Resource Pack:
Model Calibration and Validation


Overview

This resource pack, curated by the Center for Health Decision Science, provides broad exposure to empirical calibration and validation methods for mathematical models used in health decision analysis. Included are a selection of overviews, guidelines, tutorials, and applications.

Given the complexity of diseases and variation in data quality, there are invariably a number of parameters that are unobserved or cannot be estimated directly but can be inferred through the process of model calibration. Model calibration is approached uniquely for each disease model depending on the quantity (and quality) of data and complexity of the model structures. Selected resources in the pack vary from Bayesian evidence synthesis used to calibrate parameters of a complex model to methods for calibrating stochastic dynamic transmission models. Other resources were selected to address model credibility and performance. Topics include between-model comparisons, predictive validity, and assessment of external validity using data that are not used as direct inputs or in model calibration.
Selected Resources – At a Glance

TUTORIALS AND PRIMERS

Bayesian Methods for Calibrating Health Policy Models: A Tutorial

Calibration of Complex Models through Bayesian Evidence Synthesis: A Tutorial

GUIDELINES AND METHODS


Validation and Calibration of Structural Models that Combine Information from Multiple Sources
Not open access.

Likelihood Approach for Calibration of Stochastic Epidemic Models

Calibrating Models in Economic Evaluation

Empirically Evaluating Decision-Analytic Models

Validation of Population-Based Disease Simulation Models: A Review

EXAMPLES BY DISEASE AREA

Empirically Calibrated Model of Hepatitis C Virus Infection in the United States
Not open access.

Validation and Calibration of a Simulation Model of Pediatric HIV Infection

Assessing the Performance of a Computer-Based Policy Model of HIV and AIDS

The Rise and Fall of HIV in High-Prevalence Countries: A Challenge for Mathematical Modeling

Eleven Mathematical Models of TB

Reduced Burden of Childhood Diarrheal Diseases through Increased Access to Water and Sanitation in India: A Modeling Analysis

Modeling Human Papillomavirus and Cervical Cancer in the United States for Analyses of Screening and Vaccination

Health and Economic Implications of HPV Vaccination in the United States

Cost Effectiveness Analysis of Including Boys in a HPV Vaccination Programme in the U.S.

Including Boys in an HPV Vaccination Programme: A CEA in a Low-Resource Setting

Health and Economic Impact of HPV 16/18 Vaccination and Cervical Cancer Screening in Eastern Africa

Validating a Cardiovascular Disease Microsimulation Model

Not open access.
Unifying Screening Processes within the PROSPR Consortium: A Conceptual Model for Breast, Cervical, and Colorectal Cancer Screening

Development of an Empirically Calibrated Model of Gastric Cancer in Two High-Risk Countries

Contribution of H. Pylori and Smoking to US Incidence of Gastric Adenocarcinoma: A Microsimulation Model

Simulation Models of Obesity: A Review of the Literature
Not open access.
Annotated Bibliography

TUTORIALS AND PRIMERS

Bayesian Methods for Calibrating Health Policy Models: A Tutorial
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2412
This article provides a tutorial on Bayesian approaches for model calibration. It describes the theoretical basis for Bayesian calibration approaches as well as pragmatic considerations that arise in the tasks of creating calibration targets, estimating the posterior distribution, and obtaining results to inform the policy decision. These considerations, as well as the specific steps for implementing the calibration, are described in the context of an extended worked example about the policy choice to provide (or not provide) treatment for a hypothetical infectious disease.

Calibration of Complex Models through Bayesian Evidence Synthesis: A Tutorial
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2417
This tutorial demonstrates how to implement a Bayesian synthesis of diverse sources of evidence to calibrate the parameters of a complex model. To illustrate these methods, the authors demonstrate how a previously developed Markov model for the progression of human papillomavirus (HPV-16) infection was rebuilt in a Bayesian framework. Transition probabilities between states of disease severity are inferred indirectly from cross-sectional observations of prevalence of HPV-16 and HPV-16–related disease by age, cervical cancer incidence, and other published information. The authors derive a Bayesian posterior distribution, in which scenarios are implicitly weighted according to how well they are supported by the data.

GUIDELINES AND METHODS

CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2424
This paper discusses methods for the reporting of uncertainty, both in terms of deterministic sensitivity analysis techniques and probabilistic methods. Stochastic (first-order) uncertainty is distinguished from both parameter (second-order) uncertainty and from heterogeneity, with structural uncertainty relating to the model itself forming another level of uncertainty. The article describes the process of estimating model inputs, whether these are point estimates or distributions. It also explores the link between parameter uncertainty, decision uncertainty, and value-of-information analysis.

Recommendations are provided on best choices for reporting, including expected value of perfect information, which is argued to be the most appropriate presentational technique, alongside cost-effectiveness acceptability curves, for representing decision uncertainty from probabilistic analysis.

This paper is one of a 7-part series of articles on modeling good research practices based on a collaboration between the International Society for Pharmacoeconomics and Outcomes Research (ISPOR) and the Society for Medical Decision Making (SMDM). The other articles include:

- Overview: A Report of the ISPOR-SMDM Modeling Task Force-1
This paper discusses how to improve trust in the use of health care models through validation and transparency. Validation involves face validity (wherein experts evaluate model structure, data sources, assumptions, and results), verification or internal validity (check accuracy of coding), cross validity (comparison of results with other models analyzing same problem), external validity (comparing model results to real-world results), and predictive validity (comparing model results with prospectively observed events).

Recommendations are provided for nontechnical description (model type, intended applications, funding sources, structure, inputs, outputs, data sources, validation methods, results, and limitations) as well as technical documentation, which should be written in sufficient detail to enable a reader with necessary expertise to evaluate the model and potentially reproduce it.

This paper is one of a 7-part series of articles on modeling good research practices based on a collaboration between the International Society for Pharmacoeconomics and Outcomes Research (ISPOR) and the Society for Medical Decision Making (SMDM). The other articles include:

- **Overview: A Report of the ISPOR-SMDM Modeling Task Force-1**
- **Conceptualizing a Modeling: A Report of the ISPOR-SMDM Modeling Task Force-2**
- **State-Transition Modeling: A Report of the ISPOR-SMDM Modeling Task Force-3**
- **Modeling Using Discrete Event Simulation: A Report of the ISPOR-SMDM Modeling Task Force-4**
- **Model Transparency and Validation: A Report of the ISPOR-SMDM Modeling Task Force-7**

### Validation and Calibration of Structural Models that Combine Information from Multiple Sources


Not open access.

CHDS repository link: [http://repository.chds.hsph.harvard.edu/repository/2990](http://repository.chds.hsph.harvard.edu/repository/2990)

This is a review of calibration and validation methods in mathematical modeling. Such models that attempt to capture structural relationships between their components and combine information from multiple sources are increasingly used in medicine. The authors provide an overview of methods for model validation and calibration and survey studies comparing alternative approaches. Model validation entails a confrontation of models with data, background knowledge, and other models, and can inform judgments about model credibility.

Calibration involves selecting parameter values to improve the agreement of model outputs with data. When the goal of modeling is quantitative inference on the effects of interventions or forecasting, calibration can be viewed as estimation. This view clarifies issues related to parameter identifiability and facilitates formal model validation and the examination of consistency among different sources of information. In contrast, when the goal of modeling is the
generation of qualitative insights about the modeled phenomenon, calibration is a rather informal process for selecting inputs that result in model behavior that roughly reproduces select aspects of the modeled phenomenon and cannot be equated to an estimation procedure.

Current empirical research on validation and calibration methods consists primarily of methodological appraisals or case-studies of alternative techniques and cannot address the numerous complex and multifaceted methodological decisions that modelers must make. Further research is needed on different approaches for developing and validating complex models that combine evidence from multiple sources.

**Likelihood Approach for Calibration of Stochastic Epidemic Models**


The proposed method applies a linear noise approximation to describe the size of the fluctuations, and uses each new surveillance observation to update the belief about the true epidemic state. Using simulated outbreaks of a novel viral pathogen, the authors evaluate the accuracy of this method (multiple shooting for stochastic systems or MSS) for real-time parameter estimation and prediction during epidemics. They assume that weekly counts for the number of new diagnosed cases are available and serve as an imperfect proxy of incidence.

The authors compare the performance of MSS to three state-of-the-art benchmark methods: 1) a likelihood approximation with an assumption of independent Poisson observations; 2) a particle filtering method; and 3) an ensemble Kalman filter method. They find that MSS significantly outperforms each of these three benchmark methods in the majority of epidemic scenarios tested.

**Calibrating Models in Economic Evaluation**


Models based on scientific knowledge of disease use simplifying assumptions, and contain input parameters with varying levels of uncertainty. Calibration is one tool for estimating uncertain parameters and more accurately defining model uncertainty. Calibration involves the comparison of model outputs with empirical data, leading to the identification of model parameter values that achieve a good fit. The lack of standards in calibrating disease models in economic evaluation can undermine the credibility of calibration methods. In order to avoid public skepticism regarding calibration, the authors present a unified approach to the problem and report the various methods used.
Empirically Evaluating Decision-Analytic Models
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3026
To augment model credibility, evaluation via comparison to independent, empirical studies is recommended. The authors developed a structured reporting format for model evaluation and conducted a structured literature review to characterize current model evaluation recommendations and practices.

As an illustration, they applied the reporting format to evaluate a microsimulation of human papillomavirus and cervical cancer. The model's outputs and uncertainty ranges were compared with multiple outcomes from a study of long-term progression from high-grade precancer (cervical intraepithelial neoplasia [CIN]) to cancer. Outcomes included 5 to 30-year cumulative cancer risk among women with and without appropriate CIN treatment. Consistency was measured by model ranges overlapping study confidence intervals.

The structured reporting format included: matching baseline characteristics and follow-up, reporting model and study uncertainty, and stating metrics of consistency for model and study results. Structured searches yielded 2963 articles with 67 meeting inclusion criteria and found variation in how current model evaluations are reported.

Validation of Population-Based Disease Simulation Models: A Review
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2991/
This article develops a framework for validating population-based chronic disease simulation models, and reviews the principles and methods for such models. While computer simulation models are used increasingly to support public health research and policy, questions about their quality persist.

Based on the review, the authors formulated a set of recommendations for gathering evidence of model credibility. They find that evidence of model credibility derives from examining: 1) the process of model development, 2) the performance of a model, and 3) the quality of decisions based on the model. Many important issues in model validation are insufficiently addressed by current guidelines.

These issues include a detailed evaluation of different data sources, graphical representation of models, computer programming, model calibration, between-model comparisons, sensitivity analysis, and predictive validity. The role of external data in model validation depends on the purpose of the model (e.g., decision analysis versus prediction).

Examples by Disease Area
Empirically Calibrated Model of Hepatitis C Virus Infection in the United States
Not open access.
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3020
This article presents an epidemiologic model of hepatitis C in the United States. The authors used empirical calibration of model parameters to gain insights into uncertainty in the natural history of hepatitis C and to improve future projections.
The authors identified model inputs by way of a systematic review. Model simulations were conducted and model predictions were compared with epidemiologic data on infection prevalence and mortality from liver cancer. Goodness-of-fit criteria were used to identify parameter values that were consistent with these data.

Results indicated that rates of progression to advanced liver disease may be lower than previously assumed. The authors also found a wide range of plausible assumptions about heterogeneity beyond what could be explained by age and sex that were all consistent with observed epidemiologic trends.

Validation and Calibration of a Simulation Model of Pediatric HIV Infection
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2832

The authors developed a microsimulation model of pediatric HIV disease progression using the Cost-Effectiveness of Preventing AIDS Complications (CEPAC) model framework. This CEPAC-Pediatric model was then validated by varying CD4 data and comparing the corresponding model-generated survival curves to empirical survival curves obtained from the International Epidemiologic Database to Evaluate AIDS (IeDEA). The model was calibrated to other African countries by systematically varying immunologic and HIV mortality-related input parameters. In the calibration analyses, the model-generated survival curves were compared against UNAIDS data.

The findings indicated that the model-generated survival curves fit the IeDEA data well (survival at 16 months was 91.2% and 91.1%, respectively). The calibration analyses showed that increases in IeDEA-derived mortality risks were necessary to fit the UNAIDS survival data.

Based on these results, the authors conclude that the CEPAC-Pediatric model is internally valid and that the increases in modeled mortality risks that were required to match the UNAIDS data highlight the importance of pre-enrollment mortality in many pediatric cohort studies.

Assessing the Performance of a Computer-Based Policy Model of HIV and AIDS
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3027

Description of calibration processes serve to enhance the transparency of disease-specific models. This paper reports on the process of adapting a computer-based simulation model of HIV disease to the Women's Interagency HIV Study (WIHS) cohort and assesses model performance to address policy questions in the U.S. relevant to HIV-infected women when using the study data. Calibration targets included 24-month survival curves stratified by treatment status and CD4 cell count.

The authors found that assumptions around chronic HIV-associated mortality following an opportunistic infection in untreated women, effectiveness of HAART and the ability of HAART to prevent complications were the most influential. Once the authors found good-fitting parameter sets, projected rates of treatment regimen switching using the calibrated cohort-specific model closely approximated independent analyses published using data from the WIHS.

The Rise and Fall of HIV in High-Prevalence Countries: A Challenge for Mathematical Modeling
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2624

Several countries with generalized, high-prevalence HIV epidemics, mostly in sub-Saharan Africa, have experienced rapid declines in transmission. These HIV epidemics, often with rapid onsets, have generally been attributed to a combination of factors related to high-risk sexual behavior. The subsequent declines in these countries began prior to
widespread therapy or implementation of any other major biomedical prevention. This change has been construed as evidence of behavior change, often on the basis of mathematical models, but direct evidence for behavior changes that would explain these declines is limited.

In this paper, the authors look at the structure of current models and argue that the common “fixed risk per sexual contact” assumption favors the conclusion of substantial behavior changes. They argue that this assumption ignores reported non-linearities between exposure and risk. Taking this into account, they propose that some of the decline in HIV transmission may be part of the natural dynamics of the epidemic, and that several factors that have traditionally been ignored by modelers for lack of precise quantitative estimates may well hold the key to understanding epidemiologic trends.

Eleven Mathematical Models of TB
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2915
To assess the feasibility of goals to reduce TB incidence and mortality, 11 independent models were empirically calibrated and used to simulate prevention, diagnosis, and treatment strategies in China, India, and South Africa. While drivers of between-model differences were identified, public health findings were robust.

Reduced Burden of Childhood Diarrheal Diseases through Increased Access to Water and Sanitation in India: A Modeling Analysis
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2985
Each year, more than 300,000 children in India under the age of five years die from diarrheal diseases. Clean piped water and improved sanitation are known to be effective in reducing the mortality and morbidity burden of diarrhea but are not yet available to close to half of the Indian population.

This analysis estimates the health benefits (reduced cases of diarrheal incidence and deaths averted) and economic benefits (measured by out-of-pocket treatment expenditure averted and value of insurance gained) of scaling up the coverage of piped water and improved sanitation among Indian households to a near-universal 95% level. The authors use IndiaSim, a previously validated, agent-based microsimulation platform to model disease progression and individual demographic and healthcare-seeking behavior in India, and use an iterative, stochastic procedure to simulate health and economic outcomes over time.

They found that scaling up access to piped water and improved sanitation could avert 43,352 diarrheal episodes and 68 diarrheal deaths per 100,000 under 5 children per year, compared with the baseline. They estimated a savings of (in 2013 US$) $357,788 in out-of-pocket diarrhea treatment expenditure, and $1646 in incremental value of insurance per 100,000 under 5 children per year over baseline. Based on the distribution of benefits, they concluded scaling up access to piped water and improved sanitation could lead to large and equitable reductions in the burden of childhood diarrheal diseases in India.

Modeling Human Papillomavirus and Cervical Cancer in the United States for Analyses of Screening and Vaccination
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3022

This resource pack was developed the Center for Health Decision Science at the Harvard T.H. Chan School of Public Health. All materials produced by the Center for Health Decision Science are free and publicly accessible for educational use.
This paper discusses a model of human papillomavirus (HPV) and cervical cancer that incorporates uncertainty about the natural history of disease that was used to provide quantitative insight into U.S. policy choices for cervical cancer prevention. The authors developed a stochastic microsimulation of cervical cancer that distinguishes different HPV types by their incidence, clearance, persistence, and progression. For each set of sampled input parameters, likelihood-based goodness-of-fit (GOF) scores were computed based on comparisons between model-predicted outcomes and calibration targets that included age-specific prevalence of HPV by type and cervical intraepithelial neoplasia (CIN), HPV type distribution within CIN and cancer, and age-specific cancer incidence.

Approximately 200 good-fitting parameter sets were identified from 1,000,000 simulated sets and the authors used 50 good-fitting parameter sets to assess the external consistency and face validity of the model through comparison of screening outcomes to independent data not used during calibration. Modeled screening outcomes were found to be externally consistent with results from multiple independent data sources. Based on these 50 good-fitting parameter sets, the expected reductions in lifetime risk of cancer with annual or biennial screening were 76% (range 69-82%) and 69% (60-77%) and from vaccination alone was 75% (range 60-88%). The uncertainty was reduced when vaccination was combined with every-5-year screening to 89% (range 83-95%).

Health and Economic Implications of HPV Vaccination in the United States
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3047

This article reports on a study using models of HPV-16 and HPV-18 transmission and cervical carcinogenesis to compare the health and economic outcomes of vaccinating preadolescent girls in the US (at 12 years of age), and vaccinating older girls and women in catch-up programs (to 18, 21, or 26 years of age). The study also examined the health benefits of averting other HPV-16-related and HPV-18-related cancers, the prevention of HPV-6-related and HPV-11-related genital warts and juvenile-onset recurrent respiratory papillomatosis by means of the quadrivalent vaccine, the duration of immunity, and future screening practices. On the assumption that the vaccine provided lifelong immunity, the study authors found that the cost-effectiveness ratio of vaccination of 12-year-old girls was $43,600 per quality-adjusted life-year (QALY) gained, as compared with the current screening practice. Under baseline assumptions, the cost-effectiveness ratio for extending a temporary catch-up program for girls to 18 years of age was $97,300 per QALY; the cost of extending vaccination of girls and women to the age of 21 years was $120,400 per QALY, and the cost for extension to the age of 26 years was $152,700 per QALY. They report that the results were sensitive to the duration of vaccine-induced immunity; if immunity waned after 10 years, the cost of vaccination of preadolescent girls exceeded $140,000 per QALY, and catch-up strategies were less cost-effective than screening alone.

The cost-effectiveness ratios for vaccination strategies were more favorable if the benefits of averting other health conditions were included or if screening was delayed and performed at less frequent intervals and with more sensitive tests. They conclude that the cost-effectiveness of HPV vaccination will depend on the duration of vaccine immunity and will be optimized by achieving high coverage in preadolescent girls, targeting initial catch-up efforts to women up to 18 or 21 years of age, and revising screening policies.

Cost Effectiveness Analysis of Including Boys in a HPV Vaccination Programme in the U.S.
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3046

This article reports on a societal-perspective cost effectiveness analysis of including preadolescent boys in a routine human papillomavirus (HPV) vaccination programme for preadolescent girls. The analysis included girls and boys aged 12 years; interventions included HPV vaccination of girls alone and of girls and boys in the context of screening for cervical cancer. The authors found that with 75% vaccination coverage and an assumption of complete, lifelong vaccine
efficacy, routine HPV vaccination of 12 year old girls was consistently less than $50,000 per QALY gained compared with screening alone. Including preadolescent boys in a routine vaccination programme for preadolescent girls resulted in higher costs and benefits and generally had cost effectiveness ratios that exceeded $100,000 per QALY across a range of HPV related outcomes, scenarios for cervical cancer screening, and assumptions of vaccine efficacy and duration. Vaccinating both girls and boys fell below a willingness to pay threshold of $100,000 per QALY only under scenarios of high, lifelong vaccine efficacy against all HPV related diseases (including other non-cervical cancers and genital warts), or scenarios of lower efficacy with lower coverage or lower vaccine costs. The authors conclude that including boys in an HPV vaccination programme generally exceeds conventional thresholds of good value for money, even under favourable conditions of vaccine protection and health benefits.

Including Boys in an HPV Vaccination Programme: A CEA in a Low-Resource Setting
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3039
This paper looks at the cost-effectiveness of including boys vs girls alone in a pre-adolescent vaccination programme against human papillomavirus (HPV) types 16 and 18 in Brazil. Using demographic, epidemiological, and cancer data from Brazil, the authors developed a dynamic transmission model of HPV infection between males and females. Model-projected reductions in HPV incidence under different vaccination scenarios were applied to a stochastic model of cervical carcinogenesis to project lifetime costs and benefits.

They found that at 90% coverage, vaccinating girls alone reduced cancer risk by 63%; including boys at this coverage level provided only 4% further cancer reduction; at a cost per-vaccinated individual of USD 50, vaccinating girls alone was alone was <USD 200 per year of life saved (YLS), while including boys ranged from USD 810-18,650 per YLS depending on coverage. For all coverage levels, the authors concluded that increasing coverage in girls was more effective and less costly than including boys in the vaccination programme.

Health and Economic Impact of HPV 16/18 Vaccination and Cervical Cancer Screening in Eastern Africa
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3037
In this article the authors use epidemiologic data from Kenya, Mozambique, Tanzania, Uganda, and Zimbabwe to develop models of HPV-related infection and disease. For each country, they assessed HPV vaccination of girls before age 12 followed by screening with HPV DNA testing once, twice, or three times per lifetime (at ages 35, 40, 45). For women over age 30, they assessed only screening (with HPV DNA testing up to three times per lifetime or VIA at age 35). Assuming no waning immunity, mean reduction in lifetime cancer risk associated with vaccination ranged from 36 to 45%, and vaccination followed by screening once per lifetime at age 35 with HPV DNA testing ranged from 43 to 51%.

For both younger and older women, the most effective screening strategy was HPV DNA testing three times per lifetime. Provided the cost per vaccinated girl was less than $150 ($2 per dose), vaccination had an incremental cost-effectiveness ratio [$15 (international dollars)/year of life saved (YLS)] less than the country-specific per capita GDP, a commonly cited heuristic for "very cost-effective" interventions. If the cost per vaccinated girl was between $110 ($2 per dose) and $125 ($5 per dose), vaccination followed by HPV DNA testing would save the most lives and would be considered good value for public health dollars.

The authors suggest that these results should be used to catalyze design and evaluation of HPV vaccine delivery and screening programs, and contribute to a dialogue on financing HPV vaccination in poor countries.
Validating a Cardiovascular Disease Microsimulation Model
Not open access.
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/2918
This paper examines a cardiovascular disease model used to evaluate prevention and treatment of the disease. The authors perform a calibration and validation process, in which simulated results were compared to observed all-cause and CVD-specific mortality data from the National Health and Nutrition Examination Survey. Comparison was conducted using survival curves and ROC curves.

Unifying Screening Processes within the PROSPR Consortium: A Conceptual Model for Breast, Cervical, and Colorectal Cancer Screening
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3031
General frameworks of the cancer screening process are available, but none directly compare the process in detail across different organ sites. This limits the ability of medical and public health professionals to develop and evaluate coordinated screening programs that apply resources and population management strategies available for one cancer site to other sites.

This paper presents a conceptual model that incorporates a single screening episode for breast, cervical, and colorectal cancers into a unified framework based on clinical guidelines and protocols. The model covers four types of care in the screening process: risk assessment, detection, diagnosis, and treatment. Interfaces between different provider teams (e.g., primary care and specialty care), including communication and transfer of responsibility, may occur when transitioning between types of care.

The model highlights across each organ site similarities and differences in steps, interfaces, and transitions in the screening process and documents the conclusion of a screening episode. This model was developed within the National Cancer Institute–funded consortium Population-based Research Optimizing Screening through Personalized Regimens (PROSPR).

Development of an Empirically Calibrated Model of Gastric Cancer in Two High-Risk Countries
CHDS repository link: http://repository.chds.hsph.harvard.edu/repository/3023
This paper presents an empirically calibrated mathematical model of gastric cancer and H. pylori in China and Colombia to provide qualitative insight into the cost-effectiveness of gastric cancer prevention strategies. Despite studies that have established the relationship between Helicobacter pylori and gastric cancer and H. pylori treatment reducing cancer incidence among individuals without preexisting precancerous lesions, screening for H. pylori is still being debated.

The authors synthesized available data to develop a natural history model of noncardia intestinal gastric adenocarcinomas with health states such as normal gastric mucosa, chronic nonatrophic gastritis, gastric atrophy, intestinal metaplasia, dysplasia, and gastric cancer that were all stratified by H. pylori status. A likelihood-based empirical calibration approach was used to identify good-fitting parameter sets consistent with epidemiologic data. A
range of likely outcomes associated with H. pylori screening that incorporated parameter uncertainty were reflected in the results.

**Contribution of H. Pylori and Smoking to US Incidence of Gastric Adenocarcinoma: A Microsimulation Model**
CHDS repository link: [http://repository.chds.hsph.harvard.edu/repository/3036](http://repository.chds.hsph.harvard.edu/repository/3036)

Although gastric cancer has declined dramatically in the US, the disease remains the second leading cause of cancer mortality worldwide. This analysis estimates the contribution of risk factor trends on past and future intestinal-type non-cardia gastric adenocarcinoma (NCGA) incidence.

The authors developed a population-based microsimulation model of intestinal-type NCGA and calibrated it to U.S. epidemiologic data on precancerous lesions and cancer. The model explicitly incorporated the impact of Helicobacter pylori and smoking on disease natural history, for which birth cohort-specific trends were derived from the National Health and Nutrition Examination Survey (NHANES) and National Health Interview Survey (NHIS).

Between 1978 and 2008, the model estimated that intestinal-type NCGA incidence declined 60% from 11.0 to 4.4 per 100,000 men. The authors concluded that trends in modifiable risk factors explain a significant proportion of the decline of intestinal-type NCGA incidence in the US, and are projected to continue. Although past tobacco control efforts have hastened the decline, full benefits will take decades to be realized, and further discouragement of smoking and reduction of H. pylori should be priorities for gastric cancer control efforts.

**Simulation Models of Obesity: A Review of the Literature**
Not open access.
CHDS repository link: [http://repository.chds.hsph.harvard.edu/repository/2817](http://repository.chds.hsph.harvard.edu/repository/2817)

Simulation models combine information from a variety of sources to provide a useful tool for examining how the effects of obesity unfold over time and impact population health. They can aid in the understanding of the complex interaction of the drivers of diet and activity and their relation to health outcomes.

This paper provides an overview of different types of simulation models used to evaluate the potential impact of policies to address the obesity epidemic. The authors discuss the strengths and limitations of different types of models, and review existing obesity models.

The authors categorize existing models according to their focus: health and economic outcomes, trends in obesity as a function of past trends, physiologically-based behavioral models, environmental contributors to obesity, and policy interventions.