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Estimating the Underlying Infant Mortality Rates for Small Populations, Even Those Reporting Zero Infant Deaths: a Case Study of 66 Local Health Areas in British Columbia

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Abstract
A method is presented for estimating the "underlying" infant mortality rates for areas with small populations, described and illustrated in a case study that estimates infant mortality rates for 66 of 89 local health areas in British Columbia where reported births were less than 649 in 2011, including 38 reporting zero infant deaths. The method generates non-zero infant mortality rates for all 66 districts. Although some judgment is needed with the method, it has sufficient transparency that estimates can be replicated. The results support the argument that the method can produce reasonable estimates of underlying infant mortality rates for small populations subject to high levels of stochastic variation.

Résumé
Une méthode est présentée pour estimer les taux de mortalité «sous-jacents» dans des zones à population réduite. Cette méthode est décrite et illustrée à l'aide d'une étude de la mortalité infantile au sein de 66 des 89 zones de santé de la Colombie-Britannique où les naissances déclarées étaient inférieures à 649 en 2011, et parmi lesquelles 38 zones ne signalaient aucun décès avant l'âge d'un an. La méthode génère des taux de mortalité infantile non nuls pour l'ensemble des 66 districts. Bien que la méthode nécessite un certain jugement, elle est suffisamment claire pour que les estimations puissent être répliquées. Les résultats corroborent l'argument selon lequel la méthode peut produire des estimations raisonnables des taux sous-jacents de mortalité infantile pour de petites populations soumises à de fortes variations stochastiques.

Keywords Policy decisions · Monitoring health status · Small population · Beta-model · Binomial

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Mots clés Décisions politiques · Observation des états de santé · Petites populations · Modèle Beta · Binomial

1 Introduction

The infant mortality rate (IMR) is widely used. It is a measure not only used as a direct indicator of the risk of infant death, but also indirectly as an indicator of overall population health, the availability and quality of health care services, and socio-economic status differentials (Hummer 2005; Kinge and Kornstad 2014; Kitagawa and Hauser 1973; Link and Phelan 1995; Ram et al. 2016; Stockwell et al. 2005; Stockwell et al. 1987).[1] Because statistical data are often used to guide health policy decisions, it is not surprising that the IMR is used in this regard (Chen et al. 2016; Infant Mortality Review Committee 2016; Kleinman 1996; Misra et al. 2004; Stockwell et al. 1987). Moreover, as observed by VanEenwyk and Macdonald (2012), questions concerning health outcomes and related health behaviors and environmental factors often are studied within small subgroups of a population because many activities to improve health affect relatively small populations.

Fortunately, the advent of geographic information systems and high volume, fast computer-based information systems often involving the matching of records from different sources means that this type of information is technically feasible. Unfortunately, data representing small populations are subject to high levels of stochastic uncertainty, which implies lower levels of precision for small populations than those typically found in larger populations (Reeske and Razum 2011; Swanson and Tayman 2012: 216). As such, even when infant deaths are available for small populations and IMRs can be computed, these rates may not be reflective of the intrinsic (in the demographic sense) mortality regimes affecting the small populations in question. Awareness of this situation has led to a range of methods used in developing estimates of the underlying IMRs for small populations. One approach is "non-reporting," which is to simply not report IMRs for small populations, as it is the case with the Centers for Disease Control (US National Center for Health Statistics n.d.). However, this approach discards related information (e.g., reported births) that may be of use in estimating IMRs for small populations.

Another general approach is to provide an estimate by embedding small population information within a "larger context," which takes us back to the "aggregation strategy" discussed earlier. This approach is used by, among other agencies, the US National Center for Health Statistics (2018), for which the "larger context" is defined both in terms of time and space. In terms of time, the NCHS data on infant mortality rates by

[1] Murray (1996) has argued that the infant mortality rate is flawed when it is used as an index of overall mortality (i.e., the mortality regime affecting a given population) and that Disability Adjusted life Expectancy (DALE) should be used in its place. However, it has been pointed out by Reidpath and Allotey (2003) that the infant mortality rate and the DALE are so highly correlated that it merely goes to reinforce the intuition that the causes of infant mortality are strongly related to those structural factors like economic development, general living conditions, social well-being, and environmental factors, and, and such, the infant mortality rate remains a useful and comparatively inexpensive indicator of population health. Guillot et al. (2013) also note that infant mortality is responsive to changes in annual mortality conditions because it involves a short lag between the timing of mortality exposures and the timing of corresponding births.

county are aggregated for the period 2007–2015 and in terms of space, counties with small populations are aggregated. Statistics Canada (2017) uses a similar approach in that it provides a portrait of infant deaths in 2011 for provincial health regions by aggregating them over a three year period (2010–2012). One drawback to this approach is that it typically yields simple arithmetic averages and is not specific to the time and small population of interest. Related to this issue is the fact that these averages are biased unless appropriate weights or other procedures are used to reduce bias (Voss et al. 1995), steps that may not be feasible in a given situation.

Another "contextual" approach that I refer to as the "representational approach" is taken in this paper, which, unlike the "non-reporting" approach, has the potential to provide estimates of the IMRs underlying small populations, while also avoiding the drawbacks found in the aggregated approach. To this end, a publication by Link and Hahn (1996) was used as a guide in generating the approach described, tested, and applied here.[2]

2 British Columbia's Local Health Areas: a Case Study

British Columbia has 89 Local Health Areas (LHAs). The province is useful as a case study because 66 of its LHAs reported less than 649 births in 2011, marking them as "small populations" for purposes of this study. Moreover, 38 of these 66 small population LHAs reported zero infant deaths in 2011, making the province even more useful as a case study. Exhibit 1 is a map of British Columba by LHA.

3 Methods

There are two major components of method I introduce in this paper. The first part of the "Methods" section discusses the fundamental binomial nature of infant mortality rates in that they are the proportion of births that result in deaths during the first year of life that constitute a beta-binomial process. The second part of the "Methods" section looks at the second component by extending the beta-binomial process to a set of two estimates constituting samples of the mean and variance of the underlying process and argues that by averaging them, one can produce a superior estimate of the mean proportion of births that result in deaths during the first year of life.

3.1 Part I: Infant Mortality Rates as a Beta-Binomial Process

Infant mortality rates measure the proportion of births that result in deaths during the first year of life. As such, they measure the relationship between events (deaths) and trials (births) with the distribution of infant deaths in a given area i at a given time t is (approximately) binomial, with parameter d, where

$$d_{i,t} = D_{i,t}/B_{i,t} \tag{1}$$

[2] Although it uses a different context and terms, another example of the entire process can be found in Robinson (2015).

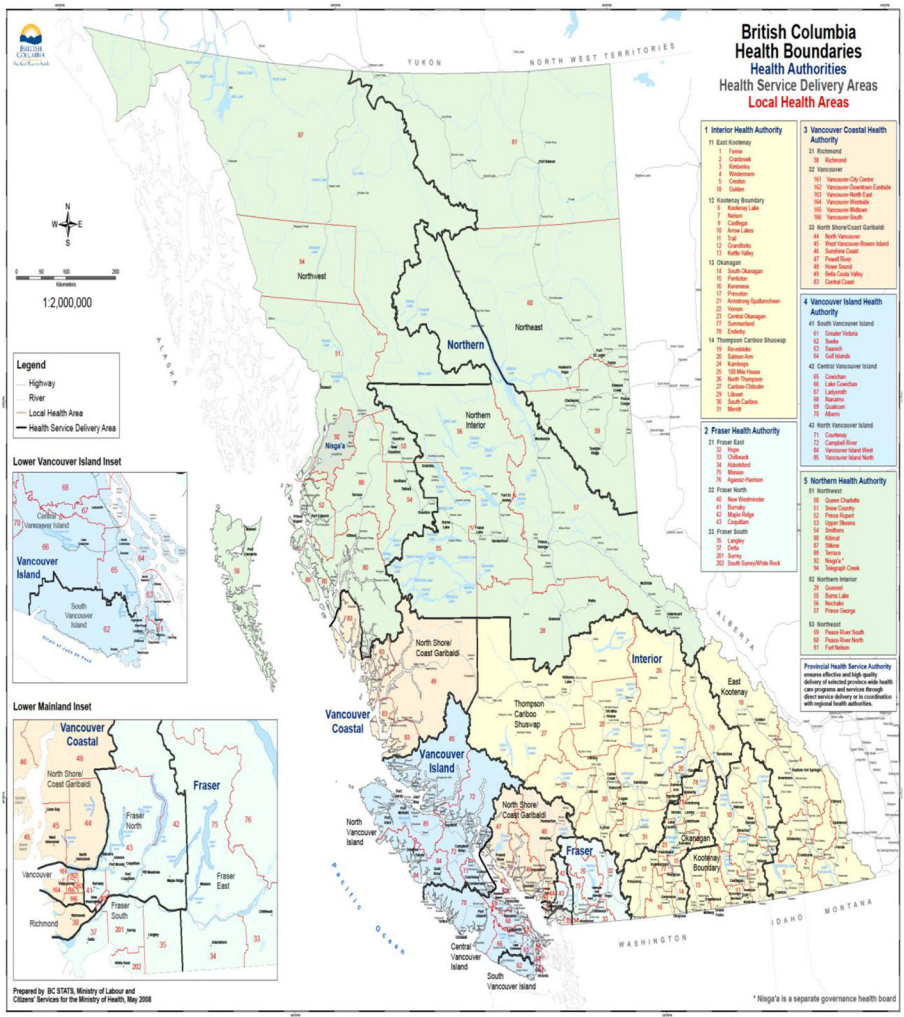


Exhibit 1 Map of British Columbia by Local Health Area. Source: British Columbia Government (https://www2.gov.bc.ca/gov/content/data/geographic-data-services/land-use/administrative-boundaries/health-boundaries)

where

i area ($i = 1$ to n)
t time
D infant deaths
B births

and is typically described as a beta-binomial random process with a probability mass function defined by two parameters: α and β. The first parameter, α, can be interpreted as the count of the event of interest, which in our case is the number of infant deaths, the number of births in which the infant dies before achieving the first year of life. The second parameter, β, can be interpreted as the count of "non-events," which in our case

is the number of children born who survive to reach 1 year of age. Note that "rate" = $\alpha/(\alpha + \beta)$, which in our case is equivalent to" infant mortality rate" = infant deaths/(infant deaths + survivors to age 1), which reduces to infant deaths/births. Thus, parameter α is the numerator in the expression defining a rate, and when added together, the parameters α and β represent the denominator. Together, IMR may be re-expressed as the compound distribution of α and β captured in the beta-binomial probability model:

$$\text{IMR} = \alpha/(\alpha + \beta) = \text{infant deaths}/(\text{infant deaths} + \text{infant survivors}) \quad (2)$$

and is typically described as a Bernoulli random process with a probability mass function defined by:

$$p = e/n \quad (3)$$

constitutes the sample mean,

$$p = p(1-p) \quad (4)$$

measures the sample variance, and

$$\text{sqrt}(p(1-p))/p \quad (5)$$

provides the coefficient of variation—a measure of the relative dispersion and stochastic uncertainty associated with the parameter estimates.

Because the IMR may be conceptualized directly using the beta-binomial model, IMRs may be thought of as stochastic processes that occur within each local health area while also contributing to higher-level meta-populations within which they are nested (Karlin and Taylor 2001; Graham and Talay 2013).

3.2 Part II: An Indirect Estimator of IMR Using Averaging of Samples from a Beta-Binomial Stochastic Process

A potential number of strategies exist for dealing with small sample size dynamics or confidentiality suppression in making estimates of infant mortality rates. First, one might simply use the state IMR in place of highly uncertain localized estimates of IMR. This would stabilize estimates for IMR on the local level, but at the expense of potentially masking heterogeneity in IMRs across geographic units. For purposes of capturing spatial patterns in IMR, a main priority in smaller-level analyses, this solution is less acceptable.

A second alternative might be to make local adjustments based on judgment. While this may improve estimates overall, especially when judgments are made by applied demographers with significant experience, this approach is subject to the criticism that non-standard methods are applied across different geographies and/or population groupings. With resource allocation decisions often tied to demographic estimates, this solution may not be satisfactory either. An ideal approach would be to utilize a principled method for adjusting local estimates of IMR. Simple model averaging based on the beta-binomial model represents a viable approach for achieving this goal.

Table 1 Reported 2011 births, infant deaths, and infant mortality rates for the 23 LHAs with "large populations"

Local Health Area	Total live births number	Total infant deaths number	IMR	IMR per 1000 births
023 Central Okanagan	1641	2	0.00122	1.2188
024 Kamloops	1022	4	0.00391	3.9139
033 Chilliwack	1029	7	0.00680	6.8027
034 Abbotsford	1733	9	0.00519	5.1933
035 Langley	1470	10	0.00680	6.8027
037 Delta	849	2	0.00236	2.3557
038 Richmond	1585	7	0.00442	4.4164
040 New Westminster	713	2	0.00281	2.8050
041 Burnaby	2277	5	0.00220	2.1959
042 Maple Ridge	945	6	0.00635	6.3492
043 Coquitlam	2095	5	0.00239	2.3866
044 North Vancouver	1251	4	0.00320	3.1974
057 Prince George	1045	5	0.00478	4.7847
061 Great Victoria	1767	8	0.00453	4.5274
062 Sooke	807	3	0.00372	3.7175
068 Nanaimo	961	4	0.00416	4.1623
161 Vancouver—City Centre	1043	2	0.00192	1.9175
163 Vancouver—North East	1043	5	0.00484	4.8356
164 Vancouver—Westside	1114	3	0.00269	2.6930
165 Vancouver—Midtown	1040	7	0.00673	6.7308
166 Vancouver—South	1224	3	0.00245	2.4510
201 Surrey	5345	18	0.00337	3.3676
202 South Surrey/White Rock	649	3	0.00462	4.6225

Source: British Columbia Vital Statistics Agency (2012)

Now that it has been established that the IMR constitutes a beta-binomial probability process, the two estimates of this process may be thought of as constituting samples of the mean and variance of the underlying process. Therefore, they may be considered as samples obtained from the same underlying mortality process. As such, it can be anticipated that a superior estimate of the mean proportion is the result of averaging them (Gardiner 1983; Brass et al. 1968; United Nations 1967). As such, the averages of two estimates based on the model may also be averaged as:

$$\mathrm{IMR}_{\mathrm{averaged}} = (\alpha_1 + \alpha_2)/((\alpha_1 + \beta_1) + (\alpha_2 + \beta_2)) \tag{6}$$

where the subscripts (1 and 2) now represent estimates of death and survivorship counts for two groups. This method can, of course, be extended to k groups as desired. Such

model averaging yields an estimate where a larger-scale and representationally appropriate model IMR is leveraged to make smaller-scale estimates more precise in a manner similar to that observed in the literature on indirect estimation in demography (Moultrie et al. 2013; Siegel and Swanson 2004; United Nations 1967). Recent attempts to extend indirect estimation based on stochastic process theory have been introduced (Baker et al. 2011), and in this paper, this idea is leveraged further in developing indirect estimates of IMR based on model averaging.

Before turning to a discussion of the data, it is appropriate here to discuss in some detail the averaging process just described. Because an IMR is typically expressed per 1000 births, it can be turned into a binomial variable by dividing it by 1000 (or more generally if IMR is expressed as infant deaths per k births, it would be divided by k). In this form, IMR is strictly bound in that it cannot be less than zero nor greater than ($0 \leq \text{IMR} \leq 1$). In practice, it is substantially less than one. Once in this form, a beta-model (binomial) can be fitted to a distribution of IMRs, which when fitted, produces two estimated parameters, α and β. The first parameter, α, can be interpreted as the count of the event of interest, which in our case is the number of infant deaths, the number of births in which the infant dies before achieving the first year of life. The second parameter, β, can be interpreted as the count of "non-events," which in our case is the number of children born who survive to reach 1 year of age. Note that "rate" = $\alpha/(\alpha + \beta)$, which in our case is equivalent to "infant mortality rate" = infant deaths/(infant deaths + survivors to age 1), which reduces to infant deaths/births. Thus, parameter α is the numerator in the expression defining a rate, and when added together, the parameters α and β represent the denominator.

The two parameters estimated by fitting the beta-model to a distribution of IMRs are then used to adjust the reported infant deaths (a) and births (b) for the population in question, even when either one or both is equal to zero. The adjustment is straightforward: adjusted IMR = $(a + \alpha)/((a + b) + (\alpha + \beta))$. Note, as stated earlier that if a = zero, then the adjusted IMR = $\alpha/(b + \alpha + \beta)$ and that if both a and b are zero, then the adjusted IMR = $\alpha/(\alpha + \beta)$.

4 Data

In regard to British Columbia, the province's 89 Local Health Areas (LHAs) are divided into two groups for purposes of this paper: (1) those with 649 or more births (23 LHAs), which are defined as "large population LHAs" and those with less than 649 births (66), which are defined as "small population LHAs." I use the first group as the "representative" set of IMS to which the beta-model will be fit. The division is based on 3rd quartile in terms of the births, which starts at 649 for all 89 LHAs.[3] Table 1 shows the births, infant deaths, and IMRs for the 23

[3] The third quartile was used as the point to distinguish between large populations and small populations because the distribution of populations across a given type of administrative area tends to be skewed. This effect is commonly known as the "rank-size rule" or "rank-size distribution" (Zipf 1949; Massey et al. 1980; Stephan and Stephan 1984; Swanson and Stephan 2004). When the births by Local Health Area were ranked in descending order and plotted, a distinct plateau is seen that starts approximately at the 74th percentile (approximately the third quartile) and continues approximately to the 11th percentile, whereupon the number again increases. The plateau suggested that those at or above this level were different in terms of size than those below this level. Other ways could be used to distinguish between large and small populations that may be useful. However, given that this paper represents an initial exploration of this method, it seems appropriate to examine other ways to distinguish large from small populations in subsequent research.

Beta Distribution Report

Dataset C:\...\BC LHA IMR PAPER\BC LHA GT 648 BIRTHS 2011.NCSS
Time Variable IMR

Parameter Estimation Section

Parameter	Method of Moments Estimate	Maximum Likelihood Estimate	MLE Standard Error	MLE 95% Lower Conf. Limit	MLE 95% Upper Conf. Limit
Minimum (A)	0	0			
Maximum (B)	1	1			
α	5.821971	5.681206	1.628485	2.489434	8.872978
β	1458.264	1423.04	426.4026	587.3059	2258.773
Log Likelihood		-115.9192			
Mean	0.003976522	0.003976428			
Median	0.003753017	0.003747455			
Mode	0.003298007	0.003281095			
Sigma	0.001644201	0.001664393			

Inverse of Fisher Information Matrix

Parameter	P	Q
P	2.651963	664.0357
Q	664.0357	181819.1

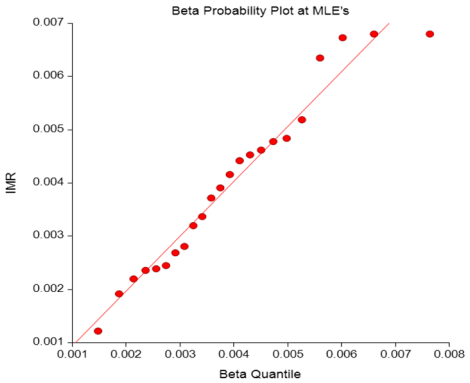


Exhibit 2 NCSS report of fit of beta-model to IMRs for the 23 LHA "representational set"

"large population" LHAs. The birth and infant death data are taken from the 2011 Vital Statistics Report produced by the British Columbia Vital Statistics Agency (2012).

5 Results

The beta-binomial model procedure found within the "survival/reliability" module of the NCSS statistical analysis package (release 8) was used to obtain the two beta-model parameters based on the infant mortality rates for the 23 LHAs used as the "large population" representative set (see Table 1). The major results of interest found in running this procedure with the data are found as Exhibit 2. Note that there are two different estimates of α and β parameters presented in the exhibit, one accomplished by the method of moments and the other by maximum likelihood estimation. The parameters of the latter are used here, namely α = 5.681206 and β = 1458.264.

Table 2 shows both the reported and estimated IMRs of the 66 "small population" LHAs. The estimated IMRs are those found by applying the two beta-parameters in conjunction with reported 2015 infant deaths (including the 38 LHAs reporting zero infant deaths) and reported births by LHA using the formulas described earlier.

Table 2 Original (reported) IMRs and estimated (revised) underlying IMRs for the 66 LHAs with "small populations"

Local Health Area	Reported (original) IMR (per 1000 births)	Revised IMR per 1000 births)
001 Fernie	0.0000	3.587
002 Cranbrook	4.4643	4.043
003 Kimberley	0.0000	3.798
004 Windermere	12.9870	4.437
005 Creston	0.0000	3.695
006 Kootenay Lake	0.0000	3.935
007 Nelson	0.0000	3.425
009 Castlegar	0.0000	3.652
010 Arrow Lakes	0.0000	3.927
011 Trail	4.8780	4.090
012 Grand Forks	18.1818	4.503
013 Kettle Valley	0.0000	3.941
014 Southern Okanagan	0.0000	3.657
015 Penticton	0.0000	3.241
016 Keremeos	0.0000	3.900
017 Princeton	0.0000	3.897
018 Golden	14.2857	4.458
019 Revelstoke	0.0000	3.763
020 Salmon Arm	0.0000	3.317
021 Armstrong—Spallumcheen	0.0000	3.743
022 Vernon	1.7301	3.329
025 100 Mile House	0.0000	3.743
026 North Thompson	0.0000	3.911
027 Cariboo—Chilcotin	7.6923	4.549
028 Quesnel	13.4529	5.256
029 Lillooet	25.0000	4.549
030 South Cariboo	16.3934	4.485
031 Merritt	0.0000	3.640
032 Hope	14.7059	4.464
045 West Vancouver—Bowen Island	0.0000	3.366
046 Sunshine Coast	4.6729	4.067
047 Powell River	0.0000	3.624
048 Howe Sound	4.1667	4.024
049 Bella Coola Valley	0.0000	3.876
050 Queen Charlotte	0.0000	3.821
051 Snow Country	0.0000	3.965
052 Prince Rupert	6.0241	4.190
053 Upper Skeena	14.7059	4.464
054 Smithers	0.0000	3.518

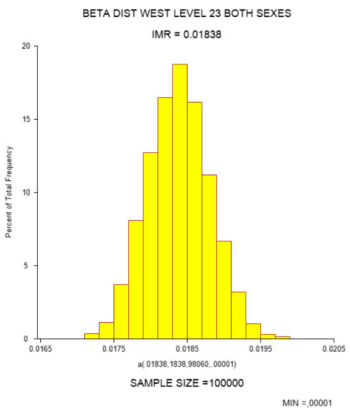
Table 2 (continued)

Local Health Area	Reported (original) IMR (per 1000 births)	Revised IMR per 1000 births)
055 Burns Lake	0.0000	3.766
056 Nechako	4.5872	4.057
059 Peace River South	8.6705	4.892
060 Peace River North	4.8622	4.244
063 Saanich	2.5189	3.659
064 Gulf Islands	0.0000	3.758
065 Cowichan	3.7383	3.912
066 Lake Cowichan	0.0000	3.871
067 Ladysmith	0.0000	3.608
069 Qualicum	8.4746	4.614
070 Alberni	2.9240	3.773
071 Courtenay	1.9048	3.420
072 Campbell River	2.5445	3.668
075 Mission	6.3158	4.560
076 Agassiz—Harrison	0.0000	3.743
077 Summerland	0.0000	3.781
078 Enderby	0.0000	3.783
080 Kitimat	22.4719	5.061
081 Fort Nelson	0.0000	3.753
083 Central Coast	0.0000	3.892
084 Vancouver Island West	0.0000	3.900
085 Vancouver Island North	0.0000	3.603
087 Stikine	0.0000	3.960
088 Terrace	8.3333	4.603
092 Nisga'a	0.0000	3.903
094 Telegraph Creek	0.0000	3.960
162 Vancouver—Downtown Eastside	3.2626	3.762

6 Discussion of Results

The estimated IMRs for the 66 LHAs reporting less than 649 births range from 3.241 (Penticton LHA) to a high of 5.256 (Quesnel LHA). This range is less than that found for original (reported) IMRs for these same 66 LHAs, which is from a low IMR of 0.00 for 38 of them to a high of 25.000 for Lillooet LHA. The reduced range for the estimated IMRs suggests that the process used to create them may, in fact, represent the IMRs underlying these 66 LHAs in that the estimates do not display as high level of variation as found in the original (reported) IMRs. This change in the range suggests a move to a lower level of stochastic uncertainty, which would be more reflective of the intrinsic mortality

Data Simulation Report
Histogram Section of Simulated Data



Descriptive Statistics of Simulated Data

Statistic	Value	Statistic	Value
Mean	0.01838248	Minimum	0.01684878
Standard Deviation	0.0004237251	1st Percentile	0.01744547
Skewness	0.07195781	5th Percentile	0.01769227
Kurtosis	2.934381	10th Percentile	0.0178332
Coefficient of Variation	0.02305049	25th Percentile	0.01808544
Count	5000	Median	0.01838394
		75th Percentile	0.01866444
		90th Percentile	0.0189272
		95th Percentile	0.01908542
		99th Percentile	0.01937772
		Maximum	0.02014658

Exhibit 3 Characteristics of the synthetic population used in the validity test

regimes affecting these "small population" LHAs. This is what the method is intended to do.

Because of the "representational context" selection, the estimates are subject to judgment. However, even still the entire process is transparent, which means that the results are not subject to arbitrary and capricious judgments that render them difficult to replication. This and the fact that estimates are valid and can be efficiently generated by the process described here suggests that they have the potential to support policy decisions in British Columbia concerning infant mortality (see, e.g., Infant Mortality Review Committee 2016) while keeping time and resource requirements low, characteristics that Swanson and Tayman (2012: 304) suggest are important components in deciding what methods to use in developing estimates.

7 Validity Test

Given that the method is producing a revised IMR that is likely to be close to the underlying IMR for a small population and therefore reflective of its intrinsic mortality regime, one would expect the method to do this where one could observe the intrinsic mortality regime. Model stable populations afford this opportunity because they have known intrinsic mortality regimes, the model

life tables associated with a given set of model stable populations. To examine how the method works in this environment, I employed the IMR associated with a model stable population found in *Manual IV, Methods of Estimating Basic Demographic Measures from Incomplete Data* (1967). For this purpose, I selected the infant mortality rate associated with West Level 23 for both sexes, which shows that of 100,000 births, 98,166 are expected to reach the first birthday. This yields an IMR of 0.0184 = 1–.98166.

Using the IMR of 0.0184 and a seed population of 100,000, a random sample of 5000 IMRs was generated using the beta-model simulation provided by the NCSS statistical system (release 8). The sample is sufficiently large to allow the simulation program the opportunity to generate outliers, which it did. As can be seen in Exhibit 3, the mean is 0.01838 with a standard deviation of 0.000423 and a coefficient of variation equal to 0.02305. The minimum IMR is .016849 and the maximum is .020147.

From the 5000 randomly generated observations, I extracted two sets of data. For the first set, I extracted the initial 43 IMR randomly generated observations from the simulation. For the second set, I rank-ordered the 5000 observations from high to low and then from low to high and extracted the eight highest IMR and seven lowest IMRs, respectively, from them. The idea is that the entire set represents a synthetic population with 58 observations while the second set of 43 simulated IMRs represents the subset of the synthetic population in which IMRs are reported, and the third set of 15 simulated IMRs represents a subset of "small populations" subject to a high level of stochastic uncertainty. These characteristics mimic the 2009–2011 IMRs reported for the 58 counties of state of California, where the results are not reported for 15 counties (due to their small populations).[4] The 42 observations are expected to be closer, on average, to the "underlying" IMR of 0.01838 and have variation, respectively, than that found in the 15 observations. For the set of 43 observations, the mean IMR is 0.01834 and the coefficient of variation is .02305. For the set of 15 observations, the mean IMR is .01855 and the coefficient of variation is .07692. Thus, the set of 42 observations has a mean and a coefficient of variation closer to the mean and coefficient of variation found in the full set of 5000 observations than does the set of 15 observations.

A beta-model was fit to the set of 43 observations, and its parameters were used to revise the IMRs in the set of 15 observations. The expectation is that the revised IMRs will yield a

[4] Note that as stated in the text, the validity test mimics the fact that for its 58 counties California reports IMRs only for 43 of them for the 2009–2011 period, leaving the remaining 15 counties without reported IMRs. As such, the validity test was set up as if there were 43 units for which IMRs were reported and 15 for which they were not. However, all of the data used in the validity test were generated from the synthetic population that is based on Model Life Table, level 23, as described in the text. The reporting structure as well as the actual data for California can be found through the Open Portal service provided by the California Health and Human Services Agency via a download of a CVS data set assembled by the California Department of Public Health. This data set can be accessed by going to https://data.chhs.ca.gov/dataset/infant-mortality-deaths-per-1000-live-births-lghc-indicator-01/resource/ae78da8f-1661-45f6-b2d0-1014857d16e3 and then clicking on the "download" tab, which downloads the file, "Infant Mortality, Deaths Per 1000 Live Births (LGHC Indicator 01) (CSV)" in CVS form. Once downloaded, it can be saved as an excel file. The data in this file include the infant mortality rates (identified as "rate" in the file) and the infant deaths (identified as "numerator" in the file) and live births (identified as "denominator" in the file) used to calculate the IMRs for all counties and other administrative areas, including the state as a whole. The data represent the period 2009–2011. A description of the methods, caveats, and so forth associated with this data set can be found on the ULR shown above.

mean IMR closer to that found for the full 5000 set of simulated observations and that the variation among these revised means will decline, yielding a smaller coefficient of observation.

The results show that the beta-model moved the initial IMR estimates for the 15 observations closer to the underlying IMR. As such, they are more reflective of the West Level 23 mortality regime that is intrinsic to them: the mean of the original IMRs for the 88 observations is 0.01855 while the mean for the revised IMRs is 0.01839, which is closer to the underlying IMR of 0.01838. In terms of variation, the coefficient of variation for the initial set of 14 IMRs is .07692, while that for the revised set is 0.00338. These results support the argument that the method described in this paper is capable of moving IMRs subject to stochastic uncertainty closer to the underlying IMRs and their respective intrinsic mortality regimes.

8 Conclusions

Because of the "representational context" selection, the estimates are subject to judgment. However, even still the entire process is transparent, which means that the results are not subject to arbitrary and capricious judgments that render them difficult to replication. This and the evidential support provided by the validity test suggest that, in fact, our method is capable of producing estimates of underlying IMRs.[5] In turn, these findings suggest that the method is not only capable of generating reasonable IMR estimates in the absence of reported infant deaths, but that these are valid in terms of the intrinsic mortality regimes affecting small populations. Because these estimates can be efficiently generated by the process described here also suggests that they have the potential to support policy decisions while keeping time and resource requirements low, characteristics that Swanson and Tayman (2012) suggest are important components in deciding what methods to use in developing estimates.[6]

[5] In the validity test, different populations are simulated from a common beta-distribution, and the result is that the two sets of populations, large and small, are normally distributed around the intrinsic mean IMR of the "population." The simulation shows that the adjusted IMRs of the small populations move closer the underlying IMR, which indicates that the method works when both the small and large populations represent samples taken from the same underlying population. If the small populations represent a sample from a different population than the sample of large population, then the adjustment may yield a "biased" estimate of the former's underlying IMR. This shows the importance of having a reference set that conceptually represents a sample from the same underlying population as the small population sample. One way to visualize the unbiased and biased outcomes is to picture the case where the method yields: (1) an "unbiased" estimate, which is when the mean IMR of the large populations is between the underlying IMR and the mean IMR of the small populations, and (2) a "biased" estimate when the method does not move the mean IMR for the small population closer to its underlying IMR, which occurs where the mean IMR of the small population is between the underlying IMR and the mean IMR of the large populations.

[6] Although Green and Armstrong (2015) discuss simple vs. complex methods in terms of forecasting, their discussion applies here in that the beta-binomial approach falls into the simple methodological category rather than the complex category. Adapting their discussion to methods in general, the work of Green and Armstrong (2015) suggests that while there is no evidence that shows complexity improves accuracy, complexity remains popular among (1) researchers, because they are rewarded for publishing in highly ranked journals, which favor complexity; (2) methodologists, because complex methods can be used to provide information that support decision makers' plans; and (3) clients, who may be reassured by incomprehensibility. We believe that the argument by Green and Armstrong (2015) can be applied to Bayesian methods, which represents the "complex" alternative to the "simple" beta-binomial approach. We prefer the beta-binomial approach, however, not only because of the argument presented by Green and Armstrong, but also because the application of a Bayesian approach can be difficult, effortful, opaque, and even counter-intuitive (Goodwin 2015).

In conclusion, it is important to keep in mind that small populations with approximately the same total number of people may have very different age compositions. For example, one may have a relatively large aged population and the other a relatively large young population. This simple example is meant to illustrate the effect of demographic heterogeneity on measures of mortality (Vaupel and Missov 2014). In situations where substantial heterogeneity may be present, a model with additional covariates may prove useful because the latter can potentially take into account the effects of demographic heterogeneity.

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