Approximating Age-Period-Cohort Estimates by Averaging Multiple Models with Varying Window Restrictions

# Abstract

Key words: Computational Sociology, Methods, Life Course, Bayesian, Culture

# Introduction

# Background

Both classic and modern studies have proposed different effects across three social dimensions of time: age, period, and cohort (Ryder 1965). These dimensions of time operate on individuals in different ways as they flow through social space. Age effects are driven either by the common experiences associated with the biological process of aging (Jackson, Weale, and Weale 2003), or persistent age-structuring institutions, like high school or retirement (Leisering 2003; Moen 2014). Period effects are responses of everyone to contemporaneous social experiences, like recessions or wars (Lam, Fan, and Moen 2014). Finally, cohort effects are socialization effects. They are broad-based historical events that stick to the populations experiencing them, even after the event has long since ended (Vaisey and Lizardo 2016). In contemporary research, cohorts are virtually always defined in terms of birth year.

These three dimensions of time sit at the center of some recurrent debates. For example, cultural sociologists are divided over whether the main driver of culture is a period process (cultural fragmentation) or a cohort process (acquired dispositions) (Vaisey and Lizardo 2016). Clinical reasearchers and biodemographers are looking for biological age—indicators of biological deterioration—but argue about confounding from cohort changes (Jackson et al. 2003). And yet others are concerned about separating long-term and short-term impacts of important events, like the Great Recession (Burgard and Kalousova 2015).

Unfortunately, it is not trivial to estimate the unique effects of age, period, and cohort to find evidence that may settle these questions and debates. The fundamental problem is one of statistical identification: these three dimensions are linearly dependent. Two of the dimensions define the third. If a researcher knows an individual’s age, and the year of the survey, cohort is also defined. Because these variables are exactly colinear, they are not estimable using classic statistical techniques. A number of solutions have been proposed to address this conundrum, these include traditional methods like block/window constraints (Anon. 2005), and new methods, including statistical transformation (the “intrinsic estimator”), and random effects models (Yang and Land 2013).

The past several years have seen a resurgence in debates surrounding these issues (Bell and Jones 2017; Luo 2013; Luo and Hodges 2016). Perhaps the most common argument is that the “constraints”, *i.e.* assumptions used to break the APC identity, produce unknown biases into the models. In reality, this presents an extreme case of multicollinearity, a well-known, though difficult problem in statistical theory (Wooldridge 2009, at p. 95-98), with numerous cautions in applied texts that separating highly colinear effects is difficult (Camm 2016, at p. 328). From a Bayesian perspective, collinearity and multicollinearity significantly reduce the ability of the data to supply information to produce the estimates, potentially introducing sensitivity to the prior (Gelman 2014, at p. 305-306), including assumtpions of linearity. To put it another way, the critique of APC models in general, and window constraints in particular (Luo and Hodges 2016), is that different sets of assumptions lead to different (and inconsistent) results. But, what if Instead of focusing on finding a *best* fitting model, we use a simple nonlinear approach (block modelling), and hundreds of assumptions? BMA allows us to do just that: run hundreds of models with differeing assumptions, and then combine them, weighted by their fit with the data.

# Bayesian Model Averaging

The theoretical backdrop of BMA applies to this curcumstance quite well. In principal, there is no one true (or best) model; instead estimates are conditional on models from the modeling space (), and have a posterior distribution, which is calculated as a weighted average of all models (Raftery 1995:144–45). It has been applied in diverse areas from weather forecasting to biology to social science (Fragoso and Neto 2015) . BMA operates under the simple fact that any particular estimate, including effect size and significance, have a posterior probability distribution which is calculated as “an average of the posterior distributions under each of the models considered, weighted by their posterior model probability.” (Hoeting et al. 1999). The major difficulties for BMA are (1) how to sample models to test, and (2) how to calculate the posterior model probability given the data (or where is the model, and is the data). For model selection, we use the Markov Chain Monte Carlo Composition (MC3) method. We use the Bayesian Information Crieterion (BIC) approximation. To implement the MC3 method, we use the following steps:

1. Define a jumping distribution , so that is non-zero for all possible window constraints.
2. Specify a starting model, , and ellicit priors for models in .
3. Given that the chain is in state , draw , and accept it with probability

otherwise, retain .

## Step One: Defining a Window Constraint Sampler

In terms of window constraints, the target model, which is inestimable, is built by estimating each unique value of age, period, and cohort, as a dummy variable series:

where is an estimated effect, , and index unique values for age, period, and cohort, and , , and stand for matricies of dummy variable series for age, period, and cohort. This model is unidentified, because, as with the continuous case, the dummy variables in any two of the matricies above fully condition the third matrix. In other words, the indicator variable in is a function of the indicators in and (in mathematical terms,the probability that any given cohort dummy variable is one or zero is exctly dependent on the values of A and P, so that ) is always exaclty zero, or exactly one, depending on the values of and ).

We can break this dependencey, however, by transofrming , , and —preferably without resulting to some prespecified arbitrary set of constraints (Gelman 2014, at p. 366). How do the window constraints break the linear dependency? By way of example, we can construct an age dummy variable series where is sliced into two groups based on some cut-point so that, for example, individuals who are older than 30 have a dummy variable of 1 and the dummy variable for those 30 or younger euqls 0. This would identify a binary dummy variable with an older and a younger group. We can generalize this expression to an arbitrary vector of cut-points, with subscript so that the window constraints of in equation \_\_ are as follows:

If the vector and have the following properties: , , and , then can describe any posible sets of window restrictions for age. The first three requirement ensures that the dummy variable series is fully defined across the entire range of the continuous variable . In particular, the first restriction ensures that the dummy variable series with the oldest ages in contains the maximum value of . Similarly, the next two restrictins ensure that the smallest window constraint in contains the minimum value of . The final constraint requires that have at least three elements. Three elements in defines a dummy variable. Using the example above, if has a range of 5 to 50, then the dummy variale distinguishing older and younger respondents can be defined by .

Generalizing cross all dimensions of APC, permuting three similar vectors (say ) will describe any model for any possible window constraints detailed in equation 1. Accordingly, all permutations of G, as defined above, constitute the model space of window constraints (). For any given set of APC variables, is finite, but it can become large. For example, 5 unique ages, periods, and cohorts allow for 3,375 unique window models[[1]](#footnote-26), and 6 unique values for each of age, period, and cohort allow for 38,304 different models. In any model space, only 1 model is inestimable because of perfect colinearity. This target model is (theoretially) the least biased, although it is almost certainly the most parsimonious. The question is how to best use information from some subset of possible models in to estimate unbiased APC effects of the target model. Bayesian Model Averaging (BMA) provides a straightforward way to combine models. need transition

There are two features of that make the MC3 algorithm provides an attractive way to sample models. can be decomposed into two parts: (1) the number of windows, and (2) the break points for each of the windows. By disaggregating into these two parts, we use the Dirchelet distribution as the jumping distribution to construct matrix to define models.

*Using the Dirichlet Distribution to Sample Window Groups (G).* As noted above, there are two basic features of vector . First, is the number of window breaks, or the rank of , and second is the location of the window breaks, or the values of . We use a uniform distribution over the range of A,P, or C to sample the number of window breaks. This is simple, straightforward, and is a noninformative prior distribution. We use the Dirichelet distributon to sample the location of window breaks. The Dirichelet is well-suited to this task, and is commonly used in classification tasks citation. In additon, Taddy et al. (2015) show that the Dirichelet is a natural prior distribution for variable selection and value-splitting in classification and regression trees (CART) algortithms, common for machine learning. Our approach is a similar, as developing is fundamentally a classificaiton task which aggregates similar ages, periods, and cohorts. In addition, one of the classical descriptions of the Dirichelet distribution, for “string-cutting,” is directly applicable to assigning various window lengths across the range of A, P, and C.

To implement our sampling scheme, we use two sets of auxiliary variables for each dimension () of APC to match the decompostion of described above. The fist is a simplex for each unique value of A, P, or C. The simplex contains a list of numbrers between 0 and 1, which sum to 1. We draw a unique simplex for each dimension , with the same length of unique elements in (). The second auxiliary variable is a scalar for each dimension, . is simply the product of times . We use a uniform distribution to sample , and a Dirchelet distribution to sample from the simplex as follows:

Where is the index number for the APC effects (the , , or of equaiton 1) is the continuous vector of values (the ,, or ). add more explanation

*Starting Model and Jumping Distribution.* The for the Dirichelet distribution are for each of the vunique values in the dimension () for APC. The Dirchelet distribution draws a random projection on the standard simplex, *i.e.* a vector of weights weights between 0 and 1 which sum to 1. Multiplying the vector of weights () by a scalar provides a set of numbers which sum to the scalar value . We transform and into matrix by selecting the unique floor rounded values of the product of the cumulative sums of :

Where is a vector of the type described in equation 2, and indexes and is a subset of the unique values in .

# A Simulation

# An Empirical Example from the GSS

# Discussion

# Conclusion

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1. A continuous variable of 5 integers can be sliced into continous window constraints in 15 ways (where | indicates a window break for dummy variables):

   2 windows, 4 combinations: 1|2345, 12|345, 123|45, 1234|5

   3 windows, 6 combinations: 1|2|345, 1|23|45, 1|234|5, 12|3|45, 12|34|5, 123|4|5

   4 windows, 4 combinations: 1|2|3|45, 1|2|34|5, 1|23|4|5, 12|3|4|5

   5 windows, 1 combination: 1|2|3|4|5

   Since the hypothetical assumes 3 variables (A,P,and C) of 15 combinations each, total combinations are . Similar calculations over an integer of 6 leads to 34 window combinations over each dimension for a total of 39,304 possible models. [↑](#footnote-ref-26)