeros will be imputed using the average of nonzero (effective) sample sizes within the group. Cannot have only zero (effective) sample sizes within the group, unless a stratified analysis is requested, in which case imputation is attempted across strata for each group and time point. Must be specified if randomVars = YES and Bayesmodel ≠ <empty>.
outcome2 =	<empty>	Optional: Variable name of second outcome	Same conditions as for the outcome variable. Use if available and when correlation between the two outcomes is to be exploited.
se2 =	<empty>	Optional: Variable name of standard error for second outcome	Same conditions as for the se variable. Use if available and when correlation between the two outcomes is to be exploited.
neff2 =	<empty>	Optional: Variable name of (effective) sample size for second outcome	Same conditions as for the neff variable. Use if available and when correlation between the two outcomes is to be exploited.
by =	<empty>	Optional: Variable name of stratification variable	To obtain separate analyses in the strata defined by the by variable
group =	<no default>	Variable name of population group variable	Missing values are not allowed. Sort order of population groups from the input data set will be retained in output tables.
time =	<no default>	Variable name of time point variable	Must be numeric. Missing values are not allowed. All groups must have the same number of time points.
slopes =	<empty>	Specifies which, if any, trend model(s) to use with maximum likelihood estimation (MLE)	If specified, must be one or more of the following seven keywords: INDEP_CUBIC, INDEP_QUAD, INDEP_LINEAR, COMMON_CUBIC, COMMON_QUAD, COMMON_LINEAR, or DROPPED. Multiple keywords should be separated by a space character. If multiple models are specified, MLE-based model averaging will be applied using the Bayesian information criterion value from each model's fit in PROC NLMIXED to approximate its Bayes factor relative to the null model. Default when only one outcome is specified is to **not** conduct MLE-based estimation but only Bayesian estimation. Default when two outcomes are specified is to conduct MLE-based model averaging over all seven models up to cubic, because Bayesian estimation is not implemented with two outcomes.

See footnotes at end of table.

Table. Enhanced modified Kalman filter macro parameters settings, default values, and functionality—Con.

Macro parameter	Default value	Description	Notes
Bayesmodel =	bma_cubic	Specifies which, if any, trend model(s) to use with Bayesian estimation	Only applicable with one outcome. If specified, must be one or more of the following 13 keywords: BMA_CUBIC, BMA_QUAD, BMA_LINEAR, FULL_CUBIC, FULL_QUAD, FULL_LINEAR, INDEP_CUBIC, INDEP_QUAD, INDEP_LINEAR, COMMON_CUBIC, COMMON_QUAD, COMMON_LINEAR, or DROPPED. Multiple keywords should be separated by a space character. If multiple models are specified, and option BayesmodelAvg = YES, then Bayesian model averaging will be applied, using a mixture prior on the regression coefficients to estimate Bayes factors. Option Bayesmodel = BMA_CUBIC is a shortcut for Bayesmodel = INDEP_CUBIC INDEP_QUAD INDEP_LINEAR COMMON_CUBIC COMMON_QUAD COMMON_LINEAR DROPPED. Option Bayesmodel = BMA_QUAD is a shortcut for Bayesmodel = INDEP_QUAD INDEP_LINEAR COMMON_QUAD COMMON_LINEAR DROPPED. Option Bayesmodel = BMA_LINEAR is a shortcut for Bayesmodel = INDEP_LINEAR COMMON_LINEAR DROPPED. If any of FULL_CUBIC, FULL_QUAD, or FULL_LINEAR are specified, then Bayesian model averaging will not be applied; instead, a "fully Bayesian" model will be applied, where prior parameters for the regression coefficients are themselves given hyperprior distributions whose parameters are estimated from the posterior.
BayesmodelAvg =	YES	Indicates whether Bayesian model averaging should be applied	Only applicable if Bayesmodel ≠ <empty>. Bayesian model averaging is always applied if one of the BMA_CUBIC, BMA_QUAD, or BMA_LINEAR keywords is specified. When BayesmodelAvg = YES, Bayesian model averaging is applied unless one of the fully Bayesian models is specified. Setting BayesmodelAvg = NO results in each Bayesian model being estimated separately. However, the formatted table in the HTML output from SAS will be based on the last model in the input sequence.
randomVars =	YES	Indicates whether variances should be treated as random variables	Applicable only when Bayesmodel ≠ <empty>. By default, sampling variances will be treated as scaled chi-squared random variables with an inverse gamma prior. Setting randomVars = NO will result in sampling variances being treated as fixed.
ARmodel =	common_ar	Indicates whether random effects should have a common distribution across groups	Common first-order autoregressive [AR(1)] parameters across groups are the only option in the MLE-based setting. In the Bayesian setting, the user can specify ARmodel = INDEP_AR so that each group would have its own set of AR(1) parameters rho and tausq, although drawn from a common prior distribution.
xtrakeep =	<empty>	Optional: List of additional variable names to retain with the data set	Any variable one wants to keep in the data while running models: weights, etc. Could also be used to retain labels for multiyear data.
out =	param	Prefix for all output data files; cannot be longer than 16 characters	Output data set names are composed of a prefix and a suffix and are saved to the work directory. For example, param_pred will contain all MKF predictions, all original values, and model parameters. param_bayes will contain MKF predictions from Bayesian modeling.
comparedto =	<empty>	Optional: Reference for disparities calculations	Both absolute and relative disparities will be calculated (that is, differences and ratios) relative to the specified reference. If the reference is not one of the values of the group variable and is not min or max, then no comparisons will be included in the printed (HTML) output. However, all comparisons will be included in the param_bayes data set (if out = param). Including disparities calculations increases computational load and data set sizes, so the user is advised to leave comparedto = <empty> until the model is finalized. Also, even if comparedto = <empty>, disparities (including measures not included in eMKF) can later be calculated post hoc from the posterior draws. Posterior draws are saved to the user's workspace when option mcmclog = YES; see below.
comparedata =	<empty>	Optional: Name of the data set to use to store disparities calculations	Default when left <empty> and when comparedto ≠ <empty> is to use param_diff (if out = param).

See footnotes at end of table.

Table. Enhanced modified Kalman filter macro parameters settings, default values, and functionality—Con.

Macro parameter	Default value	Description	Notes
`modelprint =`	`NO`	Indicates whether intermediate model results should be included in the output	If set to `YES`, then SAS default runtime printout (including convergence diagnostics) from PROC NLMIXED (in the MLE-based setting) and PROC MCMC (in the Bayesian setting) will be included.
`finalprint =`	`YES`	Indicates whether a formatted table with direct and model-based estimates for the last time point should be printed to the HTML output file	If set to `YES`, a formatted table will list all groups (and strata, if applicable) and show both the direct and the model-based estimates, together with their Wald 95% confidence intervals (CIs), relative differences, and relative root mean squared errors. If disparities were also selected, then differences and ratios relative to the specified reference will also be shown, together with their 95% CIs. For ratios, the lognormal CIs are used instead of the Wald CIs.
`pdigit =`	`4`	Number of decimal digits for the printed outputs	User can control how many significant digits to include in the formatted output tables.
`_rho_ =`	`<empty>`	Value of random effects AR(1) autocorrelation coefficient to pass to PROC NLMIXED	Applicable only in the MLE-based setting. If known, the value can be specified here. By default, this is left unspecified and will be estimated from the data.
`_tausq_ =`	`<empty>`	Value of random effects AR(1) innovation variance used to pass to PROC NLMIXED	Applicable only in the MLE-based setting. If known, the value can be specified here. By default, this is left unspecified and will be estimated from the data.
`DF =`	`10000`	Model degrees of freedom to pass to PROC NLMIXED	Applicable only in the MLE-based setting. If known, the value can be specified here. By default, this is set to a very high value.
`chains =`	`4`	Number of chains to use for the Bayesian estimation	Applicable only for Bayesian estimation. It is recommended to run four chains that are started from separate regions of the parameter space.[1] Each chain is further split in two to calculate the Gelman–Rubin diagnostic.
`GRthreshold =`	`1.01`	Threshold to use for the folded and rank-normalized Gelman–Rubin diagnostic R-hat	Applicable only for Bayesian estimation. The folded and rank-normalized R-hat modifies the traditional R-hat. It is recommended to use the threshold of 1.01 (default) instead of the more relaxed threshold of 1.10 commonly used in the literature.[1]
`seed =`	`1235`	Random number generating seed	Allows the user to reproduce the same results in the Bayesian model on different occasions. Can be set to any integer value the user desires.
`maxtune =`	`50`	Maximum number of proposal tuning loops in the random walk Metropolis sampler. If empty, PROC MCMC default value is used; if 0, tuning will be skipped.	From the SAS/STAT 14.2 User's Guide: "Specifies an upper limit for the number of proposal tuning loops. By default, `MAXTUNE = 24`."
`ntu =`	`1000`	Number of tuning iterations to use in each Markov Chain Monte Carlo (MCMC) proposal tuning phase in the random walk Metropolis sampler. If empty, PROC MCMC default value is used.	From the SAS/STAT 14.2 User's Guide: "Specifies the number of iterations to use in each proposal tuning phase. By default, `NTU = 500`."
`nbi =`	`10000`	Number of burn-in in MCMC iterations. If empty, PROC MCMC default value is used; if 0, burn-in will be skipped.	From the SAS/STAT 14.2 User's Guide: "Specifies the number of burn-in iterations to perform before beginning to save parameter estimate chains. By default, `NBI = 1000`."
`nmc =`	`50000`	Number of post-burn-in MCMC iterations. If empty, PROC MCMC default value is used.	From the SAS/STAT 14.2 User's Guide: "Specifies the number of iterations in the main simulation loop. This is the MCMC sample size if `THIN = 1`. By default, `NMC = 1000`."
`thin =`	`1`	Controls thinning rate. If empty, PROC MCMC default value is used.	From the SAS/STAT 14.2 User's Guide: "Controls the thinning rate of the simulation. PROC MCMC keeps every nth simulation sample and discards the rest. All the posterior statistics and diagnostics are calculated using the thinned samples. By default, `THIN = 1`."
`accepttol =`	`<empty>`	Tolerance for target acceptance probabilities (`targetaccept ± accepttol`). If empty, PROC MCMC defaults are used.	From the SAS/STAT 14.2 User's Guide: "Specifies a tolerance for acceptance probabilities. By default, `ACCEPTTOL = 0.075`."

See footnotes at end of table.

Table. Enhanced modified Kalman filter macro parameters settings, default values, and functionality—Con.

Macro parameter	Default value	Description	Notes
`targetaccept =`	`<empty>`	Target acceptance rate for random walk Metropolis. If empty, PROC MCMC defaults are used.	From the SAS/STAT 14.2 User's Guide: "Specifies the target acceptance rate for the random walk Metropolis algorithm (...) The numeric value must be between 0.01 and 0.99. By default, `TARGACCEPT = 0.45` for models that have one parameter; `TARGACCEPT = 0.35` for models that have two, three, or four parameters; and `TARGACCEPT = 0.234` for models that have more than four parameters (...)."
`propcov =`	`<empty>`	Method used to construct initial covariance matrix in the random walk Metropolis sampler. If empty, PROC MCMC default is used.	From the SAS/STAT 14.2 User's Guide: "Specifies the method used in constructing the initial covariance matrix for the Metropolis-Hastings algorithm. The `QUANEW` and `NMSIMP` methods find numerically approximated covariance matrices at the optimum of the posterior density function with respect to all continuous parameters. The optimization does not apply to discrete parameters. The tuning phase starts at the optimized values; in some problems, this can greatly increase convergence performance. If the approximated covariance matrix is not positive definite, then an identity matrix is used instead. Valid values are as follows: `IND`, `CONGRA`, `DBLDOG`, `QUANEW`, `NMSIMP` or `SIMPLEX` (...)." Default in PROC MCMC is to use the identity matrix (`IND`).
`init =`	`reinit`	`REINIT` resets model parameters to the user-supplied initial values after tuning. Needed to ensure the calculation of the Gelman–Rubin diagnostic will be based on starting values for each chain that are from different parts of the parameter space.[1]	From the SAS/STAT 14.2 User's Guide: "Specifies options for generating the initial values for the parameters. These options apply only to prior distributions that are recognized by PROC MCMC (...) If either of the functions GENERAL or DGENERAL is used, you must supply explicit initial values for the parameters. By default, `INIT=MODE`. The following keywords are used: `MODE`, `PINIT`, `RANDOM`, and `REINIT` (...) [The keyword] `REINIT` resets the parameters, after the tuning phase, with the initial values that you provided explicitly or that were assigned by PROC MCMC. By default, PROC MCMC does not reset the parameters because the tuning phase usually moves the Markov chains to a more favorable place in the posterior distribution."
`slicesampler =`	`NO`	Indicates whether or not to use the `slice` sampler instead of random walk Metropolis for parameters that are not included in the Gibbs sampling steps. Default is `NO` due to heavier computational load.	From the SAS/STAT 14.2 User's Guide: The `SLICE` option in the `PARMS` statement "applies the `slice` sampler to each parameter in the `PARMS` statement individually (...) PROC MCMC does not implement a multidimensional version of the `slice` sampler. Because the `slice` sampler usually requires multiple evaluations of the objective function (the posterior distribution) in each iteration, the associated computational cost could be potentially high with this sampling algorithm."
`checkSampleSize =`	`YES`	Indicates whether the number of available time points should meet minimum thresholds before proceeding	`YES` (default) checks sample size is large enough before proceeding. Minimum number of data points recommended is $k + 4$ for a degree k polynomial trend model, $k = 0,1,2,3$. Whether `checkSampleSize` is set to `YES` or `NO`, macro will return error if there is only one data point per group. The macro will also return an error if there are more than 204 groups or more than 5,508 data points (time or group combinations) per stratum. This is due to how the macro code currently implements workhorse calculations symbolically using SAS macro variables whose length cannot exceed 65,534 characters.
`orpoly =`	`YES`	Indicates whether design matrix should be pretransformed using an orthogonal polynomial transformation	`orpoly = YES` (default) will pre-transform the design matrix using the SAS IML orpol function; regression coefficients will be reverse-transformed prior to macro completion. Note that the prior parameters below are assumed to be for the coefficients of the orthogonal polynomial regression when `orpoly = YES`.
`malpha =`	`<empty>`	Common prior mean value for intercepts in the (orthogonal) polynomial regression	Mean of normal prior distribution for the intercepts. When `malpha = <empty>`, it is estimated empirically using $r/2$, where the range $r = \max - \min$ is over the outcome's values across all groups and time points.[2]
`palpha =`	`<empty>`	Common prior precision (that is, inverse variance) for intercepts in the (orthogonal) polynomial regression	Precision (that is, inverse variance) of normal prior distribution for the intercepts. When `palpha = <empty>`, it is estimated empirically using $0.000001/r^2$, where the range $r = \max - \min$ is over the outcome's values across all groups and time points.[2]

See footnotes at end of table.

Table. Enhanced modified Kalman filter macro parameters settings, default values, and functionality—Con.

Macro parameter	Default value	Description	Notes
mbeta1	= 0	Common prior mean parameter for linear coefficients in the (orthogonal) polynomial regression	Mean of normal prior distribution for the linear coefficients in the BMA_**, INDEP_**, and COMMON_** models. Mean of normal hyperprior distribution for the prior normal means of the linear coefficients in the FULL_** models. Not applicable when Bayesmodel = DROPPED. Default value is 0, reflecting a prior preference for the null (no trend) model.
pbeta1	= <empty>	Common prior precision (that is, inverse variance) parameter for linear coefficients in the (orthogonal) polynomial regression	Precision (that is, inverse variance) of normal prior distribution for the linear coefficients in the BMA_**, INDEP_**, and COMMON_** models. Precision (inverse variance) of normal hyperprior distribution for the prior normal means of the linear coefficients in the FULL_** models. Not applicable when Bayesmodel = DROPPED. When pbeta1 = <empty>, this prior precision parameter is estimated empirically using $0.000001/r^2$ in the BMA_**, INDEP_**, and COMMON_** models and $10/r^2$ in the FULL_** models, where the range r = max – min is over the outcome values across all groups and time points.[2]
mbeta2	= 0	Common prior mean parameter for quadratic coefficients in the (orthogonal) polynomial regression	Mean of normal prior distribution for the quadratic coefficients in the BMA_**, INDEP_**, and COMMON_** models. Mean of normal hyperprior distribution for the prior normal means of the quadratic coefficients in the FULL_** models. Not applicable when Bayesmodel = DROPPED, BMA_LINEAR, FULL_LINEAR, INDEP_LINEAR, or COMMON_LINEAR. Default value is 0, reflecting a prior preference for the null (no trend) model.
pbeta2	= <empty>	Common prior precision (that is, inverse variance) parameter for quadratic coefficients in the (orthogonal) polynomial regression	Mean of normal prior distribution for the quadratic coefficients in the BMA_**, INDEP_**, and COMMON_** models. Mean of normal hyperprior distribution for the prior normal means of the quadratic coefficients in the FULL_** models. Not applicable when Bayesmodel = DROPPED, BMA_LINEAR, FULL_LINEAR, INDEP_LINEAR, or COMMON_LINEAR. Default value is 0, reflecting a prior preference for the null (no trend) model.
mbeta3	= 0	Common prior mean parameter for cubic coefficients in the (orthogonal) polynomial regression	Mean of normal prior distribution for the cubic coefficients in the BMA_CUBIC, INDEP_CUBIC, and COMMON_CUBIC models. Mean of normal hyperprior distribution for the prior normal means of the cubic coefficients in the FULL_CUBIC model. Not applicable when other keywords are specified in Bayesmodel. Default value is 0, reflecting a prior preference for the null (no trend) model.
pbeta3	= <empty>	Common prior precision (that is, inverse variance) parameter for cubic coefficients in the (orthogonal) polynomial regression	Precision (that is, inverse variance) of normal prior distribution for the cubic coefficients in the BMA_CUBIC, INDEP_CUBIC, and COMMON_CUBIC models. Precision (inverse variance) of normal hyperprior distribution for the prior normal means of the cubic coefficients in the FULL_CUBIC model. Not applicable when other keywords are specified in Bayesmodel. When pbeta3 = <empty>, this prior precision parameter is estimated empirically using 4×pbeta1. This ensures cubic coefficients are shrunk to 0 more strongly than both the linear and quadratic coefficients, reflecting a prior preference for the simpler trend.
beta1l	= 0	Lower bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the linear coefficients	Applicable only for Bayesmodel keywords FULL_CUBIC, FULL_QUAD, or FULL_LINEAR. Lower bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the linear coefficients. Default value is 0.
beta1u	= <empty>	Upper bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the linear coefficients	Applicable only for Bayesmodel keywords FULL_CUBIC, FULL_QUAD, or FULL_LINEAR. Upper bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the linear coefficients. When beta1u = <empty>, default value is estimated empirically using $r/2$, where the range r = max – min is over the outcome's values across all groups and time points.

See footnotes at end of table.

Table. Enhanced modified Kalman filter macro parameters settings, default values, and functionality—Con.

Macro parameter	Default value	Description	Notes
beta2l	= 0	Lower bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the quadratic coefficients	Applicable only for Bayesmodel keywords FULL_CUBIC or FULL_QUAD. Lower bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the quadratic coefficients. Default value is 0.
beta2u	= <empty>	Upper bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the quadratic coefficients	Applicable only for Bayesmodel keywords FULL_CUBIC or FULL_QUAD. Upper bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the quadratic coefficients. When beta2u = <empty>, default value is estimated empirically using 1.5×beta1u. This ensures prior standard deviations for quadratic coefficients are larger than for the linear coefficients, reflecting increased prior uncertainty in the more complex models.
beta3l	= 0	Lower bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the cubic coefficients	Applicable only for Bayesmodel keyword FULL_CUBIC. Lower bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the cubic coefficients. Default value is 0.
beta3u	= <empty>	Upper bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the cubic coefficients	Applicable only for Bayesmodel keyword FULL_CUBIC. Upper bound for uniform hyperprior distribution of the standard deviation parameters in the normal prior for the cubic coefficients. When beta3u = <empty>, default value is estimated empirically using 2×beta1u. This ensures prior standard deviations for cubic coefficients are larger than for both the quadratic and linear coefficients, reflecting increased prior uncertainty in the more complex models.
mrho	= 0	Mean parameter for the transformed AR(1) autocorrelation parameter rho, given by psi = ln[(1 − rho)/(1 + rho)]	When ARmodel = COMMON_AR, this is the mean of the normal prior distribution for the transformed AR(1) autocorrelation parameter rho, namely, psi = ln[(1-rho)/(1+rho)]. When ARmodel = INDEP_AR, this is the mean of the normal hyperprior distribution for the mean parameter of the normal prior for the group-specific transformed AR(1) autocorrelation parameters rho_g. Default value is 0.
prho	= 1	Precision parameter for the transformed AR(1) autocorrelation parameter rho, given by psi = ln[(1 − rho)/(1 + rho)]	When ARmodel = COMMON_AR, this is the precision (that is, inverse variance) of the normal prior distribution for the transformed AR(1) autocorrelation parameter rho, namely, psi = ln[(1-rho)/(1+rho)]. When ARmodel = INDEP_AR, this is the precision (inverse variance) of the normal hyperprior distribution for the mean parameter of the normal prior for the group-specific transformed AR(1) autocorrelation parameters rho_g. The default value is 1. When ARmodel = INDEP_AR, the value $1/\sqrt{\text{prho}}$ also serves as the upper bound for the uniform hyperprior distribution of the standard deviation parameter in the normal prior distribution of the group-specific transformed AR(1) autocorrelation parameters; the lower bound is set at 0.0001 to keep away for numerical zeros.
taul	= 0.0001	Lower bound for uniform prior distribution on the innovation standard deviation in the AR(1) random effects	Lower bound for uniform prior distribution on the innovation standard deviation in the AR(1) random effects.[2]
tauu	= <empty>	Upper bound for uniform prior distribution on the innovation standard deviation in the AR(1) random effects	Upper bound for uniform prior distribution on the innovation standard deviation in the AR(1) random effects. When tauu = <empty>, default value is estimated empirically using $r/10$, where the range r = max − min is over the outcome's values across all groups and time points.[2] When ARmodel = INDEP_AR, group-specific values of tau are drawn independently from the uniform distribution with bounds taul and tauu.
vshape	= <empty>	Shape parameter for inverse gamma prior distribution of the group-specific variance parameters	Applicable only when Bayesmodel ≠ <empty> and randomVars = YES
vscale	= <empty>	Scale parameter for inverse gamma prior distribution of the group-specific variance parameters	Applicable only when Bayesmodel ≠ <empty> and randomVars = YES

See footnotes at end of table.

Table. Enhanced modified Kalman filter macro parameters settings, default values, and functionality—Con.

Macro parameter	Default value	Description	Notes
`wshape = 2`		Ignored as of the present release of eMKF (version 1.4 2024-08-10)	Applicable only with Bayesian model averaging. Common shape parameter to use for Dirichlet prior on model indicators in mixture priors, with a default value of 2 for a discrete uniform prior. As of the present release (version 1.4 2024-08-10), the Dirichlet prior has been disabled for simplicity, and model indicators are given constant prior weights (1/7 for `BMA_CUBIC`; 1/5 for `BMA_QUAD`; and 1/3 for `BMA_LINEAR`) instead of random prior weights that are generated from a Dirichlet.
`mcmcplot = NO`		Indicates whether the default within-chain trace or diagnostics plots from PROC MCMC should be included in the SAS HTML output.	Setting `mcmcplot = YES` is useful for visual diagnostics purposes, for example, if the Gelman–Rubin diagnostics at the threshold `GRthreshold` suggest poor mixing, but is not recommended to include by default for very long MCMC runs because of the higher computational burden in generating the graphics. In most cases, using the option `modelprint = YES` instead will allow the user to examine relevant diagnostics statistics without generating trace plots and histograms.
`mcmclog = NO`		Indicates whether the full posterior samples (after any thinning is applied) should be retained in the work directory for *post hoc* analyses.	Setting `mcmclog = YES` is useful for diagnostics purposes, for example, to compute across-chain mixing and convergence criteria other than the Gelman–Rubin criterion, as well as to calculate any disparities measures that are not included in the present release of eMKF. Saving the full posterior sample is disabled by default because of the resulting large file size, which could negatively interact with user settings on shared or network resources.
`cmploc = work.funcs`		Desired location of SAS language compiler (CMP) library	This is the location that SAS PROC FCMP will use to save the compiled Gibbs samplers for use during the session. Usually, this is set to `sasuser.funcs`, or to `work.funcs` if the sasuser profile folder is write-protected.

[1]Vehtari A, Gelman A, Simpson D, Carpenter B, Bürkner PC. Rank-normalization, folding, and localization: An improved R̂ for assessing convergence of MCMC (with discussion). Bayesian Anal 16(2):667–718. 2021.
[2]Setodji CM, Lockwood JR, McCaffrey DF, Elliott MN, Adams JL. The modified Kalman filter macro: User's guide. RAND Technical Report. 2011. Available from: https://www.rand.org/pubs/technical_reports/TR997.html.

NOTES: The value `<empty>` is equivalent to an empty string `%str()` in SAS. When `<no default>` is indicated, parameter values must be specified by the user, and no default values are available. MKF is modified Kalman filter. eMKF is enhanced modified Kalman filter.

SOURCE: Talih M, Rossen LM, Patel P, Earp M, Parker JD. The enhanced modified Kalman filter (eMKF) tool for small domain estimation [version 1.4 2024-08-10]. National Center for Health Statistics. 2024. Available from: https://github.com/CDCgov/eMKF.

Appendix III. Alternative Specifications in the Enhanced Modified Kalman Filter Macro

Model Averaging Based on Maximum Likelihood Estimation

The following SAS code snippet shows a call to the enhanced modified Kalman filter (MKF) macro where maximum likelihood-based model averaging is specified:

```
%mkf(data        = NHANESobesity,
     group       = Population,
     time        = Year,
     by          = Age,
     outcome     = Obesity,
     se          = SE_obesity,
     Bayesmodel  = ,
     slopes      = indep_cubic indep_quad
                   indep_linear
                   common_cubic
                   common_quad
                   common_linear dropped,
     out         = mac);
```

Because the default estimation method when only one outcome is specified is Bayesian estimation, the `Bayesmodel` macro parameter needs to be explicitly set to empty, as in the earlier MKF macro. The `slopes` parameter lists the trend model(s) to be fit using maximum likelihood (via SAS PROC NLMIXED, as explained in Appendix I, "State-space Model Formulation and Maximum Likelihood-based Estimation"). When more than one model or keyword is listed, model averaging is implemented using the Bayesian information criterion values to approximate the Bayes factors when calculating model averaging weights in the maximum likelihood-based estimation setting.

The enhanced MKF macro also ensures a common "descendant" is included in any model sequence that users provide so that all Bayes factors are relative to a common "null" trend model (the simplest model in the specified sequence). Model averaging over all seven models up to cubic is specified by listing all seven models in the `slopes` parameter, and, other than for how the sampling variances are treated (option `randomVars = NO` by default here versus `randomVars = YES` by default in the Bayesian setting), this specification is the maximum likelihood-based analog to the Bayesian model averaging specification illustrated in "Bayesian Trend Model Averaging."

Figure I displays the formatted output resulting from running the code in the example shown above, where maximum likelihood-based model averaging is specified. Note that, as in the earlier macro, the enhanced MKF macro does not give users the option to calculate disparities when maximum likelihood-based estimation is selected.

"Fully Bayesian" Models

In the earlier MKF macro, Bayesian estimation was implemented using the "fully Bayesian" linear model, where a level was added to the underlying Bayesian hierarchical model to account for the uncertainty in specifying prior means and variances for the regression coefficients, but also to reinforce borrowing strength across groups and offer a compromise between the independent and common trend cases; see Appendix I, "Bayesian Estimation of Regression Hyperparameters."

The following options for the `Bayesmodel` macro variable in the enhanced MKF macro extend the fully Bayesian linear model in the earlier macro to include quadratic and cubic trends: 1) `full_cubic`, 2) `full_quad`, and 3) `full_linear`. Those options may be considered as alternatives to cubic, quadratic, and linear Bayesian model averaging, and may be appropriate when subject-matter, statistical, or computational considerations preclude model averaging. For example, if quadratic or cubic trends are known to be inappropriate based on previous analyses or subject-matter expertise, users may wish to limit the macro to the fully Bayesian linear trend model to reduce computational burden.

Group-specific, First-order Autoregressive Coefficients

Models with group-specific, first-order autoregressive [AR(1)] coefficients are usually driven by subject-matter or statistical considerations that suggest substantial structural differences across groups (8,9). The following code snippet shows how to request group-specific AR(1) coefficients (`ARmodel = indep_ar`) to override the default of a common set of AR(1) parameters across groups. Instead of Bayesian model averaging, the fully Bayesian cubic model

(`Bayesmodel = full_cubic`) is fitted, here, for illustration:

```
%mkf(data       = NHANESobesity,
     group      = Population,
     time       = Year,
     by         = Age,
     outcome    = Obesity,
     se         = SE_obesity,
     neff       = NEFF_obesity,
     ARmodel    = indep_ar,
     Bayesmodel = full_cubic,
     out        = bfc);
```

Figure II displays the formatted output resulting from running this code.

Figure I. Output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter maximum likelihood-based model average up to the unconstrained cubic trend, with fixed sampling variances and common autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity

Age	Population	Year	Estimation type	Point estimate	RMSE	Wald 95% CI	Std. diff	Rel. RMSE
18-24	Black, non-Hispanic	2018.6	Sample	0.3387	0.0370	[0.2662, 0.4112]	~~	~~
			MKF estimate	0.3607	0.0263	[0.3091, 0.4122]	0.5929	0.7111
25-44	Black, non-Hispanic	2018.6	Sample	0.4911	0.0218	[0.4484, 0.5338]	~~	~~
			MKF estimate	0.5047	0.0177	[0.4700, 0.5394]	0.6237	0.8136
45-64	Black, non-Hispanic	2018.6	Sample	0.5724	0.0154	[0.5423, 0.6025]	~~	~~
			MKF estimate	0.5562	0.0130	[0.5307, 0.5817]	-1.0522	0.8475
65+	Black, non-Hispanic	2018.6	Sample	0.4897	0.0222	[0.4461, 0.5334]	~~	~~
			MKF estimate	0.5014	0.0200	[0.4622, 0.5405]	0.5215	0.8970
18-24	White, non-Hispanic	2018.6	Sample	0.3079	0.0520	[0.2060, 0.4099]	~~	~~
			MKF estimate	0.2888	0.0322	[0.2257, 0.3519]	-0.3675	0.6190
25-44	White, non-Hispanic	2018.6	Sample	0.4221	0.0210	[0.3809, 0.4633]	~~	~~
			MKF estimate	0.4072	0.0162	[0.3754, 0.4390]	-0.7090	0.7718
45-64	White, non-Hispanic	2018.6	Sample	0.4232	0.0296	[0.3651, 0.4813]	~~	~~
			MKF estimate	0.4471	0.0202	[0.4075, 0.4868]	0.8089	0.6822
65+	White, non-Hispanic	2018.6	Sample	0.4233	0.0229	[0.3784, 0.4681]	~~	~~
			MKF estimate	0.4142	0.0197	[0.3756, 0.4528]	-0.3964	0.8601
18-24	Other race, non-Hispanic	2018.6	Sample	0.2918	0.0491	[0.1955, 0.3881]	~~	~~
			MKF estimate	0.2273	0.0371	[0.1546, 0.3000]	-1.3133	0.7548
25-44	Other race, non-Hispanic	2018.6	Sample	0.3087	0.0259	[0.2579, 0.3595]	~~	~~
			MKF estimate	0.2776	0.0209	[0.2366, 0.3186]	-1.2011	0.8076
45-64	Other race, non-Hispanic	2018.6	Sample	0.3246	0.0428	[0.2407, 0.4084]	~~	~~
			MKF estimate	0.2562	0.0313	[0.1947, 0.3176]	-1.5997	0.7326
65+	Other race, non-Hispanic	2018.6	Sample	0.2333	0.0455	[0.1441, 0.3226]	~~	~~
			MKF estimate	0.2587	0.0365	[0.1871, 0.3303]	0.5568	0.8025

See footnotes at end of figure.

Figure I. Output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter maximum likelihood-based model average up to the unconstrained cubic trend, with fixed sampling variances and common autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity—Con.

Age	Population	Year	Estimation type	Point estimate	RMSE	Wald 95% CI	Std. diff	Rel. RMSE
18-24	Mexican American	2018.6	Sample	0.3937	0.0814	[0.2341, 0.5533]	~~	~~
			MKF estimate	0.3301	0.0376	[0.2564, 0.4038]	-0.7810	0.4617
25-44	Mexican American	2018.6	Sample	0.5265	0.0231	[0.4812, 0.5717]	~~	~~
			MKF estimate	0.5311	0.0171	[0.4976, 0.5646]	0.2005	0.7406
45-64	Mexican American	2018.6	Sample	0.5060	0.0355	[0.4365, 0.5756]	~~	~~
			MKF estimate	0.5303	0.0231	[0.4849, 0.5756]	0.6827	0.6523
65+	Mexican American	2018.6	Sample	0.4976	0.0545	[0.3907, 0.6044]	~~	~~
			MKF estimate	0.4576	0.0378	[0.3836, 0.5317]	-0.7324	0.6929
18-24	Other Hispanic	2018.6	Sample	0.3566	0.0512	[0.2563, 0.4570]	~~	~~
			MKF estimate	0.3283	0.0388	[0.2524, 0.4043]	-0.5525	0.7569
25-44	Other Hispanic	2018.6	Sample	0.3845	0.0273	[0.3311, 0.4379]	~~	~~
			MKF estimate	0.3953	0.0212	[0.3538, 0.4367]	0.3942	0.7764
45-64	Other Hispanic	2018.6	Sample	0.4464	0.0375	[0.3729, 0.5199]	~~	~~
			MKF estimate	0.4555	0.0280	[0.4006, 0.5104]	0.2417	0.7465
65+	Other Hispanic	2018.6	Sample	0.4642	0.0413	[0.3833, 0.5452]	~~	~~
			MKF estimate	0.4273	0.0318	[0.3649, 0.4896]	-0.8951	0.7703

NOTES: Obesity is indicated by a body mass index of 30.0 or higher. Body mass index is calculated from measured height and weight and defined as weight (kilograms) / [height (meters)]^2. The category “Other race, non-Hispanic” includes non-Hispanic people identifying as more than one race. The category “Other Hispanic” includes Hispanic or Latino people from origins other than Mexican American. The symbol ~~ indicates that the output is not applicable. Year = 2018.6 is the midpoint of the 2017–March 2020 cycle, which, due to the suspension of field operations for the National Health and Nutrition Examination Survey in March 2020, combines the full 2017–2018 cycle with partial data from 2019 through March 2020; see “National Health and Nutrition Examination Survey, 2017–March 2020 Prepandemic File: Sample Design, Estimation, and Analytic Guidelines” (https://www.cdc.gov/nchs/data/series/sr_02/sr02-190.pdf). Direct estimates of the proportion of adults with obesity are indicated in the rows labeled “Sample,” whereas estimates based on the selected modified Kalman filter (MKF) model are indicated in the rows labeled “MKF estimate.” Selected MKF models include a common set of autoregression parameters across population groups. RMSE is the root mean squared error; for direct estimates, RMSE is equal to the standard error because the survey-weighted sample proportion is assumed to be an unbiased estimator of the population proportion. The Wald 95% confidence interval (CI) is constructed for both direct and model-based estimates using the formula: [point estimate] ± 1.96 • RMSE. The standardized difference (Std. diff) is the difference between the model-based and direct estimates, divided by RMSE (= standard error) of the direct estimate. The relative RMSE (Rel. RMSE) is the ratio of the model-based RMSE to the direct RMSE.

SOURCE: National Center for Health Statistics, National Health and Nutrition Examination Surveys, 1999–March 2020.

Figure II. Output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter fully Bayesian cubic trend model, with random sampling variances and independent autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity

```
  Age        Population             Year      Estimation       Point        RMSE         Wald 95% CI        Std.        Rel.
                                                  type        estimate                                      diff        RMSE
###########################################################################################################################
  18-24    Black, non-Hispanic       2018.6    Sample          0.3387       0.0370     [ 0.2662,  0.4112]   ~~          ~~
                                               MKF estimate    0.3474       0.0340     [ 0.2809,  0.4140]   0.2352      0.9180
---------------------------------------------------------------------------------------------------------------------------
  25-44    Black, non-Hispanic       2018.6    Sample          0.4911       0.0218     [ 0.4484,  0.5338]   ~~          ~~
                                               MKF estimate    0.4983       0.0206     [ 0.4580,  0.5386]   0.3312      0.9441
---------------------------------------------------------------------------------------------------------------------------
  45-64    Black, non-Hispanic       2018.6    Sample          0.5724       0.0154     [ 0.5423,  0.6025]   ~~          ~~
                                               MKF estimate    0.5676       0.0145     [ 0.5393,  0.5960]   -0.3074     0.9423
---------------------------------------------------------------------------------------------------------------------------
  65+      Black, non-Hispanic       2018.6    Sample          0.4897       0.0222     [ 0.4461,  0.5334]   ~~          ~~
                                               MKF estimate    0.4943       0.0215     [ 0.4521,  0.5365]   0.2031      0.9682
---------------------------------------------------------------------------------------------------------------------------
  18-24    White, non-Hispanic       2018.6    Sample          0.3079       0.0520     [ 0.2060,  0.4099]   ~~          ~~
                                               MKF estimate    0.3160       0.0383     [ 0.2410,  0.3910]   0.1552      0.7356
---------------------------------------------------------------------------------------------------------------------------
  25-44    White, non-Hispanic       2018.6    Sample          0.4221       0.0210     [ 0.3809,  0.4633]   ~~          ~~
                                               MKF estimate    0.4190       0.0195     [ 0.3807,  0.4573]   -0.1479     0.9298
---------------------------------------------------------------------------------------------------------------------------
  45-64    White, non-Hispanic       2018.6    Sample          0.4232       0.0296     [ 0.3651,  0.4813]   ~~          ~~
                                               MKF estimate    0.4366       0.0244     [ 0.3889,  0.4844]   0.4539      0.8217
---------------------------------------------------------------------------------------------------------------------------
  65+      White, non-Hispanic       2018.6    Sample          0.4233       0.0229     [ 0.3784,  0.4681]   ~~          ~~
                                               MKF estimate    0.4179       0.0210     [ 0.3768,  0.4591]   -0.2324     0.9169
---------------------------------------------------------------------------------------------------------------------------
  18-24    Other race, non-Hispanic  2018.6    Sample          0.2918       0.0491     [ 0.1955,  0.3881]   ~~          ~~
                                               MKF estimate    0.2776       0.0406     [ 0.1982,  0.3571]   -0.2887     0.8254
---------------------------------------------------------------------------------------------------------------------------
  25-44    Other race, non-Hispanic  2018.6    Sample          0.3087       0.0259     [ 0.2579,  0.3595]   ~~          ~~
                                               MKF estimate    0.3014       0.0250     [ 0.2524,  0.3504]   -0.2819     0.9642
---------------------------------------------------------------------------------------------------------------------------
  45-64    Other race, non-Hispanic  2018.6    Sample          0.3246       0.0428     [ 0.2407,  0.4084]   ~~          ~~
                                               MKF estimate    0.3063       0.0364     [ 0.2349,  0.3777]   -0.4274     0.8510
---------------------------------------------------------------------------------------------------------------------------
  65+      Other race, non-Hispanic  2018.6    Sample          0.2333       0.0455     [ 0.1441,  0.3226]   ~~          ~~
                                               MKF estimate    0.2539       0.0375     [ 0.1804,  0.3274]   0.4514      0.8242
---------------------------------------------------------------------------------------------------------------------------
```

See footnotes at end of figure.

Figure II. Output from calling the enhanced modified Kalman filter macro code showing the modified Kalman filter fully Bayesian cubic trend model, with random sampling variances and independent autoregression parameters for adults age 18 and older with obesity, by age group and race and ethnicity—Con.

Age	Population	Year	Estimation type	Point estimate	RMSE	Wald 95% CI	Std. diff	Rel. RMSE
18-24	Mexican American	2018.6	Sample	0.3937	0.0814	[0.2341, 0.5533]	~~	~~
			MKF estimate	0.3730	0.0540	[0.2671, 0.4789]	-0.2546	0.6635
25-44	Mexican American	2018.6	Sample	0.5265	0.0231	[0.4812, 0.5717]	~~	~~
			MKF estimate	0.5246	0.0217	[0.4821, 0.5671]	-0.0806	0.9395
45-64	Mexican American	2018.6	Sample	0.5060	0.0355	[0.4365, 0.5756]	~~	~~
			MKF estimate	0.5243	0.0283	[0.4689, 0.5797]	0.5148	0.7964
65+	Mexican American	2018.6	Sample	0.4976	0.0545	[0.3907, 0.6044]	~~	~~
			MKF estimate	0.4765	0.0406	[0.3970, 0.5560]	-0.3861	0.7441
18-24	Other Hispanic	2018.6	Sample	0.3566	0.0512	[0.2563, 0.4570]	~~	~~
			MKF estimate	0.3624	0.0409	[0.2822, 0.4425]	0.1125	0.7985
25-44	Other Hispanic	2018.6	Sample	0.3845	0.0273	[0.3311, 0.4379]	~~	~~
			MKF estimate	0.3950	0.0249	[0.3462, 0.4437]	0.3832	0.9128
45-64	Other Hispanic	2018.6	Sample	0.4464	0.0375	[0.3729, 0.5199]	~~	~~
			MKF estimate	0.4518	0.0301	[0.3928, 0.5109]	0.1449	0.8031
65+	Other Hispanic	2018.6	Sample	0.4642	0.0413	[0.3833, 0.5452]	~~	~~
			MKF estimate	0.4487	0.0363	[0.3774, 0.5199]	-0.3775	0.8800

NOTES: Obesity is indicated by a body mass index of 30.0 or higher. Body mass index is calculated from measured height and weight and defined as weight (kilograms) / [height (meters)]^2. The category "Other race, non-Hispanic" includes non-Hispanic people identifying as more than one race. The category "Other Hispanic" includes Hispanic or Latino people from origins other than Mexican American. The symbol ~~ indicates that the output is not applicable. Year = 2018.6 is the midpoint of the 2017–March 2020 cycle, which, due to the suspension of field operations for the National Health and Nutrition Examination Survey in March 2020, combines the full 2017–2018 cycle with partial data from 2019 through March 2020; see "National Health and Nutrition Examination Survey, 2017–March 2020 Prepandemic File: Sample Design, Estimation, and Analytic Guidelines" (https://www.cdc.gov/nchs/data/series/sr_02/sr02-190.pdf). Direct estimates of the proportion of adults with obesity are indicated in the rows labeled "Sample," whereas estimates based on the selected modified Kalman filter (MKF) model are indicated in the rows labeled "MKF estimate." Selected MKF models include independent sets of autoregression parameters across population groups. RMSE is the root mean squared error; for direct estimates, RMSE is equal to the standard error because the survey-weighted sample proportion is assumed to be an unbiased estimator of the population proportion. The Wald 95% confidence interval (CI) is constructed for both direct and model-based estimates using the formula: [point estimate] ± 1.96 • RMSE. The standardized difference (Std. diff) is the difference between the model-based and direct estimates, divided by RMSE (= standard error) of the direct estimate. The relative RMSE (Rel. RMSE) is the ratio of the model-based RMSE to the direct RMSE.

SOURCE: National Center for Health Statistics, National Health and Nutrition Examination Surveys, 1999–March 2020.

Vital and Health Statistics Series Descriptions

Active Series

Series 1. Programs and Collection Procedures
Reports describe the programs and data systems of the National Center for Health Statistics, and the data collection and survey methods used. Series 1 reports also include definitions, survey design, estimation, and other material necessary for understanding and analyzing the data.

Series 2. Data Evaluation and Methods Research
Reports present new statistical methodology including experimental tests of new survey methods, studies of vital and health statistics collection methods, new analytical techniques, objective evaluations of reliability of collected data, and contributions to statistical theory. Reports also include comparison of U.S. methodology with those of other countries.

Series 3. Analytical and Epidemiological Studies
Reports present data analyses, epidemiological studies, and descriptive statistics based on national surveys and data systems. As of 2015, Series 3 includes reports that would have previously been published in Series 5, 10–15, and 20–23.

Discontinued Series

Series 4. Documents and Committee Reports
Reports contain findings of major committees concerned with vital and health statistics and documents. The last Series 4 report was published in 2002; these are now included in Series 2 or another appropriate series.

Series 5. International Vital and Health Statistics Reports
Reports present analytical and descriptive comparisons of U.S. vital and health statistics with those of other countries. The last Series 5 report was published in 2003; these are now included in Series 3 or another appropriate series.

Series 6. Cognition and Survey Measurement
Reports use methods of cognitive science to design, evaluate, and test survey instruments. The last Series 6 report was published in 1999; these are now included in Series 2.

Series 10. Data From the National Health Interview Survey
Reports present statistics on illness; accidental injuries; disability; use of hospital, medical, dental, and other services; and other health-related topics. As of 2015, these are included in Series 3.

Series 11. Data From the National Health Examination Survey, the National Health and Nutrition Examination Surveys, and the Hispanic Health and Nutrition Examination Survey
Reports present 1) estimates of the medically defined prevalence of specific diseases in the United States and the distribution of the population with respect to physical, physiological, and psychological characteristics and 2) analysis of relationships among the various measurements. As of 2015, these are included in Series 3.

Series 12. Data From the Institutionalized Population Surveys
The last Series 12 report was published in 1974; these reports were included in Series 13, and as of 2015 are in Series 3.

Series 13. Data From the National Health Care Survey
Reports present statistics on health resources and use of health care resources based on data collected from health care providers and provider records. As of 2015, these reports are included in Series 3.

Series 14. Data on Health Resources: Manpower and Facilities
The last Series 14 report was published in 1989; these reports were included in Series 13, and are now included in Series 3.

Series 15. Data From Special Surveys
Reports contain statistics on health and health-related topics from surveys that are not a part of the continuing data systems of the National Center for Health Statistics. The last Series 15 report was published in 2002; these reports are now included in Series 3.

Series 16. Compilations of Advance Data From Vital and Health Statistics
The last Series 16 report was published in 1996. All reports are available online; compilations are no longer needed.

Series 20. Data on Mortality
Reports include analyses by cause of death and demographic variables, and geographic and trend analyses. The last Series 20 report was published in 2007; these reports are now included in Series 3.

Series 21. Data on Natality, Marriage, and Divorce
Reports include analyses by health and demographic variables, and geographic and trend analyses. The last Series 21 report was published in 2006; these reports are now included in Series 3.

Series 22. Data From the National Mortality and Natality Surveys
The last Series 22 report was published in 1973. Reports from sample surveys of vital records were included in Series 20 or 21, and are now included in Series 3.

Series 23. Data From the National Survey of Family Growth
Reports contain statistics on factors that affect birth rates, factors affecting the formation and dissolution of families, and behavior related to the risk of HIV and other sexually transmitted diseases. The last Series 23 report was published in 2011; these reports are now included in Series 3.

Series 24. Compilations of Data on Natality, Mortality, Marriage, and Divorce
The last Series 24 report was published in 1996. All reports are available online; compilations are no longer needed.

For answers to questions about this report or for a list of reports published in these series, contact:

Information Dissemination Staff
National Center for Health Statistics
Centers for Disease Control and Prevention
3311 Toledo Road, Room 4551, MS P08
Hyattsville, MD 20782

Tel: 1–800–CDC–INFO (1–800–232–4636)
TTY: 1–888–232–6348
Internet: https://www.cdc.gov/nchs
Online request form: https://www.cdc.gov/info
For e-mail updates on NCHS publication releases, subscribe online at: https://www.cdc.gov/nchs/email-updates.htm.

U.S. DEPARTMENT OF
HEALTH & HUMAN SERVICES

Centers for Disease Control and Prevention
National Center for Health Statistics
3311 Toledo Road, Room 4551, MS P08
Hyattsville, MD 20782–2064

For more NCHS Series Reports, visit:
https://www.cdc.gov/nchs/products/series.htm

Series 2, No. 209
CS350486