

Estimating disease prevalence using census data

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SUMMARY

We describe a method of working on publicly available data to estimate disease prevalence in small geographic areas using *Helicobacter pylori* as a model infection. Using data from the Third National Health and Nutrition Examination Survey, risk parameters for *H. pylori* infection were obtained by logistic regression and validated by predicting 737·5 infections in an independent cohort with 736 observed infections. The prevalence of *H. pylori* infection in the San Francisco Bay Area was estimated with the probabilities obtained from a predictive logistic model, using risk parameters with individual-level 1990 U.S. Census data as input. Predicted *H. pylori* prevalence was also compared to gastric cancer incidence obtained from the Northern California Cancer Center and showed a positive correlation with gastric cancer incidence ($P < 0\cdot001$, $R^2 = 0\cdot87$), and no statistically significant association with other malignancies. By exclusively using publicly available data, these methods may be applied to selected conditions with strong demographic predictors.

INTRODUCTION

In the United States, significant resources are devoted to conducting large population-based surveys. These surveys can be health-oriented, such as the National Health and Nutrition Examination Survey (NHANES) and the Nurses' Health Study, or general surveys such as the Decennial Census [1, 2]. In the interest of maximizing their value, data from such studies are made available to other investigators. These data are often highly desirable, because of the large sample sizes and careful study design. Even for very large studies, however, the amount of information collected is finite, and the number of hypotheses considered in the design must be limited.

Moreover, although these large health-oriented surveys give an excellent picture of national trends, they are not always suited for extrapolation down to the local level. For example, NHANES may describe the distribution of body mass index at the national level, but the unique attributes of the population of any particular census tract preclude the direct application of NHANES results to understanding the health status of that tract's population. Recent developments in epidemiological methodology have highlighted the importance of smaller scale, neighbourhood-level factors as health determinants [3–5]. Ordinarily, estimates of the prevalence of risk factors at the local level require direct sampling of that population. This estimation is done at great expense and the results cannot be generalized to other geographic areas. Existing methods for estimating disease prevalence or incidence in small-area units involve interpolation and smoothing and their associated limitations [6, 7].

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Table 1. *Demographics of study populations*

Demographic	Category	NHANES III (<i>n</i> = 6769)	Validation cohort (<i>n</i> = 1355)	Census (<i>n</i> = 4 294 389)
Age (yr)	18–24	14	23	12
	25–34	20	40	26
	35–44	18	22	23
	45–54	12	8	15
	55–64	13	4	11
	64–74	13	2	8
	≥75	11	1	5
Median annual household income	<\$10 000	19	—	6
	\$10 000–\$19 999	27	27	9
	\$20 000–\$29 999	18	30	11
	\$30 000–\$39 999	13	—	13
	\$40 000–\$49 999	9	17	12
	≥\$50 000	14	25	48
Race	White	73	92	70
	Black	25	2	8
	Other	2	6	22
Ethnicity	Hispanic	28	80	15
	Non-Hispanic	72	20	85
Place of birth	Native (USA)	82	20	75
	Foreign	18	80	25

NHANES III, Third National Health and Nutrition Examination Survey. Values are percentages.

Here, we describe a method of using the size and strengths of multiple large-scale population-based surveys to address such limitations. This is not an attempt to link individual records across databases, but rather to develop an understanding of disease using one dataset, then apply that knowledge to make inferences using another. Specifically, we used data from NHANES III to develop a model of demographic risk factors for *Helicobacter pylori* infection, then used data from the U.S. Census Bureau to estimate the prevalence of infection. The initial model was validated using an independent cohort, and the prevalence estimates were compared with the incidence rates of gastric cancer – a malignancy directly attributable to *H. pylori* infection [8–11].

MATERIALS AND METHODS

Modelling *H. pylori* using NHANES III data

NHANES III (1988–1994), was conducted on a nationwide probability sample of about 33994 persons aged ≥2 months, and was designed to obtain

nationally representative information on the health and nutritional status of the population of the United States [2]. Serum samples from 7465 adults were tested for the presence of anti-*H. pylori* IgG antibodies [12]. These samples were collected during the first phase of the survey, from 1988 to 1991. The presence of antibodies was tested using a commercial IgG ELISA with a sensitivity of 91% and specificity of 96%. For each individual, numerous demographics and health statistics were also collected, including age, race, ethnicity, country of birth and annual household income. A total of 6769 participants had complete data for these variables and were included in the analysis (Table 1).

Logistic regression was used to model the relationship between *H. pylori* infection status and demographic predictor variables. An individual was defined as *H. pylori*-infected if seropositive for *H. pylori* using a commercial IgG ELISA as described in the NHANES protocol [12]. Testing of this assay against biopsy samples from 268 biopsy-confirmed patients with *H. pylori* and 105 patients without *H. pylori* revealed a sensitivity of 91% and a specificity of

96%. The logistic model used the five demographic risk factors of age, income, race, ethnicity and place of birth from the NHANES dataset, and also included two interaction terms: race \times income and race \times ethnicity. The five risk factors were selected *a priori*, being well-established risk factors for *H. pylori* infection. Interaction terms were added during the logistic modelling process. Marginal odds ratios for specific levels of each demographic predictor were calculated together with associated 95% confidence intervals (CI). Calculations were performed with SAS version 9 (SAS Institute, Cary, NC, USA).

Validation of the infection model

To validate the infection model, we predicted the infection status of members of a 1355-person cohort. As part of an ongoing community-based survey, individuals presenting at one of 17 medical clinics in the Silicon Valley (Southern part of San Francisco Bay Area, CA, USA) for acute gastroenteritis and members of their households completed a questionnaire and underwent IgG serological testing for *H. pylori* [13]. This assay was 91% sensitive and 98% specific for infection in adults [14]. Acute gastroenteritis was clinically defined as loose or watery stool occurring ≥ 5 times/day in a child aged < 2 years or ≥ 3 times/day in a person aged 2 years or at least one instance of vomiting in a person of any age. Demographic data collected included age, race/ethnicity, country of birth and annual household income. A probability of *H. pylori* infection was calculated for each individual using the model parameters derived from the NHANES III data. The model parameters were held fixed, and the logistic model was used in a predictive manner with cohort data as input. The expected number of infections for this cohort was calculated as the sum of these probabilities for the cohort and a receiver operating characteristic (ROC) curve was generated.

Applying census data to the infection model to estimate infection prevalence

To estimate the prevalence of infection, we first obtained a special tabulation of the 1990 U.S. Decennial Census. This dataset consisted of aggregate statistics for each county in the Silicon Valley area, stratified by age (seven categories), household income (six categories), race (three categories), ethnicity (Hispanic or

non-Hispanic), and country of birth (United States or other). Categories were selected to match available NHANES III data. Only individuals aged ≥ 18 years were included.

The aggregate census data were converted to individual profiles based on the categories used. As the census data was stratified in five dimensions, each cell was converted into the appropriate number of individuals with the five-dimensional profile of the cell. For example, aggregate data for San Francisco county might report a total of 500 for the stratification: native-born, non-Hispanic whites between ages 55–64 with income of \$10 000–\$19 999. Although this is an aggregate statistic, it can be converted into 500 individuals with the specified demographic profile. The nine counties in our study area yielded 4 294 389 individual profiles (Table 1).

In the same process as the validation cohort, a probability of *H. pylori* infection was calculated for each individual profile using the model parameters derived from the NHANES III data. The predicted prevalence of infection for a given county was calculated as the average of the infection probabilities for the region's population.

Correlation of estimated *H. pylori* prevalence and observed cancer incidence

In an ecological manner, the estimated prevalence of *H. pylori* was correlated with the incidence of several malignancies. Using the above methods, the prevalence of *H. pylori* was estimated for the nine counties that comprise the catchment's area of the Northern California Cancer Center's (NCCC) Greater Bay Area Cancer Registry (San Francisco, San Mateo, Marin, Alameda, Contra Costa, Santa Clara, Santa Cruz, Monterey and San Benito). From the NCCC, we obtained age-adjusted rates and case counts of leukaemia, gastric and oesophageal cancers for each county for the period 1988–1997. For gastric cancer, only non-cardia cases were included in the analyses. For oesophageal cancer, adenocarcinoma and squamous cell carcinoma were analysed separately. For each county, age-adjusted rates were calculated for the 10-year period using the 1990 Standard Million. This incidence rate of each cancer was used as the dependent factor in an ordinary least-squares regression, with the predicted prevalence of *H. pylori* infection as the independent factor.

Table 2. Odds ratios from logistic regression using NHANES III data with the outcome of *H. pylori* infection. (The model included two interaction terms: ethnicity \times race and income \times race.)

Risk factor	OR	95% CI
Age (yr)		
18–24	1.0	Reference
25–34	1.6	1.3–1.9
35–44	2.2	1.8–2.6
45–54	3.2	2.6–4.0
55–64	4.9	4.0–6.0
65–74	5.8	4.7–7.2
≥ 75	8.0	6.4–10.1
Race*		
White	1.0	Reference
Black	3.9	2.6–5.7
Other	3.5	1.2–10.2
Ethnicity*		
Hispanic	3.6	3.1–4.2
Non-Hispanic	1.0	Reference
Place of birth		
Foreign	1.9	1.6–2.2
Native (USA)	1.0	Reference
Income*		
\$0–\$9999	2.6	2.1–3.3
\$10 000–\$19 999	2.0	1.6–2.5
\$20 000–\$29 999	1.8	1.4–2.2
\$30 000–\$39 999	1.4	1.1–1.8
\$40 000–\$49 999	1.1	0.9–1.5
\geq \$50 000	1.0	Reference
Income (Black)		
\$0–\$9999	0.6	0.4–0.9
\$10 000–\$19 999	0.8	0.5–1.3
\$20 000–\$29 999	0.9	0.5–1.4
\$30 000–\$39 999	0.7	0.4–1.2
\$40 000–\$49 999	1.1	0.6–1.9
\geq \$50 000	1.0	Reference
Income (Other)		
\$0–\$9999	0.2	0.1–0.8
\$10 000–\$19 999	0.6	0.2–1.9
\$20 000–\$29 999	0.4	0.1–1.5
\$30 000–\$39 999	1.0	0.2–4.7
\$40 000–\$49 999	0.6	0.1–3.0
\geq \$50 000	1.0	Reference
Ethnicity (Black)		
Hispanic	0.2	0.1–0.5
Non-Hispanic	1.0	Reference
Ethnicity (Other)		
Hispanic	0.4	0.2–0.9
Non-Hispanic	1.0	Reference

NHANES III, Third National Health and Nutrition Examination Survey.

OR, Odds ratio; CI, confidence interval.

* Denotes variables with interaction terms in the model.

RESULTS

The logistic regression using NHANES III data on *H. pylori* infection and demographic factors yielded odds ratios consistent with previous studies (Table 2). Increasing age, decreasing income, non-White race, Hispanic ethnicity and non-US place of birth were all associated with increased risk of infection. Everhart *et al.* [12] previously described *H. pylori* prevalence and demographic risk factors in this cohort.

When the NHANES III-derived logistic model was used to predict the infection status of a 1355-member cohort, the total number of infections predicted was 737.5, compared to an observed 736 infections, as determined by serology. This corresponds to a predicted prevalence of 54.4% vs. an observed prevalence of 54.3%. Subgroup analysis showed that the model tended to slightly overestimate the number of infections in subgroups associated with high risk of infection and slightly underestimate the number of infections in subgroups associated with low risk of infection (Table 3).

The area under the ROC curve was 0.69 (Fig. 1). The cutpoint with the best balance between sensitivity and specificity was 0.57. This cutpoint corresponded to a sensitivity of 0.62, specificity of 0.66, positive predictive value of 0.68 and a negative predictive value of 0.59.

When the NHANES III-derived logistic model was used in conjunction with 1990 census data, the predicted prevalence of *H. pylori* infection for the nine counties in the study area was about 36% on average (Fig. 2). Prevalence rates for the nine counties were normally distributed.

Using age-adjusted cancer incidence rates for each county derived from the registry of the NCCC, aggregated for the period 1988–1997, predicted *H. pylori* prevalence showed a positive correlation with gastric cancer incidence ($P < 0.001$, $R^2 = 0.87$, Fig. 3). We observed a negative association with esophageal adenocarcinoma incidence, and a positive association with esophageal squamous cell carcinoma incidence, although neither were statistically significant ($P = 0.063$ and $P = 0.051$, respectively). There was no association between the predicted *H. pylori* prevalence and leukaemia incidence ($P = 0.56$).

We also compared gastric cancer incidence to *H. pylori* prevalence modelled using a subset of the risk factors included in the final model. While some models showed a stronger correlation (age, race, and Hispanic ethnicity, $R^2 = 0.89$), these models were less

Table 3. Comparison of the predicted and observed numbers of infections using the NHANES III-derived infection parameter estimates and the validation dataset. Displayed are the predicted number of infections for each category and the observed number of infections with associated standard error (S.E.)

	Total number	Predicted <i>H. pylori</i> infections	Observed <i>H. pylori</i> infections (S.E.)
Overall	1355	737.5	736 (22.0)
Subgroups			
Age (yr)			
18–24	309	141.4	150 (8.5)
25–34	547	311.0	334 (11.2)
35–44	296	161.8	149 (7.8)
45–54	113	63.7	54 (4.7)
55–64	52	33.4	30 (3.1)
65–74	28	19.4	14 (2.2)
≥75	10	6.9	5 (1.3)
Income			
\$0–\$9999	0	—	—
\$10 000–\$19 999	371	236.3	233 (9.0)
\$20 000–\$29 999	413	255.5	260 (9.6)
\$30 000–\$39 999	0	—	—
\$40 000–\$49 999	227	112.0	128 (7.2)
≥ \$50 000	344	133.6	115 (8.4)
Race			
White	1252	686.0	702 (16.5)
Black	28	13.5	12 (2.6)
Other	75	38.0	22 (4.1)
Ethnicity			
Hispanic	1081	647.2	678 (15.6)
Non-Hispanic	274	90.3	58 (7.2)
Place of Birth			
Foreign	1083	657.4	677 (15.7)
Native (USA)	272	80.1	59 (7.2)

NHANES III, Third National Health and Nutrition Examination Survey.

accurate at predicting the infection prevalence of the validation cohort (predicted 52.7%, observed 54.3%). The final model made the most accurate estimate of prevalence in the validation cohort and had one of the highest correlations with gastric cancer incidence. The simplest model with both a high R^2 and accurate estimate of prevalence included the two risk factors age and place of birth, with an R^2 of 0.52 and predicted prevalence of 56.5%.

DISCUSSION

The results of this study illustrate the capability of these methods to use large datasets to make prevalence estimates for small-area units. They were

relatively simple to implement and provided excellent results, especially when considering the minimal investment required in obtaining them. We were able to replicate the results of previous studies using a small fraction of the resources they required. These methods offer the potential to use existing data sources to conduct novel epidemiological studies.

H. pylori has been designated a Group 1 carcinogen by IARC for its role in the development of gastric cancer, in part because of ecological studies demonstrating an association between the infection and cancer [15]. Our study replicated the results of previous work describing this ecological correlation [16, 17]. Our methods, however, appear much more robust. These studies relied on using limited samples

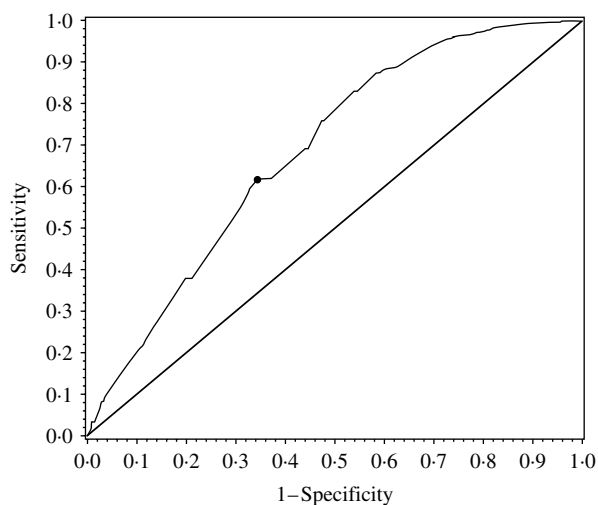


Fig. 1. ROC curve for validation dataset. Sensitivity and specificity refer to the prediction of *H. pylori* infection using demographic risk factors with serology as the reference standard. The black dot (●) represents the greatest balance between sensitivity and specificity. The area under the curve is 0.69.

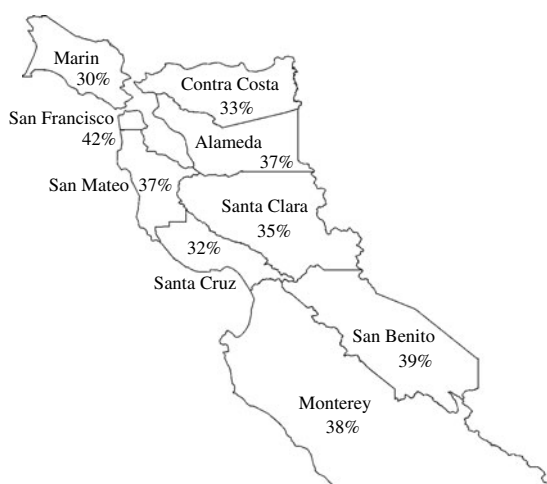


Fig. 2. Map of study area. Percentages indicate the predicted prevalence of *H. pylori* infection in that county.

of individuals to represent very large areas. In one case, samples of fewer than 200 individuals represented entire countries [17]. In prior studies, the correlation between *H. pylori* and gastric cancer was modest, with an R^2 range of 0.12–0.34. In contrast, our analysis showed a far stronger correlation between *H. pylori* prevalence and gastric cancer incidence ($R^2=0.87$).

The model created using the NHANES III data was qualitatively consistent with previous studies, and was extremely accurate at predicting the prevalence of

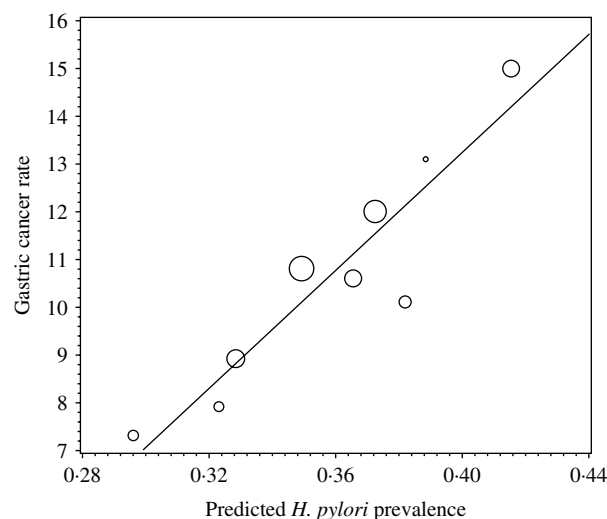


Fig. 3. Regression plots of *H. pylori* and age-adjusted gastric cancer rates. Each open symbol (○) represents a county, with the size of the symbol proportional to the population of the county. The regression was weighted by population and has the equation: gastric cancer rate = $-11.76 + 63.172 \times H. pylori$ prevalence.

infection in the cohort. Given that this cohort was completely independent of the population used to derive the model parameters, as well as some stark demographic differences between the two groups (Table 1), the NHANES III-derived model can be considered highly effective for use in predictive analyses. Although our final model was the most accurate in predicting the prevalence of the validation cohort, it is worth noting that a model consisting of just age and place of birth was quite accurate in its prevalence estimates (56.5% predicted, 54.3% observed) and had a relatively strong correlation with gastric cancer ($R^2=0.52$).

We also found a negative correlation between *H. pylori* and incidence of oesophageal adenocarcinoma – a phenomenon reported in other studies [18, 19] – although this finding was not statistically significant. Similarly, there is some evidence that *H. pylori* (particularly CagA-positive strains) is positively associated with oesophageal squamous cell carcinoma [19]. We observed this association, but as with adenocarcinomas, the observed correlation did not meet the 0.05 standard for statistical significance. There is no compelling evidence that *H. pylori* is associated with leukaemia, and as expected, this study found no statistically significant association. Thus, our findings were specific and could not be construed to reflect factors related to carcinogenesis more generally. We found that although we could create

models that yielded a higher R^2 , their estimates of the infection prevalence in the validation cohort were not nearly as accurate as the final model.

Using existing data exclusively, we were able to estimate the prevalence of *H. pylori* infection and find a positive correlation with gastric cancer incidence. By structuring our model to match categories and risk factors available in the U.S. Census, it is possible to accurately estimate the prevalence of disease at any level of geography for which census data are available. These regions can be as large as states or counties, or as small as a census block group. Conducting a traditional epidemiological survey of disease prevalence at a scale as fine as a census block group for an area the size of even one county would be prohibitively expensive. Using a pre-fit risk model not only precludes the need to collect samples, but also should permit geographic portability—for example, the same study could easily be done with populations in New York, Texas or Iowa.

To develop our predictive model, we obtained risk parameters using a large national dataset. While many such studies are collecting an increasingly large set of variables, specific risk factors may not be present in these datasets, particularly those that do not have a well-established association with disease. Although we used a national dataset to maximize generalizability, it is not a strict requirement of the methodology—risk parameters can be fit using a dataset of any size.

Unlike some methods of applying national data to the local level, we are able to avoid the ‘ecological fallacy’ [20]—the potential for incorrect conclusions when extrapolating aggregate data to a more specific level (e.g. using national data to make inferences about counties). Although the census data was provided to us in aggregated form, the tables were stratified, allowing us to build individual profiles. The NHANES model was derived from individual-level data, and we applied individual profiles from census data, thus avoiding this concern.

With further development and validation, these methods could be used to conduct low-cost pilot studies, the results of which, although not definitive proof, would serve as evidence to justify more rigorous studies using traditional epidemiological methods. Once our estimates of infection prevalence were made for each county, it was relatively simple to compare prevalence with several different malignancies. The marginal effort to add additional analyses was negligible. While the association between

H. pylori and gastric cancer is well-established, by using existing data, we could have conducted this study *de novo* and highlighted gastric cancer above all others as worthy of further investigation.

Although these methods offer quick estimates of prevalence, the results cannot be definitively confirmed without more detailed studies. The obligation to subsequently conduct these studies would eliminate the advantage of using this methodology. To inspire confidence in the results, the risk parameters of the predictive model should be extensively validated, as we did with an independent dataset. If surprising results do emerge, they may serve to justify more detailed studies. This type of analysis is not intended to supplant observational or experimental studies.

In addition to research, these small-area estimates of disease prevalence and incidence have applications in health services. The potential for a high level of geographic resolution could allow for improved targeting of outreach or service delivery programmes. The use of existing data would eliminate survey costs, leaving more resources available for interventions. This could be particularly beneficial for rural areas, which due to their geographic size and low population density are difficult to survey efficiently.

This methodology is not limited to analysis of *H. pylori* prevalence, although *H. pylori* may be particularly well-suited for this method, as it has well-established demographic risk factors. Any disease or condition that has strong demographic predictors could be modelled in this way. Other likely candidates include smoking and cardiovascular disease, and preliminary studies have shown that smoking may be particularly amenable to these methods. These results provide quantitative evidence that demographics can be used to predict disease, and we have demonstrated that existing datasets provide the information needed to estimate the prevalence of disease in a population.

DECLARATION OF INTEREST

None.

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