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Identifying the Most Significant Microbiological Foodborne Hazards to Public Health: A New Risk Ranking Model

Michael B. Batz, Sandra A. Hoffmann,
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Abstract:

In order to help facilitate a risk-based food safety system, we developed the Foodborne Illness Risk Ranking Model (FIRRM), a decisionmaking tool that quantifies and compares the relative burden to society of 28 foodborne pathogens. FIRRM estimates the annual number of cases, hospitalizations, and fatalities caused by each foodborne pathogen, subsequently estimates the economic costs and QALY losses of these illnesses, and, lastly, attributes these pathogen-specific illnesses and costs to categories of food vehicles, based on outbreak data and expert judgment. The model ranks pathogen-food combinations according to five measures of societal burden. FIRRM incorporates probabilistic uncertainty within a Monte Carlo simulation framework and produces confidence intervals and statistics for all outputs. Gaps in data, most importantly in regards to food attribution and the statistical uncertainty of incidence estimates, currently limit the utility of the model. Once we address these and other problems, however, FIRRM will be a robust and useful decisionmaking tool.

Key Words: foodborne illness, risk ranking, pathogens, health valuation, QALYs, cost of illness, uncertainty, modeling, Monte Carlo

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Introduction

The National Academies of Science, federal food safety agencies, the U.S. General Accounting Office, and numerous other expert bodies embrace the goal of a science- and risk-based food safety system (NRC 1998, 2003; GAO 1997, 2001). In such a system, risk managers prioritize food safety hazards and preventive interventions using the best available data on the distribution of risk and on how risk can be reduced most effectively and efficiently (Taylor and Hoffmann 2001). This requires taking a more integrated systems approach to reducing foodborne illness. Regulators must understand the many factors that contribute to the causation and prevention of foodborne illness from the point of production to the point of consumption and must be able to systematically target efforts in ways that contribute most effectively to risk reduction.

This approach to food safety requires decisionmaking tools and data that, with few exceptions, do not currently exist (Taylor et al. 2003). Specifically, decisionmakers need tools to: (1) identify the most significant risks from a public health perspective; (2) prioritize opportunities to reduce risk, taking into account the feasibility, effectiveness, and cost of possible interventions; and (3) allocate their efforts and resources accordingly.

* Hoffmann is the corresponding author and can be reached at hoffmann@rff.org. All other authors except J. Glenn Morris can be reached at Resources for the Future, 1616 P Street NW, Washington, DC 20036. Morris is the chair of the department of epidemiology and preventive medicine, University of Maryland School of Medicine, Baltimore, Maryland.

To address the first need, we created the Foodborne Illness Risk Ranking Model (FIRRM), an analytical software tool designed to enable decisionmakers to identify, compare, and rank the relative public health impact of 28 foodborne pathogens. Specifically, FIRRM is intended to rank pathogen-food combinations according to five measures of public health impact: estimated number of cases, hospitalizations, and deaths, as well as estimated economic impact and loss of Quality Adjusted Life Years (QALYs). FIRRM is the first comprehensive model to attribute estimates of microbiological foodborne illness to specific pathogen-food combinations, to employ economic and QALY valuation, and to use Monte Carlo simulation to quantify uncertainty.

In doing so, the model combines and furthers much of the research on the topic. This research includes estimates of the incidence of foodborne illness by the Centers for Disease Control and Prevention, or CDC, (Mead et al. 1999) and cost-of-illness studies by the USDA's Economic Research Service, or ERS, (Buzby et al. 1996, Buzby and Roberts 1996, Buzby and Roberts 1997, Frenzen 1999, ERS 2003). It also employs risk assessments by the Food and Drug Administration (FDA), USDA's Food Safety and Inspection Service (FSIS), and others (CFSAN 2000, CFSAN 2003, FSIS 1998, FSIS 2001) and a dataset created by the Center for Science in the Public Interest (CSPI) in which outbreaks are linked to causal food vehicles (DeWaal and Barlow 2002).

Materials and Methods

Presently, FIRRM focuses solely on microbiological foodborne hazards. Chemical as well as waterborne and environmental microbiological risks are clearly important, but require distinct modeling efforts that can be incorporated into the model later. From a regulatory and policy perspective, it is essential that we know which foods are responsible for specific illnesses as well as the relative contribution of these foods to the total disease burden associated with specific foodborne pathogens. Consequently, the

model addresses pathogen-food combinations rather than focusing solely on pathogens. Incidence estimates alone are not sufficient for the comparison of illnesses because different symptoms and severities are associated with different pathogens. The model therefore includes economic and QALY valuation, which incorporate public preferences, to provide a way of comparing different illnesses using a common metric. Finally, the model builds uncertainty into its input variables and results through Monte Carlo simulation, as point estimates exaggerate confidence and may misrepresent the true state of knowledge.

We created FIRRM using Analytica software, a visual modeling and Monte Carlo simulation environment in which mathematical models are developed using functional influence diagrams. Analytica was explicitly designed for risk analysis and risk-informed decisionmaking and is therefore well suited to our functional model needs. Analytica's visual approach and features also meet our usability objectives of transparency, flexibility, adaptability, and accessibility.

Modeling Approach: FIRRM uses a "top-down" epidemiological approach rather than a "bottom-up" microbiological approach to estimating illnesses. To estimate illnesses due to pathogen-food combinations, FIRRM uses surveillance data on pathogen illnesses and then traces these illnesses back to food origin. This is distinguished from conventional risk-assessment approaches, which use food contamination data, predictive microbiology, and consumption patterns to estimate illnesses.

As we are most concerned with ranking public health impacts, we decided to start with observable data gathered as close to these health outcomes as possible, rather than rely on predictions of illnesses based on modeling of microbial risk. In addition, using a predictive microbiological approach would imply performing separate risk assessments on thousands of individual pathogen-food combinations, a frankly impossible task. Finally, for the purpose of risk ranking, computations and data should

be consistent across ranked items. A top-down approach ensures identical methodology across pathogen-food combinations; individual risk assessments are not nearly so directly comparable. Although the top-down approach is preferable for a big-picture comparison of foodborne risks, it is inadequate to isolate the causes of illness along the farm-to-table pathway.

Model Design: FIRRM is composed of three major modules: incidence, valuation of health impacts, and food attribution. In the first module, the annual number of cases, hospitalizations, and deaths from 28 foodborne pathogens are estimated from public health surveillance data; this module includes estimates for the United States as a whole, as well as for the state of Maryland. In the second module, the economic cost and QALY loss associated with a single case of illness are computed for individual pathogens. The third module consists of pathogen-specific food attribution percentages; illnesses from each pathogen are attributed, by percentage, to some set of food vehicles. As discussed in depth at a recent FSRC workshop (FSRC 2003), a fully adequate source for such food-attribution data does not currently exist. Consequently, the model includes two approaches and data sources: (1) outbreak data, which are easily accessible but can offer a distorting picture of risks as cases not tied to an outbreak are ignored and (2) an expert elicitation, which develops attributions based on judgments of food safety experts and may, to some extent, depend on outbreak data (see FSRC 2003 for more detail on these approaches). We have also worked on development of an algorithm to estimate food-attribution percentages based on levels of microbial contamination and food consumption. However, at its current state of development (and reliance on the inconsistent data on food contamination available from published sources), the algorithm does not provide useable solutions.

Estimates of National Incidence: Estimates of the national incidence of pathogen-specific foodborne illnesses are based on the data and methods described in detail in Mead et al. (1999). This approach relies heavily on multiplicative parameters

representing his best judgment on underreporting. Rather than include only his final estimates, Mead's approach and data were built into the model to allow these parameters to be changed, data to be updated, and to allow for the incorporation of uncertainty into Mead point estimates.

Mead bases his estimates on incidence data on 28 bacterial, viral, and parasitic pathogens (see Table 1) from active, passive, and outbreak surveillance sources. The average values of this data are then multiplied by underreporting factors to obtain estimates of the annual number of cases, hospitalizations, and deaths associated with each pathogen.¹ These estimates are multiplied by the percent of illnesses due to each pathogen estimated to come from foodborne sources. Thus, following the Mead approach, annual foodborne cases of illness ($fbcases_p$) of pathogen p can be expressed as

$$fbcases_p = repcases_p * curf_p * surf_p * pctfb_p, \quad (1)$$

where $repcases_p$ is the average annual number of reported cases of illness cause by pathogens, $curf_p$ is the pathogen-specific underreporting factor based on illness symptom severity, $surf_p$ is a sporadic underreporting factor for illnesses estimated from outbreak data, and $pctfb_p$ is the percent of total illnesses estimated to be due to foodborne sources. Similarly, hospitalizations ($fbhosps_p$) and deaths ($fbdeath_p$) due to these foodborne pathogens can be represented by

$$fbhosps_p = repcases_p * rephrate_p * hurf_p * pctfb_p, \text{ and} \quad (2)$$

$$fbdeath_p = repcases_p * repdrate_p * durf_p * pctfb_p, \quad (3)$$

¹ Of 28 pathogens included, estimates for 11 are based on active surveillance data, seven are based on passive surveillance data, and six are based on outbreak surveillance data. Four are based on nonsurveillance data: estimated annual cases due to *Toxoplasma gondii*, *Norovirus*, *Rotavirus*, and *Astrovirus* are based on estimated infection rates applied to the U.S. population. Hospitalizations and deaths for these four pathogens plus *Giardia lamblia* are similarly computed from nonsurveillance data. Incidence estimates based on nonsurveillance data do not use underreporting factors.

where $rephrate_p$ is the reported hospitalization rate ($hurfp$) is the hospitalization underreporting factor ($repdrate_p$) is the reported death rate, and $durf_p$ is the underreporting factor for deaths.

Mead uses point values for all estimates and thus excludes uncertainty from the analysis. For example, Mead reports the range of underreporting associated with *Escherichia coli* O157:H7 cases from a single study to be between 13 and 27, but only uses the midpoint of 20 in calculations. As a result, although Mead estimates 62,458 annual cases of foodborne *E. coli* O157:H7, the uncertainty associated with the underreporting factor implies a possible range of cases from 41,598 to 84,318, or a range of plus-or-minus 35% around the point estimate. Placeholder variables for uncertainty are built into the structure of the model, but as Mead does not report uncertainty values for many key parameters, these variables are largely devoid of values. Using the model's default settings, therefore, estimates of national foodborne incidence are point estimates.

Estimates of Maryland Incidence: The model estimates incidence of nine pathogens for the state of Maryland based on active surveillance data collected as part of the CDC's FoodNet program (CDC 1997, 2003).² This submodule was designed to provide an example of how annual FoodNet data could be used to produce regularly updated estimates of incidence, in contrast to Mead's snapshot estimates (1999).

The dataset included over 1,500 entries of culture-confirmed cases in 1998 and 1999, cleaned of personal identifiers, with the following variables: isolate, serotype, sex, age, sample location, sample source (stool, blood, and so on), month, dates of hospitalization, and outcome (recovered, died, unknown). From these data, we counted the annual number of total reported cases, reported hospitalized cases, reported

² The nine FoodNet pathogens are: *Campylobacter* spp., *Cryptosporidium* spp., *Cyclospora*, *E. coli* O157:H7, *Listeria monocytogenes*, non-typhoidal *Salmonella*, *Shigella* spp., *Vibrio* spp., and *Yersinia enterocolitica*.

physician visits, and reported cases resulting in death. To estimate illnesses from reported data, we used underreporting factors taken from the national 1998 FoodNet Physician Survey and the national 1998–99 FoodNet Community Survey (Imhoff et al. 2000). Whereas Mead’s underreporting factors are pathogen-specific but static over time, FoodNet underreporting factors change over time but are not pathogen-specific.

The total number of annual cases of illness ($cases_{pt}$) for pathogen p and year t is defined as

$$cases_{pt} = hvis_{pt} + phvis_{pt} + nophvis_{pt} . \quad (4)$$

For pathogen p and year t annual physician visits ($phvis_{pt}$) are estimated by multiplying the number of reported physician visits by an underreporting factor to account for the fact that doctors don’t submit samples for every case of diarrheal illness. This underreporting factor is defined as a uniform distribution between two estimates: one drawn from the physician survey and one drawn from the community survey (Imhoff et al. 2000). A small percent of reported physician visits result in hospitalization; these cases must be subtracted from the count of physician visits and included in estimates of the more severe category of hospitalizations. We define the percent of miscategorized physician visits as a uniform distribution between zero and an estimate of this percent from the community survey (Imhoff et al. 2000). Annual hospitalizations ($hvis_{pt}$) are therefore defined as the sum of reported hospitalizations and miscategorized physician visits. Estimated cases with no medical attention ($nophvis_{pt}$) are estimated by multiplying estimated physician visits by an underreporting factor based on the community survey that estimates the number of illnesses in the community for each illness resulting in physician care.

FoodNet collects no data on underreporting of deaths, therefore estimated deaths ($death_{pt}$) is assumed equal to reported deaths.

As Maryland FoodNet data was collected in 1998 and 1999 only for the Baltimore metropolitan area, incidence estimates are scaled up to statewide estimates using U.S. Census county-level population data. Estimates of total annual foodborne cases ($fbcases_p$) may be therefore be expressed as

$$fbcases_p = pctfb_p * \frac{1}{T} \sum_t^T cases_{pt} * \frac{PopM_t}{PopB_t}, \quad (5)$$

where $PopM_t$ is the population of Maryland in year t , $PopB_t$ is the population of Baltimore for the same year, $pctfb_p$ is the estimated percent foodborne, as drawn from Mead, and T is the total number of years of data. Foodborne hospitalizations ($fbhosps_p$) and deaths ($fbdeath_p$) are calculated similarly. While national incidence estimates are point values, Maryland incidence estimates are distributions.

Economic Valuation of Health Effects: FIRRM includes two alternative measures of the economic value of avoiding adverse health effects: cost-of-illness (COI) and willingness-to-pay (WTP). COI is defined as the direct market costs of illness, primarily medical costs and labor market productivity losses. It is widely used in regulatory analysis because it is easy to estimate, but economists agree that it undercounts the economic value of avoiding illness. Economists generally recognize WTP as a more complete health valuation measure. It measures the value that individuals place on specific risk reductions in order to obtain the benefits of such risk reductions (Freeman 2003).

COI and WTP measures are used to value outcomes from health-outcome trees developed in studies from the USDA Economic Research Service (ERS) on the costs of bacterial foodborne disease (Buzby et al. 1996, Buzby and Roberts 1996, Buzby and Roberts 1997, Frenzen 1999, ERS 2003). In these health-outcome trees, total cases of illnesses from a particular pathogen are mapped by symptom, severity, and medical attention required into health-outcome trees unique to each pathogen. Rates of hospitalization, death, and other health effects are used to estimate the annual number

of cases of each health state in the outcome tree. For each health state i , the number of cases is multiplied by the economic value per case of avoiding that health state ($valperhs_i$). Thus, the economic impact of foodborne illnesses due to pathogen p ($fbval_p$) may be expressed as

$$fbval_p = fbcases_p \sum_i^I (valperhs_i * pchsi), \quad (6)$$

where $fbcases_p$ is the number of foodborne cases of pathogen p as defined in equations (1) and (4), and $pchsi$ is the likelihood of health state i . The total number of health states (I) varies by pathogen.

FIRRM includes health-outcome trees for four pathogens – *Campylobacter*, *Escherichia coli* O157:H7, *Listeria monocytogenes*, and nontyphoidal *Salmonella* – drawn directly from ERS studies. We did not create health-outcome trees for additional pathogens due to resource limitations. Although most data in the health-outcome trees are drawn from ERS studies, the two major exceptions are the hospitalization rate and fatality rate. Both national and Maryland estimates of these rates are derived from incidence estimates. Some assumptions in FIRRM also differ from those of ERS. These differences are described in detail in internal model documentation and can easily be changed in the model by the analyst to match ERS assumptions.

COI and WTP estimates for the economic impact of health states are drawn from existing studies, with those on cost-of-illness drawn from ERS studies. Deriving estimates for WTP values is highly resource-intensive, and therefore they are not available for all health states. Estimates of WTP to reduce mortality risk are much more common than those for morbidity. Estimates of WTP to reduce mortality risk (commonly referred to as the value of a statistical life (VSL)) are taken from several studies, some of which vary by age and some of which do not (Krupnick et al. 2002; Landefeld and Seskin 1982; Mrozek and Taylor 2002; Viscusi 1993; EPA 1997, 1999). These include studies used by ERS and the Environmental Protection Agency in their

regulatory benefits analysis. For health states without available WTP values, empty placeholder variables are built into the model; COI estimates are used as default values. Further research is needed to provide estimates of WTP to fill in these placeholder variables.

QALY Valuation of Health Effects: FIRRM also includes valuation of health effects in Quality Adjusted Life Years (QALY), an alternative to economic valuation commonly used in the public health community (Gold 1996). QALY loss is computed in the model similarly to economic cost; health states in a pathogen’s health-outcome tree are individually valued and summed. Thus, the QALY loss of foodborne illnesses ($fbqaly_p$) due to pathogen p , may be expressed as

$$fbqaly_p = fbcases_p \sum_i^I (qalyperhs_i * pcths_i), \quad (7)$$

where $qalyperhs_i$ is the per-case QALY loss of a health state i , and the remaining variables are the same as defined in equation (6).

QALYs are estimated for a health state by multiplying a health index, defined as a value between zero for death and one for perfect health, by the duration of the health state in years. There are numerous health indices available to estimate QALYs based on different approaches and assumptions. FIRRM uses the Quality of Well-Being (QWB) index, which is based on four component scores – Mobility, Physical Activity, Social Activity, and Symptom/Problem Complex – that are computed for each health state (Kaplan et al. 1979, Kaplan et al. 1998). The QWB index was selected for ease of use and because resource limitations precluded the extensive research required to implement the Health Utility Index (Feeny et al. 1996; Furlong et al. 1998) or other indices.

In our model, QALY loss is defined as the difference between the baseline health index of a population and the health index associated with a particular negative health state, multiplied by the average duration of the health state. Thus, the per-case QALY loss ($qalyperhs_i$) of health state i , as required for equation (7), can be expressed as

$$qalyperhs_i = (qwb_{baseline} - qwb_i) * dur_i, \quad (8)$$

where $qwb_{baseline}$ and qwb_i are the QWB scores for the baseline health state and a health state, i , respectively, and dur_i is the duration of that health state.

Food Categories for Food Attribution: To attribute illnesses to foods, FIRRM relies on a two-tier food categorization scheme adapted from the scheme developed by Center for Science in the Public Interest (CSPI) for their analyses of outbreak data from CDC and other sources (DeWaal and Barlow 2002). We modified the CSPI food categorization scheme to make it more appropriate for the model; the final scheme is shown in Table 2. The model's food categories are explained in more detail in FSRC (2002) and in internal model documentation.

Food Attribution from Outbreak Data: The outbreak method of food attribution is based on analysis of CSPI's compilation of outbreak data, in which each outbreak has been traced to an implicated food vehicle. These data include primarily unpublished CDC data obtained through Freedom of Information Act requests, but also include additional outbreak reports collected and verified by CSPI. Of the 2,472 outbreaks listed in the September 2002 Outbreak Alert, 300, or 12.1%, were not from CDC sources (DeWaal and Barlow 2002). After pathogens not in FIRRM were excluded, the dataset contained entries for 1,977 outbreaks, representing 83,619 individual cases of foodborne illness.

The food vehicles in the outbreak attribution dataset were categorized into the two-tier scheme previously discussed. For each pathogen, food-attribution percentages were computed by dividing the number of cases due to each pathogen-food combination by the total number of cases due to that pathogen. Food-attribution percentages therefore sum to 100% for a single pathogen across all food categories.

Food Attribution from Expert Elicitation Results: We designed and implemented an expert elicitation survey, in which experts were asked to estimate, for

each pathogen, the percentage of illnesses attributable to each food vehicle. The survey was developed, with the aid of Dr. Paul Fischbeck, Carnegie Mellon University, a recognized authority in the field of expert elicitation, using standard methodologies found in the literature (Morgan et al. 1990; Cooke 1991). The survey included 11 major pathogens and elicited uncertainty bounds around responses.³ The survey was sent to a peer-reviewed list of 101 scientists, public health officials, and food safety policy experts; we received 45 responses. The model includes an average of experts' best judgment estimates of attribution percentages. Work is under way to further analyze survey results.⁴

Computing Rankings: To compute risk rankings, the model combines results from the three aforementioned modules. For each pathogen, foodborne incidence from the first module and valuation of health outcomes from the second module are multiplied by the food attribution percentages from the third module to obtain incidence and valuation by pathogen-food combination. The primary output of the model is a risk ranking of pathogen-food combinations, sorted by one of the five measures of estimated annual public health burden: number of total cases, number of hospitalizations, number of deaths, economic cost, and QALY loss.

³ The survey asked respondents to give low, high, and best-guess estimates and asked them to rate their expertise on individual pathogens and individual food categories on a scale from 1 to 5.

⁴ The model also includes the option of using the results of a series of risk assessments on *Listeria monocytogenes* in 23 ready-to-eat (RTE) foods performed by FDA, USDA, and CDC (CFSAN 2003). The risk assessments estimated the number of annual illnesses due to *Listeria* in each food item, which were classified into the major food categories in the model. Food attribution percentages were computed by dividing the number of estimated cases in each food category by the total estimated cases of *Listeria* from all 23 risk assessments.

Results and Discussion

The results produced by FIRRM are only preliminary. There are a significant number of areas in which data are missing or thin; there are other modules, namely in valuation and food attribution, that have yet to be fully designed and programmed; and uncertainty is not fully incorporated into many model input variables. Thus, it would be premature for us to draw strong policy conclusions from the ranking results produced by the model. Nonetheless, results strongly support the value of the underlying methodology to food safety policy analysis and highlight the importance of some key attributes of the model.

Pathogen-Food Combinations: The results show quite clearly how risk rankings are sensitive to whether pathogens or pathogen-food combinations are being ranked. For example, Table 3 shows that while only three pathogens cause the vast majority of annual foodborne hospitalizations, these illnesses are spread across a large number of foods. The top-ranked pathogen may be *Norovirus*, but *Salmonella* in egg dishes is the most significant pathogen-food combination. This type of ranking enables the comparison of specific disease pathways in the food safety system and points towards development of more efficient intervention strategies.

Measures of Public Health Burden: The results show that rankings are sensitive to the outcome measure. For the four pathogens for which economic and QALY valuation were completed, Table 4 shows that while *Campylobacter* causes more cases of foodborne illness than any of the other pathogens, *Salmonella* causes the most hospitalizations and deaths and is likewise the most expensive. Economic valuation is driven largely, though not entirely, by the value of statistical life (VSL) used to value mortality risks. The default VSL is \$2.39 million (2001\$), drawn from Mrozek and Taylor (2002); if a significantly lower VSL is chosen, such as Krupnick's \$720,000 (2001\$) estimate (2002), *Campylobacter* becomes the most expensive pathogen due to its greater incidence. *Salmonella* and *Listeria* have similar economic costs for although *Salmonella* is

associated with far more hospitalizations; *Listeria* hospitalizations are far more severe and costly. Estimates of QALY loss for the two pathogens differ greatly, however, because of the difference in the age distributions of those affected. As those who die from *Salmonella* are, on average, much younger than those who die from *Listeria*, the number of life years lost per case (assuming a baseline population lifespan) are greater for *Salmonella*.

Food attribution complicates the matter. Table 5 shows the same pathogen-food combinations shown in Table 3 for all five health-outcome measures, sorted by hospitalizations. There is little agreement as to which is the most significant public health risk; *Salmonella* from egg dishes, *Norovirus* from shellfish, and *Listeria* from luncheon meats all rank highest by different outcome measures. As the model only includes economic valuation for four pathogens, these values are missing for some key pathogen-food combinations. Indeed, these missing values suggest the importance of completing economic valuation components of the model for both *Norovirus* and *Toxoplasma*.

Methods of Food Attribution: Table 6 shows food-attribution percentages for *Campylobacter* and *Listeria* using the expert elicitation, outbreak data, and a series of *Listeria* risk assessments. According to outbreak data, only 16% of *Campylobacter* illnesses are due to the food category of “Poultry.” Experts note the limitations of outbreak data for a largely sporadic illness with few outbreaks and estimate that percentage to be nearly 70%, citing a reliance on case control data. Percentages for *Listeria* show greater similarities across attribution methods, though they still differ. *Listeria* outbreaks were recorded only in four food categories, whereas experts associate at least minor *Listeria* risk with every food category. Food-attribution percentages drawn from the CFSAN/FSIS risk assessment on *Listeria monocytogenes* are also shown, though they are not directly comparable to the other two approaches, as the risk assessments were only performed on 23 ready-to-eat food items in only five of the

model's food categories. Nonetheless, the risk assessments agree with the two other approaches that luncheon meats and dairy are the two most important food categories for *Listeria*.

Uncertainty: The model includes various measures of statistical uncertainty for output variables, but too few input parameters are currently defined with uncertainty distributions to make formal analyses meaningful. To produce ranking results with appropriate measures of uncertainty, the model must be further developed to include input uncertainties associated with a number of variables, including reported disease incidence, incidence underreporting multipliers, food attribution from outbreaks and expert elicitation data, and others. Currently, the primary driver of uncertainty bounds around model outputs is that associated with per-case valuation estimates. Under default settings, the estimated annual mean cost of foodborne *Salmonella* and *Campylobacter* are \$1.6 billion and \$1.4 billion, respectively. The fifth and 95th percentile values for *Salmonella* COI are \$1.4 billion to \$1.8 billion. Those for *Campylobacter* COI are far broader – \$730 million to \$2 billion. The bounds around these mean values will increase dramatically when uncertainty associated with incidence estimates and food attribution is included.

Conclusion: Although FIRRM is in a preliminary stage of development and is too incomplete to use to make policy recommendations, the ranking results highlight both the long-term potential of the model as a policy tool and the areas in which there is a critical need for further data collection and parameter estimation. In making Mead's incidence estimates transparent, the model underscores the need for explicitly considering uncertainty about underreporting multipliers. The model demonstrates how active surveillance data from FoodNet might be used to produce continually updateable estimates of incidence at a state or national level and provides a tool for comparing FoodNet data with incidence estimates derived using Mead's methodology. The model demonstrates the importance of economic valuation of illnesses, as the most

costly illnesses may not be those that are the most common, while also showing that the costs of illness vary greatly depending on assumptions about the value of reducing mortality risk. Perhaps most strikingly, the model highlights the inadequacy of existing food attribution data and shows explicitly how different attribution methods and data sources can lead to profoundly distinct outcomes. Overall, however, the model successfully integrates disparate data sources in a transparent and straightforward manner and will have increasing utility as additional – and better – data are added and its structure is further refined.

Tables

Table 1: Pathogens in FIRRM (Mead Pathogens)

Bacteria		Parasites
<i>Bacillus cereus</i>	<i>Salmonella typhi</i>	<i>Cryptosporidium parvum</i>
<i>Brucella</i> spp.	<i>Salmonella nontyphoidal</i>	<i>Cyclospora cayetanensis</i>
<i>Campylobacter</i> spp.	<i>Shigella</i> spp.	<i>Giardia lamblia</i>
<i>Clostridium botulinum</i>	<i>Staphylococcus</i> spp.	<i>Toxoplasma gondii</i>
<i>Clostridium perfringens</i>	<i>Streptococcus</i> spp.	<i>Trichinella spiralis</i>
<i>E. coli</i> O157:H7	<i>Vibrio cholerae</i> toxigenic	Viruses
<i>E. coli</i> non-O157 STEC	<i>Vibrio vulnificus</i>	Norovirus
<i>E. coli</i> enterotoxigenic	<i>Vibrio</i> other	Rotavirus
<i>E. coli</i> other diarrheogenic	<i>Yersinia enterocolitica</i>	Astrovirus
<i>Listeria monocytogenes</i>		Hepatitis A

Table 2: Food Categories Used in the Foodborne Illness Risk Ranking Model

Major category	Subcategory	Major category	Subcategory
Seafood	Finfish	Breads and Bakery	Breads
	Molluscan Shellfish		Bakery
	Other Seafood		Breads and Bakery Combo
	Seafood Dishes	Game	Game
	Seafood Combo	Beef	Ground Beef
Eggs	Eggs		Other Beef
	Egg Dishes		Beef Dishes
	Eggs Combo	Poultry	Chicken
Produce	Fruits		Turkey
	Vegetables		Other Poultry
	Produce Dishes		Chicken Dishes
	Produce Combo	Turkey Dishes	
Beverages	Juices	Pork	Ham
	Other Beverages		Other Pork
	Beverage Combo		Pork Dishes
Dairy	Milk	Luncheon/ Other Meats	Luncheon Meats
	Cheese		Other Meats
	Ice Cream		Other Meat Dishes
	Other Dairy	Multi-Source	USDA
	Dairy Combo		FDA
Multi-ingredient	Salads	Multi-Source	Both USDA/FDA
	Rice/Beans/Stuffing/Pasta Dishes		Unattributable
	Sandwiches		
	Sauces/Dressings/Oils		
	Other Foods		
	Multi-ingredient Combo		

Table 3: Top Pathogens and Pathogen-Food Combinations, Ranked by Estimated Annual Hospitalizations, Using Default Model Settings

Rank	Pathogen	Hospitalizations ^a	Pathogen-Food Combination	Hospitalizations ^b
1	<i>Norovirus</i>	20,000	<i>Salmonella</i> nontyphoidal / Egg dishes	4,219
2	<i>Salmonella</i> nontyphoidal	15,610	<i>Norovirus</i> / Molluscan shellfish	3,247
3	<i>Campylobacter</i>	10,540	<i>Norovirus</i> / Multi-Ingredient salads	3,053
4	<i>Toxoplasma gondii</i>	2,500	<i>Norovirus</i> / Produce dishes	2,963
5	<i>Listeria monocytogenes</i>	2,298	<i>Campylobacter</i> / Vegetables	2,623
6	<i>E. coli</i> O157:H7	1,843	<i>Toxoplasma gondii</i> / Unattributable food	2,500
7	<i>Staphylococcus</i>	1,753	<i>Campylobacter</i> / Milk	2,045
8	<i>Shigella</i>	1,246	<i>Norovirus</i> / Fruits	1,881
9	<i>Yersinia enterocolitica</i>	1,105	<i>Campylobacter</i> / Chicken	1,522
10	<i>E. coli</i> non-O157 STEC	921	<i>Norovirus</i> / Vegetables	1,299
11	Hepatitis A	542	<i>Campylobacter</i> / Produce dishes	1,148
12	Rotavirus	500	<i>Salmonella</i> nontyphoidal / Vegetables	1,085
13	<i>Giardia lamblia</i>	500	<i>Listeria monocytogenes</i> / Luncheon meats	990
14	<i>Salmonella typhi</i>	494	<i>Norovirus</i> / Bakery	937
15	<i>Streptococcus</i>	356	<i>E. coli</i> non-O157 STEC / Unattributable food	921

^a Mean estimated annual foodborne hospitalizations for the United States.

^b Mean estimated annual foodborne hospitalizations for the United States, attributed to food sub-categories using outbreak data. The food category “Unattributable food” implies that there were not enough outbreaks of that pathogen in the outbreak dataset to attribute estimated illnesses from that pathogen to food categories.

**Table 4: Measures of Public Health Burden for Four Major Pathogens,
Using Default Model Settings^a**

Pathogen	Cases	Hospital- izations	Deaths	Cost (\$Millions)	QALY Loss
<i>Campylobacter</i>	1,963,141	10,539	103	1,397	8,727
<i>E. coli</i> O157:H7	62,458	1,843	52	232	2,003
<i>Listeria monocytogenes</i>	2,493	2,298	499	1,604	8,795
<i>Salmonella</i> nontyphoidal	1,341,873	15,608	551	1,607	14,400

^a Mean annual foodborne estimates for the United States. Costs are in 2001 dollars.

Table 5: Rankings of Pathogen-Food Combination by Measures of Public Health Burden, Sorted by Hospitalizations, Using Default Model Settings^a

Pathogen-Food Combination	Hospital				
	-izations	Cases	Deaths	Cost ^b	QALY ^b
<i>Salmonella</i> nontyphoidal / Egg dishes	1	10	3	3	1
<i>Norovirus</i> / Molluscan shellfish	2	1	19	N.A.	N.A.
<i>Norovirus</i> / Multi-ingredient salads	3	2	24	N.A.	N.A.
<i>Norovirus</i> / Produce dishes	4	3	25	N.A.	N.A.
<i>Campylobacter</i> / Vegetables	5	6	12	4	4
<i>Toxoplasma gondii</i> / Unattributable food	6	25	1	N.A.	N.A.
<i>Campylobacter</i> / Milk	7	9	20	5	5
<i>Norovirus</i> / Fruits	8	4	33	N.A.	N.A.
<i>Campylobacter</i> / Chicken	9	12	28	7	6
<i>Norovirus</i> / Vegetables	10	5	38	N.A.	N.A.
<i>Campylobacter</i> / Produce dishes	11	17	34	8	9
<i>Salmonella</i> nontyphoidal / Vegetables	12	28	6	9	8
<i>Listeria monocytogenes</i> / Luncheon/other meats	13	160	2	1	2
<i>Norovirus</i> / Bakery	14	7	41	N.A.	N.A.
<i>E. coli</i> nonO157 STEC / Unattributable food	15	60	13	N.A.	N.A.

^a Mean annual foodborne estimates for the United States, attributed to food sub-categories using outbreak data. The food category “Unattributable food” implies that there were not enough outbreaks of that pathogen in the outbreak dataset to attribute illnesses to food categories.

^b Economic valuation and QALY loss are currently estimated in FIRRM only for four pathogens and therefore rankings by dollars and QALYs are “Not Available (N.A.)” for *Norovirus*, *Toxoplasma gondii*, and *E. coli* non-O157 STEC.

Table 6: FIRRM Food Attribution Percentages for Illnesses from Foodborne *Campylobacter* and *Listeria monocytogenes*

Food Category	<i>Campylobacter</i>		<i>Listeria monocytogenes</i>		
	Outbreak Cases	Expert Elicitation	Outbreak Cases	Expert Elicitation	RTE Risk Assessments ^a
Seafood	9.1	0.9	0.0	6.8	1.3
Eggs	0.0	2.3	0.0	0.3	N.A.
Produce	39.3	5.1	0.0	8.4	14.1
Beverages	0.0	0.0	0.0	0.2	N.A.
Dairy	21.0	7.4	32.0	22.8	24.5
Breads and Bakery	0.0	0.0	6.3	0.2	N.A.
Multi-ingredient/Other	6.8	3.9	0.0	3.7	0.1
Game	0.0	1.9	0.0	0.3	N.A.
Beef	5.0	4.2	0.0	1.5	N.A.
Poultry	16.4	69.4	4.3	2.6	N.A.
Pork	0.7	4.1	0.0	1.2	N.A.
Luncheon/Other Meats	1.8	0.9	57.3	52.1	60.1
Total	100.0	100.0	100.0	100.0	100.0

^a CFSAN/FSIS risk assessments for *Listeria* were solely for ready-to-eat foods, and therefore did not include foods in all categories (CFSAN 2003). As a result, food attribution percentages are “Not Available (N.A.)” for certain food categories.

Note: Columns do not total 100 because of rounding.

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