FSIS Risk Assessment for Guiding Public Health-Based Poultry Slaughter Inspection: An Implementation Scenario-Based Approach

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EXECUTIVE SUMMARY

Background

The Food Safety and Inspection Service (FSIS) conducted this risk assessment to help inform proposals to change allocation of inspection personnel in poultry slaughter establishments.

FSIS on-line inspectors currently conduct hands-on appraisals of every poultry carcass to ensure each carcass is unadulterated, free of feathers, bruises, and defects and disease. FSIS off-line inspectors verify that establishments maintain sanitary operations and perform other public health -related assignments. However, many of these on-line inspection tasks are in fact related to food quality, rather than aligning with the FSIS mission of food safety. This risk assessment considers scenarios that might allow FSIS to target resources more efficiently, by allowing FSIS inspection personnel more time and flexibility to perform off-line inspection tasks based on human health risk factors specific to individual establishments, with the goal of providing net public health benefit.

This risk assessment updates a 2008 risk assessment (FSIS, 2008a), originally presented in conjunction with a review by the National Advisory Committee on Meat and Poultry Inspection (NACMPI, 2008; FSIS 2011) with more recent data and a modified modeling approach. This risk assessment takes into consideration public and stakeholder comments on the 2011 version [Docket No. FSIS-2011-0012], and has been modified in response to an independent peer review completed in August 2012.

Risk Management Questions

- *Can FSIS reallocate inspection activities in young chicken slaughter establishments without significant negative impact on microbial prevalence in the establishments?*
- *How will the relocation of on-line inspectors to off-line duties, or other areas within or outside the establishment, affect human illness?*
- *Where within the establishment can relocated inspection activities have the most impact toward reducing microbial prevalence and corresponding human illness?*
- *What is the uncertainty about these effects?*

Structure and Scope

This is a quantitative probabilistic food safety risk assessment. It examines the relationships between variations in inspection activities in FSIS-regulated poultry slaughter establishments and the prevalence of both *Salmonella* and *Campylobacter* on poultry (specifically young chicken and young turkey). The model predicts the probability of changes in prevalence of these pathogens that would subsequently be directly translated into changes in attributable human illnesses.

Figure ES-1 provides an overview of the two analytical stages conducted as part of this risk assessment. In Stage 1, a regression model uses historical data to characterize the relationship between specific categories of off-line inspection procedures and contamination of chicken or turkey carcasses with either *Salmonella* or *Campylobacter* (specifically, four product-pathogen pairs: young chicken-*Salmonella*, young chicken-*Campylobacter*, young turkey-*Salmonella*, and young turkey-*Campylobacter*). The four categories of off-line inspection procedures examined in the regression model are: 1) scheduled-and-performed procedures [SP]; 2) scheduled-and-not-performed procedures [SNP]; 3) unscheduled procedures [U]; and observed and recorded non compliances [NC].

The relationship characterized in Stage 1 is then used as input to Stage 2 of the risk assessment, the simulation model. The simulation model is designed to explore the effect of various potential changes in those same four categories of off-line inspection activities (SP, SNP, U and NC; termed the decision variables in the simulation model) on changes in human *Salmonella* or *Campylobacter* illnesses attributable to the consumption of young chicken and young turkey. In that way, scenarios representing different potential changes in those inspection activities that FSIS might consider—that is, different values in the decision variables—can be modeled to evaluate how relocation of on-line to different off-line duties would change the proportion of samples testing positive from poultry carcasses, thereby changing the probability of human illnesses.

Two approaches to changing the decision variables are the main focus of this risk assessment. In the first approach, referred to as the "indiscriminant scenario," allows the values of decision variables (that is, the percentage increase of each of the four categories of inspection procedures input into the model) to vary for each iteration or run of the statistical model within a broad range of expected values. This scenario estimates the range of potential effects associated with increasing any combination of its inspection procedures. It is important to note that with this indiscriminant scenario alternately selects from among the four off-line procedure categories identified above, without targeting any one. As such, this scenario includes exploration of the effect of an increase of procedures that might conceivably be correlated with an increase in contamination that is observed and recorded non compliances [NC]. This indiscriminant scenario

does, however, allow the sensitivity of the model to the four decision variables to be investigated to identify the types of offline inspection procedures that could have the greatest public health impact.

The second approach, referred to as the "discriminate scenario," focuses on the probability of changes in prevalence of the pathogens if one specific category of inspection procedures, unscheduled procedures, is targeted for increase. To do that, the value of the decision variable for unscheduled procedures [U] is increased while the values of the other three decision variables [SP, SNP and NC] are kept constant at baseline levels. Unscheduled procedures are increased in establishments in the HACCP Inspection Models Project (HIMP); therefore, increasing the unscheduled procedures in the simulation model allows estimation of the probability that having other establishments increase those procedures would change the prevalence of the pathogens that would subsequently be translated into changes in attributable human illnesses. In addition, there are data-driven reasons to focus on increasing unscheduled procedures. As discussed later, the regression analysis conducted in Stage 1 of this assessment indicated that the unscheduled decision variable had the most consistent strong correlation with product contamination. That correlation suggests that increasing unscheduled procedures would have the greatest likelihood (that is, would likely be the most effective) of decreasing product contamination leading to benefits. Focusing on this decision variable, therefore, allowed characterization of the relocation of inspection activities most likely to have a beneficial impact.

Data used in the risk assessment include:

1. Inspection activity data recorded in FSIS' PBIS database, paired with *Salmonella* and *Campylobacter* prevalence data for the same establishments and timeframes. The sources of the pathogen data are:
    - Young chicken data:
        - *Salmonella* and *Campylobacter* data from FSIS' Young Chicken Baseline study (rehang and post chill samples) (July 2007 through September 2008) (6,558 samples for each pathogen); and
        - *Salmonella* data from the FSIS PR/HACCP verification program (post chill samples) (July 2007 through September 2010) (16,115 *Salmonella* samples)[1].
    - Young turkey data:
        - *Salmonella* and *Campylobacter* data from FSIS' Young Turkey Baseline study (rehang and post chill samples) (August 2008 through July 2009) (2,884 samples for each pathogen); and
        - *Salmonella* data from the PR/HACCP verification program (post chill samples) (July 2007 through September 2010) (5,865 *Salmonella* samples).

[1] FSIS' PR/HACCP verification program did not analyze poultry samples for Campylobacter until July, 2011.

2. Human illness data, i.e. estimates for the mean number of human *Salmonella* and human *Campylobacter* illness attributable to young chicken and turkey consumption, based on distribution parameters from Centers for Disease Control and Prevention (CDC) total foodborne illness and outbreak data (CDC, 2001-2007).

As can be seen above, the number of samples for each product-pathogen pair varies. There is greater confidence in the results of the analyses for those product-pathogen pairs with larger sample sizes. Greater certainty in model estimates, therefore, should be given to estimates based on those larger sample sizes.

The number of inspection procedures also varies among the four procedure categories (i.e., SP, SNP, U and NC). There are fewer procedures that are scheduled-and-not-performed [SNP] or observed and recorded non compliances [NC] than scheduled-and-performed [SP] or unscheduled [U]. That variability affects the confidence in estimates and should also be considered when interpreting the model results.

The risk model incorporates the uncertainty about: (i) the initial analyses and data used; (ii) the expected changes in off-line inspection activities with the proposed inspection system, and (iii) current estimates of human illnesses, into its predictions about the change in human illnesses expected to occur as a result of implementation of the proposed inspection system. Table ES-1 summarizes the information available and assumptions in the risk assessment. Table ES-2 summarizes key uncertainties in the risk assessment.

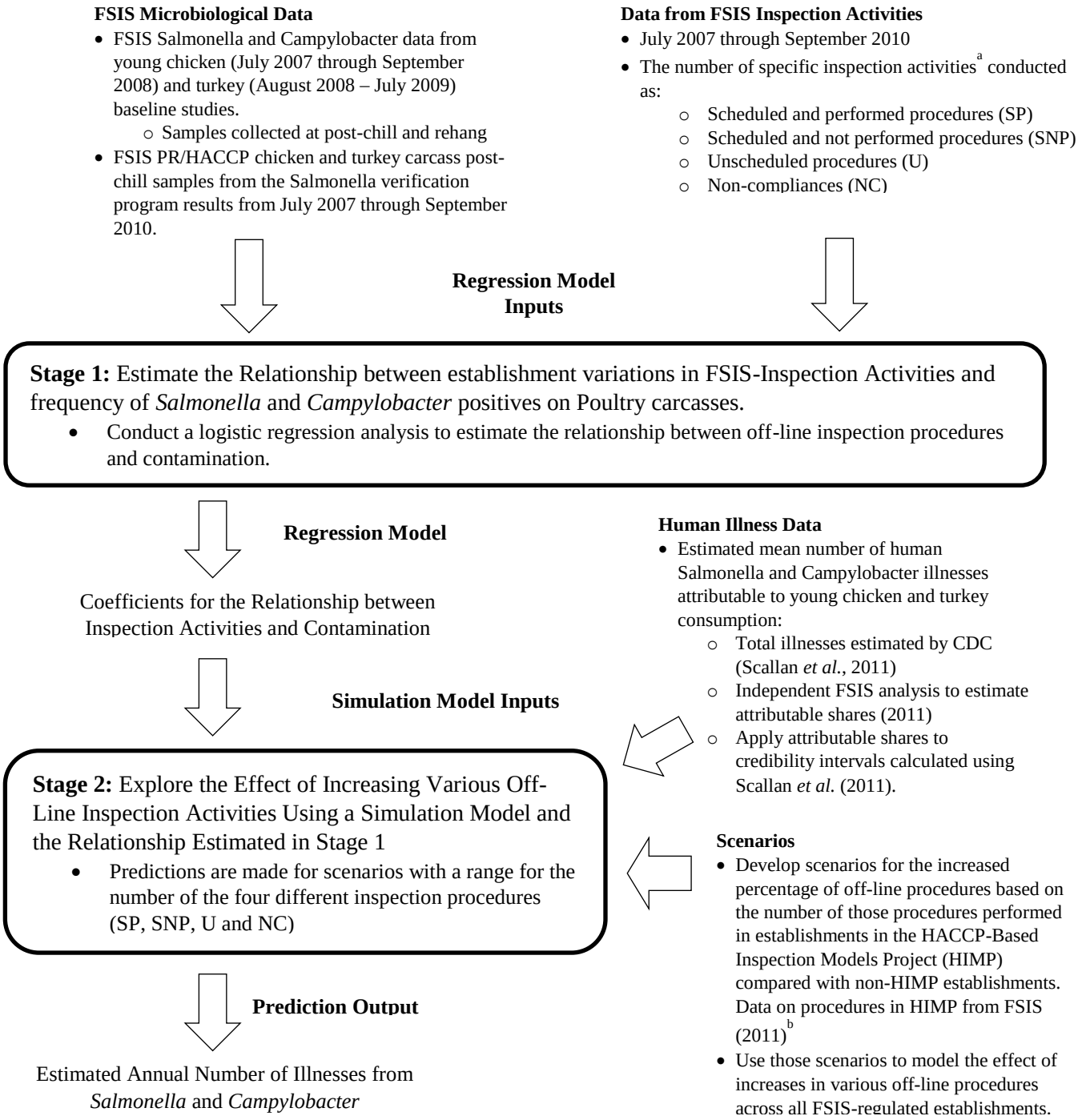

Figure ES-1. Overview of the Risk Assessment.
The figure summarizes the two major stages of the risk assessment of alternative scenarios, and the inputs and outputs from those stages.

[a] The ten specific inspection activities analyzed are: sanitation(01), HACCP (03), wholesomeness/economic consumer protection (04), sampling (05), other inspection requirements (06), sanitation performance standards (06D01), raw ground (03B), raw not ground (03C), fecal checks (03J), and economic poultry kill (04C04).

[b] *Evaluation of the HACCP-Based Inspection Models Project* (FSIS, 2011a) is available at http://www.fsis.usda.gov/shared/PDF/Evaluation_HACCP_HIMP.pdf.

Table ES-1. Available Information and Assumptions in the Risk Assessment

Information Required	Available Data	Assumptions
Stage 1: Estimate Relationship Between Establishment Variations in FSIS-Inspection Activities and Frequency of *Salmonella* and *Campylobacter* Proportions Positives on Poultry Carcasses using a Production Volume-weighted logistic regression model.		
Inspection Data	• FSIS establishment-level data on the number of specific inspection activities[a] conducted from July 2007 through September 2010, stored in PBIS	Data are representative of the young chicken and turkey slaughter establishments
Microbiological Data	• FSIS establishment-level *Salmonella* and *Campylobacter* data from young chicken (July 2007 through September 2008) and turkey (August 2008 – July 2009) baseline studies (post-chill and rehang) • Establishment-level FSIS PR/HACCP chicken and turkey carcass post-chill samples from the Salmonella verification program results from July 2007 through September 2010 (post-chill)	Data are representative of the young chicken and turkey slaughter establishments
Production Volume Data	• FSIS establishment-level production volume data	
Stage 2: Explore the potential implications for risk of Increasing Various Off-Line Inspection Activities Using a Simulation Model and the Statistical Relationship Estimated in Stage 1 and the Relationship between *Salmonella* and *Campylobacter* Contamination and human illness		
Estimated mean number of human *Salmonella* and *Campylobacter* illnesses attributable to young chicken and turkey consumption	• Independent FSIS analysis to estimate attributable shares (2011)[b]	
	• The total annual number of *Salmonella* and *Campylobacter* illnesses in the United States is estimated by CDC (Scallan *et al.*, 2011). Then apply attributable shares (FSIS, 2011b)[b] to credibility intervals calculated using Scallan *et al.* (2011)	• Human illnesses can be modeled as a Poisson process because in microbial food safety, sporadic exposure events are considered independent events and chronic exposures to pathogens are not considered
Relationship between *Salmonella* and *Campylobacter* on chicken and turkey carcasses and human *Salmonella* and *Campylobacter* illnesses	• The relationship between product contamination and human illnesses has been published previously[c]	• The probability that exposure to a random contaminated serving would produce illness is constant regardless of changes in the frequency of exposure to the pathogen on a per serving basis (that is, dose levels at consumption are independent of the frequency of contamination)[d]
Distribution of establishments that would accept the proposed inspection system	• No empirical data, therefore, use estimates from FSIS' Preliminary Regulatory Impact Analysis (PRIA) of the proposed poultry slaughter rule.	• All establishments perform offline inspection procedures after implementation at levels equivalent to HIMP establishments within the data range used.

Information Required	Available Data	Assumptions
Percentage of off-line inspection procedures that would be conducted in each establishment under the proposed inspection system	• No empirical data available, therefore, different scenarios were developed on the basis of the increased percentage of off-line procedures performed in establishments in the HIMP compared with non-HIMP establishments (FSIS, 2011a)[b]. Those scenarios are used to model the effect of increased off-line procedures across all FSIS-regulated establishments and compared to the 'baseline' of current establishment activities. Assumptions specific to the two different scenarios are outlined below.	• There would be a shift of the majority of on-line inspectors to off-line inspection duties while leaving one inspector on-line for final carcass inspection.[e] The proposed increase in off-line inspectors is expected to increase scheduled and performed procedures.[f] Similarly, increased availability of off-line inspectors should increase unscheduled procedures while reducing scheduled but not performed procedures.[g] • An estimate of the distribution for off-line inspection activities performed upon implementation of the proposed inspection system would reflect the distribution for off-line inspection activities observed in establishments currently operating under HIMP
	Indiscriminate Scenario (No assumption of how FSIS might emphasize or de-emphasize activities in proposed inspection system)	• SP and U procedures: assumed the most likely change is an increase of 25%, a minimum of no change and a maximum of a 60% increase • SNP procedures: assumed the most likely change is a decrease of 10%, a minimum of no change and a maximum of 100% reduction
	Discriminate Scenario (assumes FSIS would emphasize the performance of unscheduled procedures in proposed inspection system	• Unscheduled procedures increase while other three (SNP, SP, NC) are fixed to baseline levels

[a] The ten specific inspection activities analyzed are: sanitation(01), HACCP (03), wholesomeness/economic consumer protection (04), sampling (05), other inspection requirements (06), sanitation performance standards (06D01), raw ground (03B), raw not ground (03C), fecal checks (03J), and economic poultry kill (04C04).
[b] FSIS (2011b). Potential Public Health Impact of *Salmonella* and *Campylobacter* Performance Guidance for Young Chickens and Turkeys. Available at: http://www.fsis.usda.gov/wps/wcm/connect/335168ad-ff20-4885-8ee3-4ad983ae486c/Potential_Public_Health_Impact_Sal_Campy_Performance_Guidance_Broilers_Turkeys_2011.pdf?MOD=AJPERES.
[c] Williams M.S., Ebel, E.D., Vose, D. 2011. Framework for Microbial Food-Safety Risk Assessments Amenable to Bayesian Modeling Risk Analysis. *Risk Analysis*, Vol. 31, no. 4, 548-565.
[d] This assumption is supported by empiric evidence. FSIS chicken carcass baseline results indicate that the average concentration of *Salmonella* per ml of rinsate had not changed from 1995 in 2007, but the prevalence of positive carcasses was different. Similar results have been seen by others (Crouch *et al.*, 2009; Withee *et al.*, 2009) and in FSIS' *Campylobacter* data.
[e] This shift in inspectors is from the Preliminary Regulatory Impact Analysis (PRIA) of the proposed poultry slaughter rule.
[f] This assumption follows from the observation that there are fewer scheduled but not performed procedures and more unscheduled procedures performed when establishments are fully staffed and off-line inspectors are not required to fill line positions
[g] Based on analysis of the HACCP Inspection Models Project (HIMP) (FSIS, 2011a).
Abbreviations: HIMP, HACCP-Based Inspection Models Project; NC, non-compliances; SNP, scheduled and not performed procedures ; SP, scheduled and performed procedures; Unscheduled procedures.

Table ES-2. Summary of Key Uncertainties in the Risk Assessment

Contributors to Uncertainty in the Model	Symbol	Classification	Handling of Uncertainty in the Model	Relative Importance
Regression coefficients	$\boldsymbol{\beta}$	Statistical	Modeled as multivariate normal distributions	
Adjustment parameters to reflect the number of future off-line inspection activities	A_i	Modeling	Modeled as Pert uncertainty distributions	Most Influential uncertainty assumptions
Baseline Annual Number of *Salmonella* and *Campylobacter* Illnesses	λ_{ill}	Modeling	Independently calculate a 90% credibility interval from Scallan *et al.* (2011), and use that interval in a putative lognormal distribution to reflect uncertainty about attributable illnesses	Least Influential uncertainty assumptions
Fraction of *Salmonella* and *Campylobacter* Illnesses Attributable to Poultry	N/A	Modeling	Not modeled explicitly, awaiting further development of the parameter by CDC and other Agencies	N/A

Abbreviations: N/A, not applicable.

Change scenarios predict how prevalence of both *Salmonella* and *Campylobacter* on poultry, and ultimately annual human illnesses, might be expected to change based on four categories of inspection procedures:

1. scheduled-and-performed procedures [SP]
2. unscheduled procedures [U]
3. scheduled-not-performed procedures [SNP] and
4. observed and recorded non compliances [NC]

To identify the types of offline inspection procedures that could have the greatest public health impact the model ran an "indiscriminate" scenario where the relative frequencies of all four categories of these inspection procedures are increased or decreased independently of any other information or pre-determined assumption about their relative impact on prevalence of pathogens in the establishment. Uncertainty distributions about changes in four categories of inspection procedures are developed using information provided in the FSIS HACCP-Based Inspection Models Project (HIMP) report (young chickens only)(FSIS, 2011a), which informed the development of the new poultry inspection system. The model also ran a "discriminate" scenario, where only the unscheduled offline procedures (U) are targeted for increased inspection activity. It was observed from the historical data that in HIMP establishments up to 60% more offline procedures are performed than in non-HIMP establishments. The model assumes that an estimate of the distribution for off-line inspection activities performed upon implementation of the alternative inspection scenario would reflect the distribution for off-line inspection activities observed in establishments currently operating under HIMP.

Findings

The risk assessment attempts to model answers to each of the four risk management questions posed at the outset.

- *Can FSIS reallocate inspection activities in young chicken slaughter establishments without significant negative impact on microbial prevalence in the establishments?*

Depending on how reallocation of inspection activities is implemented, it is likely that changes in off-line inspection could result in a decrease in the numbers of positive microbial samples in FSIS-regulated young chicken and young turkey establishments. Specifically, the ***discriminate scenario***, which only increases unscheduled inspection procedures, performs much better than the indiscriminate scenario, which does not target specific types of procedures.

Under the ***indiscriminate scenario*** in young chicken establishments, when off-line inspection procedures are increased, the model predicts an average decline of 2% in the proportion of samples testing *Salmonella* positive. However, when the substantially less robust *Campylobacter* data available at the time of the assessment are used, the model suggests a 0.2% increase in the proportion of samples testing *Campylobacter* positive. This very small increase is likely a function of the instability of this model, which is due to the combination of both small sample sizes and allowing the option of increasing off-line procedures that do not necessarily directly influence contamination rates. Under the ***discriminate scenario***, where only unscheduled inspection procedures are targeted for increase, the model in young chicken slaughter establishments predicts an average decline of 2% in the proportion of samples testing *Salmonella* positive, and an average decline of 0.44% in the proportion of samples testing *Campylobacter* positive.

Under the ***indiscriminate scenario*** in young turkey slaughter establishments, when off-line procedures are increased, the model predicts an average decline of 6% in the proportion of samples testing *Salmonella* positive, and an average decline of 26% in the proportion of samples testing *Campylobacter* positive. Under the ***discriminate scenario***, where only unscheduled inspection procedures are targeted for increase, the model in young turkey slaughter establishments predicts an average decline of 3% in the proportion of samples testing *Salmonella* positive, and an average decline of 19% in the proportion of samples testing *Campylobacter* positive.

However, the results under the discriminate scenario indicate that more than 90% confidence that the combined annual illnesses avoided under the scenario that increases unscheduled procedures exceeds zero (i.e., the 10^{th} percentile of the combined *Campylobacter* illnesses avoided would be 30).

- *How will the relocation of on-line inspectors to off-line duties, or other areas within or outside the establishment, affect human illness?*

We assume that the total annual *Salmonella* and *Campylobacter* illnesses rates attributed to poultry are about 174,686 and 169,005, respectively (1).

Under the ***indiscriminate scenario***, where no specific category of procedures was targeted for increase, the model estimates an average decrease of 4,440 annual *Salmonella* illnesses attributable to young chicken and young turkey establishments combined, or an estimated prevention of 2.5% of those illnesses per year. The same scenario estimates an average increase of 170 annual *Campylobacter* illnesses (0.1% of illnesses) attributable to young chicken and turkey establishments combined.

Under the ***discriminate scenario***, where only unscheduled procedures are targeted for increase, the model estimates an average decrease of 3,980 annual *Salmonella* illnesses (2.3%) attributable to young chicken and young turkey establishments, and an average decrease of 840 annual *Campylobacter* illnesses (0.5%) attributable to young chicken and turkey establishments combined.

- *Where within the establishment can relocated inspection activities have the most impact toward reducing microbial prevalence and corresponding human illness?*

The modeling and scenario analysis results suggest that increasing unscheduled procedures (i.e, the discriminate scenario) would be most effective in reducing pathogen occurrence on carcasses because of consistency in that decision variable parameter's effect across all models. The other decision variables suggest ambiguous effects from their intended changes when those effects are considered across all four pathogen-product models. This seems due to variable model parameter precision from variable sample sizes and non-uniform data quality. When targeting unscheduled inspection procedures in young chicken establishments, the estimated decrease in prevalence was 2% for *Salmonella* and 0.5% for *Campylobacter*. For young turkey establishments, the corresponding decrease in prevalence was 3% and 19% respectively.

- *What is the uncertainty about these effects?*

Our modeling approach includes the inherent uncertainty about the relationship between the frequency of inspection activities and pathogen prevalence, about the actual change in future inspection activities that would likely be observed, and about the representativeness of the rates of human *Salmonella* and *Campylobacter* illness attributable to poultry.

INTRODUCTION

The Food Safety and Inspection Service (FSIS) conducted this risk assessment to help inform proposals to change allocation of inspection personnel in poultry slaughter establishments. This risk assessment considers scenarios that might allow FSIS to target resources more efficiently, by allowing FSIS inspection personnel more time and flexibility to perform off-line inspection tasks based on human health risk factors specific to individual establishments. If the proposed change reduces the occurrence of foodborne pathogens such as *Salmonella* and *Campylobacter* on finished poultry products, then a net public health benefit may result.

This risk assessment updates a 2008 risk assessment (FSIS, 2008a)—originally presented in conjunction with a review by the National Advisory Committee on Meat and Poultry Inspection (NACMPI, 2008)—with more recent data and a modified modeling approach. This version of the risk assessment takes into consideration public and stakeholder comments and has been modified in response to an independent peer review completed in August 2012.

The risk management questions were:

- *Can FSIS reallocate inspection activities in poultry slaughter establishments without significant negative impact on microbial prevalence in the establishments?*

- *How will the relocation of on-line inspectors to off-line duties, or other areas within or outside the establishment, affect human illness?*

- *Where within the establishment can relocated inspection activities have the most impact toward reducing microbial prevalence and corresponding human illness?*

- *What is the uncertainty about these effects?*

METHODS

Logistic regression analysis is performed to estimate the relationship between off-line inspection procedures (described below) and contamination of young chicken and young turkey carcasses with either *Salmonella* or *Campylobacter* (Stage 1). Subsequently, a stochastic simulation model uses the coefficient estimates from that logistic regression to predict the effect of changes in off-line inspection categories on changes in the annual rate of human *Salmonella* or *Campylobacter* illnesses attributable to the consumption of young chicken and young turkey (Stage 2). The simulation model incorporates uncertainty about the regression coefficients, the expected change in off-line inspection activities associated with the model scenarios and its estimate about the current rate of human illnesses, into predictions about the change in human illnesses. The overall

prediction model for estimation of illnesses avoided is presented here as a two-stage model: the regression model and the model to predict the effect of increased inspection procedures.

Stage 1: Characterizing the Relationship between FSIS Inspection Activities and Product Contamination using a Regression Model

An overview of the logistic regression model is provided here. More detail about the regression model can be found in the Appendix to this report.

The first stage is a daily production volume-weighted logistic regression model with the regression coefficients estimated from the maximum quasi-likelihood equations of the Fisher scoring algorithm using standard SAS software[2].The regression model predicts the conditional likelihood that there would be a change in the proportion of samples testing positive given the structural and decision variable input values. The independent variables consist of categorical and continuous structural variables that differ in number among the four models (i.e. young chicken/*Salmonella*; young chicken/*Campylobacter*; Young turkey/*Salmonella*; young turkey/*Campylobacter*) and four inspection variables (i.e. scheduled-and-performed procedures [SP]; unscheduled procedures [U]; scheduled-not-performed procedures [SNP] and; observed and recorded non compliances [NC]). The estimating equations predicting prevalence of positive samples then enter the second stage of the process.

Prevalence estimates are derived from a weighted average prevalence estimate across all data points. Multivariate normal estimating equations averaged across all data points are iterated 100,000 times; each iteration estimates a population prevalence that becomes an element in the prevalence distribution that is transformed in the second stage into a distribution of illnesses avoided.

The model relates occurrences of *Salmonella* and *Campylobacter* among poultry carcasses to four decision variables—each representing a category or grouping of off-line inspection procedures—and several structural variables, which are variables that describe differences in plant design, inspection system and other demographic characteristics. In the model structural variables are treated as given or constant, and, by intent, do change with changes in modeled scenarios.

Young chicken data are comprised of the *Salmonella* and *Campylobacter* results of the FSIS Young Chicken Baseline study (post-chill and rehang samples) (July 2007 through September 2008) (FSIS, 2008b) and PR/HACCP *Salmonella* verification program (post chill samples) (July

[2] Proc logistic SAS 9.1.3 Service Pack 1 Copyright (c) 2002-2003 by SAS Institute Inc., Cary, NC, USA

2007 through September 2010). Young turkey data are comprised of the *Salmonella* and *Campylobacter* results of the FSIS Young Turkey Baseline study (post-chill and rehang samples) (August 2008 through July 2009) (FSIS, 2009) and PR/HACCP *Salmonella* verification program (post chill samples) (July 2007 through September 2010) [3].

The four decision variables categories identified are:

Scheduled and Performed Procedures (SP)
Scheduled procedures are those that follow a random scheduling procedure from headquarters and performed or not performed accordingly as time and inspection personnel were available. The decision variable *Scheduled and Performed* (SP) procedures is the number of procedures that are scheduled at headquarters and that the inspector completes in the specified establishment.

Scheduled and Not Performed Procedures (SNP)
Scheduled procedures are those that follow a random scheduling procedure from headquarters and performed or not performed accordingly as time and inspection personnel were available. The decision variable *Scheduled and Not Performed* (SP) procedures is the number of procedures that are scheduled at headquarters but that the inspector does not complete in the specified establishment.

Unscheduled Procedures (U)
Unscheduled procedures are procedures not on the scheduled list for each establishment but that may be performed in response to possible establishment non-compliance with regulations or simply an expansion of routine inspection procedures when time and personnel are available. More unscheduled procedures are performed when establishments are fully staffed and off-line inspectors are not required to fill line positions.

Observed and Recorded Non-Compliances (NC)
An NC may be observed and recorded when performing scheduled and unscheduled procedures. Unlike the above three categories of inspection activities, which are indications of the number of the tasks an inspector is performing, *Observed and Recorded Non-Compliances* (NC) capture the results of the inspection task and the value is a function of not only of how frequently FSIS conducts inspection tasks, but also the establishment's food safety practices. That is, they capture when an inspector finds that an establishment is not properly implementing its sanitation, food safety processes and other controls. Because some of those non-compliances are directly related to carcass contamination, this decision variable, might be expected to be positively associated with an increase in product contamination. That is, the contamination rate of an establishment that does not have consistently good food safety practices in place might be expected to be increased compared with an establishment with good food safety practices. If such a correlation exists, then using that correlation to estimate or predict what would occur if

[3] FSIS' PR/HACCP verification program did not analyze poultry samples for Campylobacter until July, 2011.

the number of observed and recorded non-compliances were to increase would lead to an increase in illnesses.

Those four categories serve to group the six Inspection System Procedure (ISP) Codes into mutually exclusive classes. The ISP codes refer to (i) sanitation, (ii) HACCP, (iii) wholesomeness/economic consumer protection, (iv) sampling, (v) sanitation performance standards, and (vi) emergency procedures. Each ISP code is further delineated into more precise activities and most activities are noted as either SP, SNP, U or NC (see Appendix for details). The four decision variables represent the sum of activities on each establishment day across the various ISP codes as follows (see detailed description in Table A-3 in the Appendix):

1. SP = scheduled and performed procedures for sanitation (01), HACCP (03), wholesomeness/economic consumer protection (04), sampling (05), other inspection requirements (06), sanitation performance standards (06D01), raw ground (03B), raw not ground (03C), fecal checks (03J), economic poultry kill (04C04)
2. SNP = scheduled not performed procedures for sanitation(01), HACCP (03), wholesomeness/economic consumer protection (04), sampling (05), other inspection requirements (06), sanitation performance standards (06D01), raw ground (03B), raw not ground (03C), fecal checks (03J), economic poultry kill (04C04)
3. U = unscheduled procedures performed for sanitation (01), HACCP (03), wholesomeness/economic consumer protection (04), sampling(05), other inspection requirements(06), sanitation performance standards (06D01), raw ground (03B), raw not ground (03C), fecal checks (03J), economic poultry kill (04C04), emergency procedures (08)
4. NC = observation and reporting by inspection personnel of non-compliant procedures for sanitation (01), HACCP (03), wholesomeness/economic consumer protection (04), sampling (05), other inspection requirements (06), sanitation performance standards (06D01), raw ground (03B), raw not ground (03C), fecal checks (03J), economic poultry kill (04C04)

These four defined categories were chosen because the expected/intended effect of the modeled scenarios was consistent for inspection procedures within each category. For example, a proposed increase in off-line inspectors is expected to increase scheduled and performed procedures. Similarly, increased availability of off-line inspectors should increase unscheduled procedures while reducing scheduled but not performed procedures. This assumption follows from the observation that there are fewer scheduled but not performed procedures and more unscheduled procedures performed when establishments are fully staffed and off-line inspectors are not required to fill line positions. The model also assumes that – in the long-run – reported non-compliances would decrease with more off-line inspectors in slaughter establishments because such establishments would attain appropriate process control through increased inspection scrutiny and also through likely industry innovation. Although an alternative approach that collapsed decision variables according to the six ISP classes of off-line procedures was explored, this approach created confusion about the intended effect of the modeled scenarios within each class. For example, a random variable that summarized HACCP procedures would

need to increase scheduled and performed procedures (and unscheduled procedures) but also decrease scheduled but not performed procedures (and non-compliances).

After considering several alternative sets of decision variables, this treatment of decision variables avoids some potential problems with collinearity in the model. It also avoids over-interpretation of specific procedures that simply reflect random associations that can occur with over-parameterized models.

Versions of the regression analysis on the extensive dataset including more than 40 decision variables representing specific ISP codes were considered but ultimately rejected. The analysis of these complicated models was indeterminate and therefore unsuitable because these variables could be correlated with each other. Such collinearity made inferences about specific coefficients potentially invalid.

Previous versions also attempted to simplify inferences about specific variables by developing submodels that eliminated other variables and isolating the effect of the variable of interest. Nevertheless, predictions from submodels required consideration of the implications across all submodels such that each submodel would be weighted as part of a whole. Such a weighting scheme was deemed too complicated and potentially fraught with error to pursue.

Instead, the regression approach used in this assessment estimates a single regression equation for each product-pathogen pair (i.e., young chicken-*Salmonella*, young chicken-*Campylobacter*, young turkey-*Salmonella*, and young turkey-*Campylobacter*). This is a valid approach to making predictions from each model. The four decision variables (SP, SNP, U and NC) are included in each regression model. For one of those decision variables to be found statistically significant in the model, all inspection procedures within the category must be strongly associated with pathogen occurrence. Consequently, inferences made about significant variables are stronger, but more general, than inferences from previously considered models (see Appendix) with more decision variables.

Stage 1: Regression Model Outputs

Table 1 presents the results of the regression analysis for the four decision variables categories of inspection activities (SP, SNP, U and NC) for each of the four product-pathogen pairs. This analysis evaluates the correlation between each of those inspection activities and product contamination. Estimates of the regression coefficient vary among each of the decision variables and among the four product-pathogen pair .

Looking at SNP procedures, if more off-line personnel are available to complete scheduled procedures there should be fewer SNP procedures. The coefficient sign for SNP is positive in 3

of the 4 product-pathogen pair models (chicken-*Salmonella*, chicken-*Campylobacter* and turkey-*Campylobacter*), suggesting that decreasing occurrences in this category would decrease pathogen prevalence in these product classes. In contrast, the sign of the coefficient of the significant SNP variable in the turkey-*Salmonella* model is negative, suggesting, that reducing SNP could actually increase *Salmonella* prevalence in young turkey. However, even though the magnitude of the SNP coefficient in each model is large compared to the other coefficients, in each model the magnitude of expected change over all establishments is less than one SNP procedure per day. In addition, the SNP variable is the most unpredictable of the four decision variables because relatively small number of SNP procedures relative to the other three decision variables in each model, which leads to an instability in results of increasing *Salmonella* prevalence by decreasing scheduled-but-non performed procedures. The smaller number of turkey samples also contribute to lower confidence in this result relative to the chicken-*Salmonella* results.

All four product-pathogen pair models support the expectation that increased unscheduled activities (the U category) would reduce pathogen prevalence (i.e., the coefficient sign is negative for all pairs). The U variable is highly significant in the chicken-*Salmonella* model and the turkey-*Campylobacter* models, but not significant (at a p=0.05 significance level) in the other two models. Nevertheless, the p-value for these other two models does not entirely reject the possibility that the U variable may be importantly associated with pathogen occurrence.

The regression coefficient for the scheduled and performed procedures (SP) decision variable is significant only for turkey-*Campylobacter* product-pathogen pair model. The other models suggest—although the variables are not statistically significant at the p=0.05 level—that increasing this variable would increase pathogen prevalence.

As can be seen in Table 1, the regression coefficients for the non-compliance (NC) decision variable is positive for both the chicken and the turkey *Salmonella* product pairs (a significant positive correlation for turkey), suggesting that decreasing occurrences in this category would decrease pathogen prevalence in these product classes. In contrast, the coefficient for both the chicken and the turkey *Campylobacter* product pairs is negative (a significant negative correlation for chicken), suggesting that decreasing occurrences in this category would increase pathogen prevalence in these product classes. Both anticipating the effect of changes in NC procedures and interpreting the estimated changes to non-compliance (NC) episodes in establishments is complicated. The number of non-compliances reported is a function of failures in process control *and* the availability of inspection personnel to detect these failures. As such, the non-compliance decision variable is different from the other three decision variables because it partly reflects occurrences (i.e., failures) that are *not* controlled by off-line inspectors. In contrast, the other decision variables are directly amenable to change simply by changing inspection resources (e.g., unscheduled procedures can increase or decrease directly with the

number of off-line inspectors – these do not require detection of establishment failures).Taking those aspects into account, on the one hand, FSIS expects that increased off-line inspection resources would generate improved process control within establishments that adopt the proposed change. Improved process control should, in the longer term, result in fewer non-compliance reports from these establishments. On the other hand, these increased off-line inspectors would also have more time and opportunity to identify non-compliant activities and thereby generate more non-compliance reports, at least in the short term. Differential long-term versus short-term effects may be what is reflected in the difference in NC reporting between *Salmonella* and *Campylobacter* testing. Regardless of whether that is the case, as stated previously the number of *Salmonella* testing results compared with the number *Campylobacter* test results at the time of this assessment provide more confidence in the analysis of the *Salmonella* results. On the basis of an analysis of the HACCP Inspection Models Project (HIMP) (FSIS, 2011a) it would be anticipated that fewer non-compliances would occur following implementation of the proposed change. Nevertheless, the regression model results observed here are inconsistent across the four models.

The mean values for each of the four inspection categories indicate the average number of daily instances across the population of all establishments for each category of off-line inspection procedures represented in the data (Table 1). For example, the average number of scheduled and performed procedures used as explanatory variables in the chicken-*Salmonella* model is ~13 per establishment per day. Similarly, the average number of unscheduled procedures is ~29 per establishment per day. Comparing these values with the chicken-*Campylobacter* data suggests similarities (e.g., 31 vs. 29 for U) and differences (e.g., ~7 vs. ~13 for SP). Differences highlight the fact that the dataset for chicken-*Salmonella* is augmented with testing data generated from the PR/HACCP testing while the chicken-*Campylobacter* model only includes data from the Young chicken Baseline study. A similar explanation applies to comparisons between the two young turkey datasets.

Table 1. Results of the Regression Analyses for each Decision Variables from Four Product-Pathogen Pairs

Product-Pathogen Pair	Decision Variable	Regression Coefficient Estimate	Std Error	p-value	Variable Mean	Variable Std Dev
Young chicken – *Salmonella*	SP	0.0021	0.0021	0.1587	12.9624	6.0291
	SNP	0.0461	0.0093	<0.0001*	0.5536	1.0524
	U	-0.0032	0.0009	0.0002*	29.1353	20.5648
	NC	0.0091	0.0096	0.1716	0.7834	1.1422
Young chicken - *Campylobacter*	SP	0.0076	0.0065	0.1212	6.5629	0.8762
	SNP	0.0198	0.0107	0.0321*	0.6929	0.2600
	U	-0.0014	0.0011	0.1016	31.0927	7.3283
	NC	-0.0157	0.0074	0.0170*	1.3634	0.3212
Young turkey – *Salmonella*	SP	0.0054	0.0121	0.3277	10.7622	6.3381
	SNP	-0.0805	0.0408	0.0243*	0.4945	1.0889
	U	-0.0208	0.0190	0.1368	6.9431	3.1892
	NC	0.0581	0.0223	0.0046*	1.8542	3.6883
Young turkey - *Campylobacter*	SP	-0.0344	0.0203	0.0451*	10.8187	4.2699
	SNP	0.0444	0.0573	0.2192	0.9022	1.3254
	U	-0.1027	0.0303	0.0004*	8.8464	3.1642
	NC	-0.0548	0.0801	0.2470	0.5374	1.0612

*Significant difference for two-sided t-test on the regression coefficient

SP = scheduled and performed procedures

SNP = scheduled not performed procedures

U = unscheduled procedures performed

NC = observation and reporting by inspection personnel of non-compliance

Source: FSIS analysis of Agency generated data

Stage 2: Model to Predict the Effect of Increased Inspection Procedures

Stage 2 of the risk assessment predicts the estimated change in pathogen prevalence for different changes in inspection activities. Specifically, it used results of the regression model in Stage 1 to predict the probability of a change in pathogen prevalence, and the mathematically maps that change in the conditional likelihood of prevalence to the attendant estimated change in the annual rate of human illnesses. This mapping directly mirrors the signs and magnitudes of the conditional regression coefficients from Stage 1, which is reflected in the probability of illness reduction estimated from Stage 2.

The modeling framework in Stage 2 stems from the three primary determinants of adverse human health outcomes from foodborne pathogens; 1) the frequency of exposure to the pathogen; 2) the distribution of pathogens in a random exposure event on a per serving basis; and 3) the probability that a random exposure event causes the adverse human health outcome (Cox, 2006; Haas, 1996). In microbial food safety, sporadic exposure events are considered independent events and chronic exposures to pathogens are historically not considered. These characteristics support modeling the occurrence of human illnesses as a Poisson process.

A prevalence-based model estimates changes in annual illness counts based on changes in the frequency of occurrence of the pathogen among food commodities (Williams *et al*., 2011). The basic model is:

$$P(ill) = P(ill \mid exp)P(exp)$$

where $P(ill)$ is the probability of illness from a product-pathogen pairing across a population, $P(ill \mid exp)$ is the probability that exposure to a random contaminated serving would produce illness[4] and $P(exp)$ is the frequency of exposure to the pathogen on a per serving basis[5]. This basic model enables a simple estimation of annual illnesses avoided ($\lambda_{avoided}$) resulting from an intervention that reduces prevalence.

A model to predict the effect of the increased off-line poultry inspection procedures is defined as follows:

[4] $P(ill \mid exp)$ is the solution to the integral where $R(D)$ is the dose-response function and the exposure distribution of doses (D > 0 organisms) is the probability density $f(D)$.

[5] Exposure to a contaminated serving can be defined at any point in the farm-to-table continuum assuming that $P(exp)$ is proportional to the percent of positive units observed at some point prior to consumption (i.e., these measures of occurrence differ by a multiplicative constant). In food safety applications, the best data for measuring frequency is usually at the point of commercial production (e.g., retail-ready raw chicken carcasses).

$$\lambda_{avoided} = \left(1 - \frac{Prev(scenario)}{Prev(baseline)}\right) \times \lambda_{ill}$$

where $\lambda_{avoided}$ is the annual rate of product-pathogen illnesses avoided following modeled alternative scenarios; λ_{ill} is the current annual rate of product-pathogen illnesses (i.e., illnesses in the baseline); $Prev(scenario)$ is the post-chill prevalence of pathogen-contaminated poultry carcasses projected following implementation of a modeled scenario; $Prev(baseline)$ is the post-chill prevalence of pathogen-contaminated poultry carcasses projected prior to modeled changes[6].

The advantage of this modeling approach is that it avoids the need to estimate an exposure distribution or a dose-response relationship. A critical assumption needed to apply such a prevalence-based approach is that dose levels at consumption are independent of the frequency of contamination (in other words, the level of contamination is independent of pathogen prevalence). This assumption asserts that $P(ill \mid exp)$ is constant regardless of changes in $P(exp)$. Although the prevalence-based model may not always hold, in this instance the use of the prevalence based model is supported, as only small changes in microbial concentration are observed despite large changes in prevalence. Furthermore, there is empiric evidence that supports the independence of prevalence and contamination levels at the end of the production of raw poultry carcasses. For example, in rinse samples of young chicken carcasses that test positive, the average concentration of *Salmonella* per ml of sample rinsate was 0.16 and 0.14 colony forming units (cfu) in the 1995 and 2007 baseline surveys, respectively (FSIS, 1996; FSIS, 2009). Yet, the prevalence of positive carcasses was substantially different (20% vs. 7.5%) in those surveys. Similarly, those same surveys found the average concentration of *Campylobacter* per ml of sample rinsate was 21 and 9.1 cfu in 1995 and 2007, respectively; despite a dramatic reduction in the prevalence of positive carcasses from 88% to 11%. Other studies have drawn similar conclusions with respect to other product-pathogen pairs (Crouch *et al*., 2009; Withee *et al*., 2009).

The baseline prevalence is defined as

$$Prev(baseline) = \sum_{j=1}^{n} w_j \times \frac{e^{\alpha+\beta_1 X_{1j}+\ldots+\beta_i X_{ij}+\ldots+\beta_n X_{nj}}}{1+e^{\alpha+\beta_1 X_{1j}+\ldots+\beta_i X_{ij}+\ldots+\beta_n X_{nj}}}$$, where

[6] Note that $\lambda_{avoided}$ might be negative if $Prev(scenario) > Prev(baseline)$. In such cases, the negative sign would reflect an increase in that rate parameter (although the negative sign would not directly enter a Poisson distribution).

the variables and coefficients are estimated via the logistic regression models described above, n represents the number of sampling occasions for the specific product-pathogen pair (e.g., $n = 22,671$ for the Young chicken-*Salmonella* model) and w_j is a fractional weight given to each sampling occasion to reflect the *annual* production volume (carcasses slaughtered per year) for each sampled establishment. Because the logistic regression model predicts the probability of an individual sample being positive (given the X_{ij} values for that sample), this equation is summed to calculate prevalence across the entire population of samples.

The modeled prevalence following implementation of a given scenario is,

$$Prev(scenario) = \sum_{j=1}^{n} w_j \times \frac{e^{\alpha+\beta_1 X_{1j}+\ldots+\beta_i X_{ij} A_i+\ldots+\beta_n X_{nj}}}{1+e^{\alpha+\beta_1 X_{1j}+\ldots+\beta_i X_{ij} A_i+\ldots+\beta_n X_{nj}}}$$ where

one or more of the random variables are adjusted by A_i to account for a change that occurs following modeled scenario implementation. To forecast post-chill prevalence, the rehang structural variable in the regression model is adjusted to reflect post-chill testing (i.e., its value is set to one) when estimating both $Prev(baseline)$ and $Prev(scenario)$.

There is uncertainty associated with the inputs λ_{ill}, $Prev(baseline)$, $Prev(scenario)$ and A_i in this assessment. To assess the overall uncertainty about $\lambda_{avoided}$, a Monte Carlo model[7] was developed to propagate those sources of uncertainty to a prediction about the future annual rate of illnesses avoided, in this way determining which source of inherent uncertainty had the greatest impact on the public health estimate from this model. In this model, uncertainty about regression coefficients is modeled as $\boldsymbol{\beta} \sim Normal\ \boldsymbol{\mu}, \boldsymbol{\Sigma}$ where $\boldsymbol{\mu}$ is a vector of mean β coefficients and $\boldsymbol{\Sigma}$ is the variance-covariance matrix generated from the regression analysis[8]; uncertainty about A_i is modeled as $\boldsymbol{A}_i \sim Pert(min, mode, max)$; uncertainty about λ_{ill} is modeled as

$\lambda_{ill} \sim lognormal\ \mu, \sigma$. Because $\lambda_{avoided}$ is a function of the ratio of $Prev(scenario)$ and $Prev(baseline)$ - and these random variables can be reasonably assumed to be correlated – each

[7] All Monte Carlo simulations were completed using Palisade's @Risk software in Microsoft Excel. Each simulation comprises 100,000 iterations; this number of iterations produces outputs that change by <1% from one simulation to the next.

[8] Random values from this multivariate normal distribution are generated using the Cholesky decomposition method (Press *et al.* 2007).

iteration of a simulation paired the estimates of $Prev(scenario)$ and $Prev(baseline)$ such that each estimate reflected the same uncertain coefficient values from the regression model (thus the baseline and each modeled scenario is run in parallel with each other).

Estimates of λ_{ill} are needed for all four product-pathogen pairs. Uncertainty about the total *Salmonella* and *Campylobacter* illnesses per year attributable to young chickens and young turkeys is modeled by considering the uncertainty in the total annual domestically acquired foodborne illnesses estimated by CDC (Scallan *et al.*, 2011). The mean estimated total cases (and 90% credibility interval) for *Salmonella* and *Campylobacter* were 1,027,561 (644,786 – 1,679,667) and 845,024 (337,031 – 1,611,083), respectively.

As presented in Table 2, previous analysis estimated that the fractions of total *Salmonella* and *Campylobacter* illnesses per year attributable to young chicken as 16.33% (167,831/1,027,561) and 19.91% (168,291/845,024), respectively (FSIS, 2011b).[9] That analysis also estimated the fraction of total *Salmonella* and *Campylobacter* illnesses per year attributable to young turkeys as 0.67% (6855/1,027,561) and 0.08% (714/845,024), respectively. These attribution fractions are applied to the credibility intervals of Scallan *et al*. (2011) to determine the 5th and 95th percentiles of a putative lognormal distribution that describes uncertainty about the annual cases of these pathogens attributed to each poultry class (Table 2). This treatment, however, does not consider uncertainty associated with the fraction of illnesses attributed to each poultry class. Consideration of this source of uncertainty awaits further development of this parameter by CDC and other food safety agencies.

[9] Following completion of this assessment, the Centers for Disease Control published Painter J.A., Hoekstra R.M., Ayers T., Tauxe R.V., Braden C.R., Angulo F.J, Griffin P.M. (2013). Attribution of foodborne illnesses, hospitalizations, and deaths to food commodities by using outbreak data, United States, 1998–2008. *Emerging Infectious Diseases*, 19(3):407-415. http://dx.doi.org/10.3201/eid1903.111866.. Our assumed attribution for *Salmonella*-poultry is within the range estimated by Painter *et al.* (2013), but our *Campylobacter*-poultry attribution (19.71%) is substantially larger than reported by Painter *et al.* (2013) 7.6%. Painter *et al.* (2013) explain that outbreak data under-represent poultry as a source of *Campylobacter* spp. infection and further note that studies of sporadic infections implicate consumption of poultry as a more significant risk factor.

Table 2. Estimated Number of Annual *Salmonella* and *Campylobacter* Illnesses, with Uncertainty Bounds, from Young Chicken and Young Turkey.

Product-Pathogen	Estimated attributed annual illnesses[1]			Lognormal distribution parameters[2]	
	Mean	5th percentile	95th percentile	Mu	Sigma
Young chicken - *Salmonella*	167,831	105,313	274,340	12.043	0.291
Young chicken - *Campylobacter*	168,291	66,413	317,473	11.886	0.476
Young turkey - *Salmonella*	6,855	4,320	11,254	8.850	0.292
Young turkey - *Campylobacter*	714	283	1,353	6.428	0.477

Source: FSIS analysis of data from Scallan et al., 2011.

[1]These distribution parameters are estimated from total illness data and attribution fractions for *Salmonella* and *Campylobacter* (Scallan *et al*., 2011; FSIS, 2011).

2 This parameterization assumes ln(annual illnesses) ~ Normal (Mu, Sigma). The lognormal distribution parameters were estimated using a percentile fitting algorithm:

$\mu = \frac{\ln(95th\%ile) + \ln(5th\%ile)}{2}, \sigma = \frac{\ln(95th\%ile) - \mu}{Z_{0.95}}$ where $Z_{0.95}$ is the 95th percentile of a standard Normal distribution.

One objective of this risk assessment is to estimate the adjustment parameters A_i that reflect the expected change in the decision variables following implementation of the proposed change. To establish baseline prevalence estimates, it is assumed that each decision variable simply reflects the data used to estimate the regression models. For the scenarios it is assumed that the data for each random decision variable would be adjusted as follows:

- Scheduled and performed (SP) and unscheduled procedures (U) in an establishment could either increase, decrease, or stay the same, once an establishment adopts the inspection system in the proposed change. FSIS inspection records in HIMP establishments are considered a good indicator of what the proposed FSIS inspection system might look like under the proposed change. On average, FSIS inspectors performed 14,136 offline verification inspections per HIMP establishment in CY2010 versus an average of 8,724 offline verification inspections per non-HIMP establishment. This varied from 1.6 times more offline verification inspection procedures in HIMP establishments than in non-HIMP establishments to 3.2 times more HACCP verification inspection procedures. Because a fraction of establishments already participate in HIMP and another fraction of establishments would choose not to adjust in response to the proposed change, it is assumed that a most

likely value of a 25% increase in SP and U procedures in our modeled scenario. At a minimum, it is assumed that there would be no change and at a maximum that there would be a 60% increase in these procedures. Therefore, for the SP and U decision variables, $A_i \sim Pert(1.0, 1.25, 1.6)$ is modeled. Note: although conceptually there is no reason why SP and U procedures could not decrease, because they are "decision variables" and it is not anticipated, operationally, that the number of those inspection activities would decrease, it was elected to truncate the Pert distributions at a lower limit of 1; assuming a worst case scenario of "no increase' in either of these off-line inspection procedures.

- Scheduled-but-not performed procedures would most likely decline under the proposed inspection system, as the primary reason for SNPs in an establishment is limited personnel to complete the offline procedure. Because the proposed inspection system may result in fewer scheduled procedures, it is difficult to compare current HIMP data on SNP procedures. It was assumed that these SNP procedures would most likely be reduced by 10%, but could be reduced by 100% or not change at all. Therefore, for the SNP decision variable, $A_i \sim Pert(0.0, 0.9, 1.0)$ is modeled. Note: a minimum value of 0.5 for this change variable was also considered, but the results were not significantly altered and only the above distribution is used in the final analysis.

The discussion above examines the uncertainty in how recorded non-compliances might change in establishments under different inspection scenarios. Data from HIMP establishments were used to model that change (FSIS, 2011a). On average, HIMP broiler establishments have 26% fewer reported public health-related non-compliances than do non-HIMP broiler establishments. Nevertheless, it remains possible that under the modeled scenario that non-compliances may be reduced by 100% or not change at all. Therefore, for the NC decision variable, $A_i \sim Pert(0.0, 0.74, 1.0)$ is modeled. In this case an alternative minimum value of 0.74, and a mean value of 0.9 for this change variable were also considered, but the results again were not significantly altered and only the above distribution is used in the final analysis.

Stage 2: Implementation Scenarios

To predict how annual illness rates might change following implementation of the proposed change, it is assumed that the four decision variables (that is the inspection categories SP, SNP, U and NC) would all change according to the assumptions outlined above. Those assumptions were then modeled using two different implementation scenarios.

An "***indiscriminate scenario***" is used to identify the types of offline inspection procedures that could have the greatest public health impact and to determine the sensitivity of the model to the different decision variables. In this scenario, no preference is provided for how FSIS might

emphasize or de-emphasize particular decision variables in the regression models. In other words, this scenario does not specify the implementation strategy employed, just that some combination of the four categories of inspection procedures would increase, with no inspection category more heavily emphasized than others. Note that it is not clear whether increasing NCs would actually be expected to increase illness.

A second scenario, termed the "***discriminate scenario***", models an increase in unscheduled procedures (i.e. Increase U) similar to what currently occurs in HIMP establishments. This model estimates how human illness might change if this particular category of inspection procedures (i.e., decision variable), is altered while leaving other decision variables unchanged. This scenario is modeled such that the A_i parameter for the U decision variable is the same as explained above while the A_i parameter values for the other decision variables are fixed at a value of one, to indicate no change from the baseline in the other inspection activities. The decision to consider this alternative scenario is based, in part, on the output of Stage 1 of this risk assessment. In that stage the outputs of the regression model for the unscheduled procedures decision variable was the most consistently negatively correlated with contamination across all four product-pathogen models, with that correlation being statistically significant in one chicken and one turkey model. That suggests that this decision variable is the most likely to decrease prevalence and, subsequently, human illnesses. In addition, operationally there is an assumption that FSIS would alter performance of the equivalent of unscheduled procedures.

RESULTS

Estimated Annual Changes in *Salmonella* and *Campylobacter* Prevalence in Young Chicken Establishments:

Under the ***indiscriminate scenario***, this risk model predicts an average decline of 2 % in the proportion of positive *Salmonella* samples and an increase of 0.2% in the proportion of positive *Campylobacter* samples. However, recall that the *Campylobacter* models are substantially less precise due to sample sizes, and the indiscriminate model includes procedures that, as discussed previously, would not always be expected to reduce contamination (i.e., NC activities) and categories of procedures that are infrequent (i.e., SNP).

Under the ***discriminate scenario***, when only unscheduled inspection procedures in young chicken slaughter establishments are targeted for increase, the risk model predicts an average decline of 2% in the proportion of positive *Salmonella* samples, and a decline of 0.44% in the proportion of positive *Campylobacter* samples if (Table 3).

Estimated Annual Changes in *Salmonella* and *Campylobacter* Prevalence in Young Turkey Establishments:

Under the ***indiscriminate scenario***, this risk model predicts an average decline of 6% in the proportion of positive *Salmonella* samples and a decline of 26% in the proportion of positive *Campylobacter* samples when off-line procedures are changed in young turkey slaughter establishments.

Under the ***discriminate scenario***, when only unscheduled inspection procedures in young turkey slaughter establishments are targeted for increase, the risk model predicts an average decline of 3% in the proportion of positive *Salmonella* samples and a decline of 19% in the proportion of positive *Campylobacter* samples (Table 3).

Table 3. Estimated Reductions in Prevalence of *Salmonella* and *Campylobacter* in Young Chicken and Young Turkey Slaughter Establishments

	Estimated Reduction in prevalence: mean (10th percentile, 90th percentile)			
	Indiscriminate Scenario		**Discriminate Scenario**	
	Salmonella	*Campylobacter*	*Salmonella*	*Campylobacter*
Young chicken establishments	0.020 (0.006,0.041)	-0.002 (-0.010,0.006)	0.0210 (0.008,0.036)	0.004 (-0.0001,0.0099)
Young turkey establishments	0.060 (-0.024,0.141)	0.260 (0.137,0.386)	0.030 (-0.005,0.079)	0.190 (0.080,0.310)

Source: FSIS analysis of Agency generated data
Summary statistics derived using Monte Carlo simulations of the indiscriminate and Increase Unscheduled procedures scenarios across the four product-pathogen models.

Estimation of Changes in Human Illness

The estimated changes in human illness are summarized in Figures 1-4 and Tables 4 and 5. The figures depict the cumulative probability plots for the indiscriminate and alternative scenarios across the four product-pathogen pairs.

The first focus is on the ***indiscriminate scenarios***, where any combination of the four inspection categories is increased without consideration or targeting of those that would be expected to decrease illnesses. The model predicts that implementation of the indiscriminate scenario would net a small decrease in illnesses. Mean estimates from the indiscriminate scenario suggest an estimated reduction of 4,020 in annual *Salmonella* illnesses and 350 additional annual

Campylobacter illnesses in young chicken establishments. The mean estimates for young turkey establishments under the indiscriminate scenario show an annual decline of 420 and 180 *Salmonella* and *Campylobacter* illnesses, respectively.

The model also includes an estimate of the probability (percentage) that there will be an increase in illnesses and the probability that there will be a decrease in illnesses with the implementation of the indiscriminate scenario. That percentage represents the likelihood of having a positive change in illnesses, without consideration of the magnitude of that change (in other words, it indicates the likelihood of an increase of *any size*, even one illness). Under the ***indiscriminate scenario,*** the models (with the exception of the young chicken-*Campylobacter* prediction) suggest a high probability that the scenario modeled might result in a decrease in human illnesses. The probability that illnesses might *increase* by at least one illness (i.e., a negative value for illnesses avoided) is 0.04, 0.63, 0.18, 0.01 for the young chicken-*Salmonella*, young chicken-*Campylobacter*, young turkey-*Salmonella* and young turkey-*Campylobacter* models, respectively (Table 3). Stated a different way, there is a 96%, 37%, 82%, and 99% chance that illnesses would *not* increase by even one illness for the young chicken-*Salmonella*, young chicken-*Campylobacter*, young turkey-*Salmonella* and young turkey-*Campylobacter* models, respectively.

It is important to note that the young chicken-*Campylobacter* model results are ambiguous under the ***indiscriminate scenario***. The possibility of a predicted increase in *Campylobacter* illnesses is primarily driven by the SP decision variable and by the statistically significant NC decision variable. For both of these variables, the expected changes serve to increase prevalence, and their effects tend to overwhelm the prevalence-decreasing effects of expected changes to the SNP and U decision variables. It would only take a slight change in any of these decision variables to impact illness predictions because, compared to the young chicken-*Salmonella* model, the *Campylobacter* model is based on a considerably smaller sample, leading to less precision. Therefore, we have less confidence in the *Campylobacter* model results. In addition, as discussed previously, the effect of increasing non-compliances procedures on illness rates, particularly in the short term, is poorly understood and decreases the confidence in the model results that adjust that variable.

The Monte Carlo simulation results reflect the aggregate estimated change in total illnesses across young chicken and young turkey slaughter industries. To estimate this aggregate value, the $\lambda_{avoided}$ values for the young chicken-*Salmonella* and young turkey-*Salmonella* models were summed for each iteration of a Monte Carlo simulation. This same approach was used for the *Campylobacter* models (Table 4). These results imply a 97% probability that aggregate human *Salmonella* illnesses would be unchanged or decrease following a change to inspection procedures under the ***indiscriminate scenarios*** described. However, the indiscriminate scenario suggests a 54% probability that *Campylobacter* illnesses associated with both young chicken and young turkey establishments might increase, even by less than one illness, if such an implementation strategy were to be adopted.

Table 4. Estimated Human Illnesses Avoided from Monte Carlo Simulations of the ***Indiscriminate Scenario*** across the Four Product-Pathogen Models[a,b]

Statistic	Attributable to Young Chicken Establishments		Attributable to Young Turkey Establishments		Combined Illnesses Avoided	
	***Salmonella* illnesses avoided**	***Campylobacter* illnesses avoided**	***Salmonella* illnesses avoided**	***Campylobacter* illnesses avoided**	***Salmonella* illnesses avoided**	***Campylobacter* illnesses avoided**
Mean	4,020	-350	420	180	4,440	-170
Median	3,650	-260	390	150	4,090	-90
Mode	3,200	-310	250	130	3,580	-150
Std Deviation	2,800	1,180	520	120	2,850	1,180
10th percentile	920	-1,690	-160	70	1,260	-1,520
90th percentile	7,640	860	1,060	330	8,120	1,060
Probability of any increase in illnesses [c]	4.23%	63.28%[b]	17.81%	0.12%	3.11%	54.30% [b]

Source: FSIS analysis of Agency generated data

[a] Predicted changes in illness rounded to the nearest 10.

[b]This indiscriminate scenario does not target any inspection activity category to increase. It shows the range of illnesses avoided if any combination of inspection activity category is increased.

[c]This percentage represents the probability that an increase in illness of any size, even one illness, will occur. In other words, it is the likelihood that the decrease in illnesses will be negative.

[d]Sensitivity analyses indicate that much of the probability of seeing an increase in illnesses in the indiscriminate scenario is driven by the NC decision variable. The underlying reason for seeing what might be thought of as a counterintuitive results is, at least in part, a results of the statistical model and the unclear relationship between non compliances and product contamination. As discussed previously, an increase in the value of that variable would not necessarily be expected to be associated with a decrease in illnesses. In fact, the results from the regression analysis in Stage 1 of this risk assessment show either positive or negative correlations between NCs and contamination depending on the product-pathogen model. Furthermore, increasing the number of FSIS inspection tasks conducted would not, automatically, increase the number of NCs because the true value is a function of not only of how frequently FSIS conducts inspection tasks, but also the establishment's food safety practices. Those factors make the effect of increasing NCs poorly understood and uncertain, and could contribute to increase in estimated illnesses. The fact that indiscriminately increasing the decision variables results in some probability of increasing illnesses supports exploring the effect of targeting specific procedures for increase that logically, and according to the Stage 1 regression analysis, are more likely to be associated with decreased illnesses, specifically unscheduled procedures.

These results can be compared with those associated with the discriminate scenario in which only unscheduled procedures are increased. Table 5 shows that under the ***discriminate scenario***, that combined mean *Salmonella* illnesses could be reduced by as much as 3,980 annually (3,740 attributable to young chicken establishments and 240 attributable to young turkey establishments)(Table 5). Similarly, combined mean *Campylobacter* illnesses could be reduced by 840 annually (710 attributable to young chicken establishments and 130 attributable to young turkey establishments).

The discriminate model also minimizes the probability (i.e., the likelihood) that illnesses would increase by even one illness. In the young chicken-*Salmonella* model, the probability that the *Salmonella* illness rate would increase is down from 4.23% under the ***indiscriminate scenario*** to 0.013% for the discriminate scenario. Furthermore, the similarity of the uncertainty distributions for the "indiscriminate" and "discriminate" scenario results reinforce the importance of the "U" decision variable in the indiscriminate scenario (Figure 1).

Of great interest is the fact that under the discriminate scenario, run on the young chicken-*Campylobacter* data, the probability that the *Campylobacter* illness rate would increase is significantly lower than under the indiscriminate scenario (i.e., it drops from 63% to 10%). That is because the discriminate scenario does not include the effect of decreasing non-compliances. In fact, the discriminate scenario suggests the potential for avoiding substantially more *Campylobacter* illnesses if FSIS emphasizes increased unscheduled procedures.

When compared to the indiscriminate scenario, the discriminate scenario, in which the unscheduled procedures are specifically targeted for increase, the young turkey-*Salmonella* model suggests a small reduction in the probability that the *Salmonella* illness rate would increase (i.e., from 18% to 14%). The alternative scenario in the young turkey-*Campylobacter* model suggests only a minor change relative to the indiscriminate analysis.

For the discriminate scenario, the combined illnesses avoided results show a substantially lower probability that illnesses might increase (i.e., down from 3% to 0.03% for *Salmonella* and down from 54% to 6% for *Campylobacter*). These results suggest that aggregate human illnesses would be unchanged or decrease—with approximately 100% and 94% probabilities for *Salmonella* and *Campylobacter* respectively—if FSIS emphasized increases in unscheduled procedures in inspection resource allocation.

Table 5. Estimated Human Illnesses Avoided from Monte Carlo Simulations of the ***Discriminate Scenario*** that Specifically Increases Unscheduled Procedures across the Four Product-Pathogen Models[a].

Statistic	Attributable to Young Chicken Establishments		Attributable to Young Turkey Establishments		Combined Illnesses Avoided	
	Salmonella illnesses avoided	***Campylobacter*** illnesses avoided	***Salmonella*** illnesses avoided	***Campylobacter*** illnesses avoided	***Salmonella*** illnesses avoided	***Campylobacter*** illnesses avoided
Mean	3,740	710	240	130	3,980	840
Median	3,300	510	200	110	3,550	650
Mode	2,550	240	120	80	2,350	300
Std Deviation	2,260	850	280	100	2,280	850
10th percentile	1,300	-10	-30	40	1,510	100
90th percentile	6,690	1,720	590	250	6,960	1,860
Probability of any increase in illnesses[b]	0.013%	10.45%	13.68%	0.04%	0.03%	6.21%

Source: FSIS analysis of Agency generated data

[a] Predicted changes in illness rounded to the nearest 10.

[b]This percentage represents the probability that an increase in illness of any size, even one illness, will occur. In other words, it is the likelihood that the decrease in illnesses will be negative.

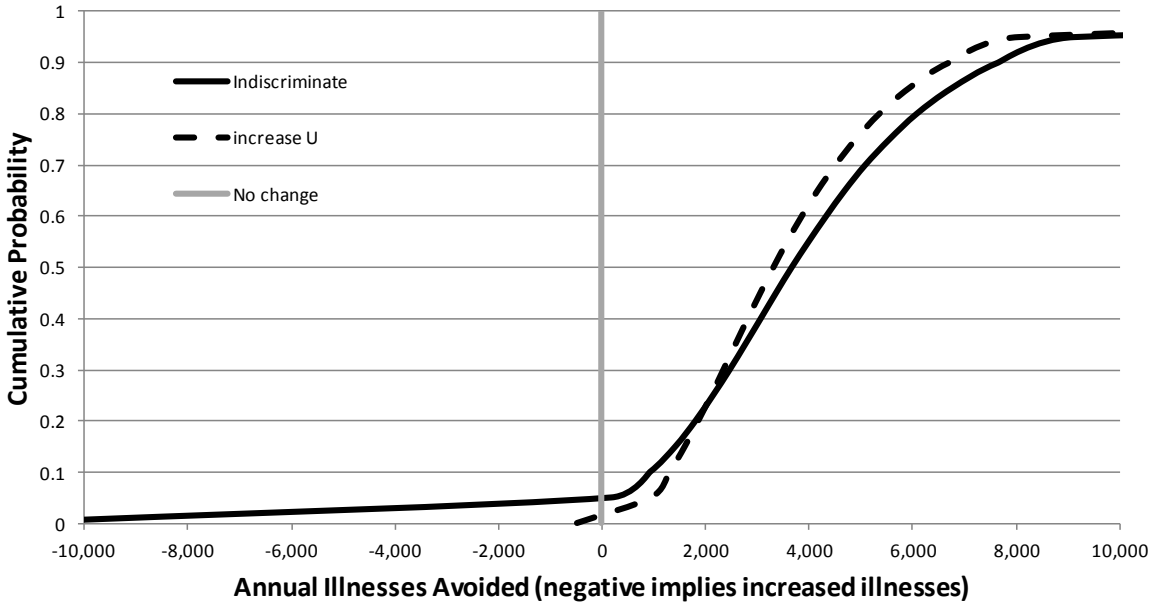

Figure 1. Estimated Change in the Annual *Salmonella* Human Illness Rate when Off-line Inspection Procedures are Increased in Young Chicken Establishments.
Data depicted for the indiscriminate scenario and the discriminate scenario that increased unscheduled procedures (labeled above as "Increase U"). Note that model uncertainty and data variability cannot statistically distinguish the two distributions.
Source: FSIS analysis of Agency generated data.

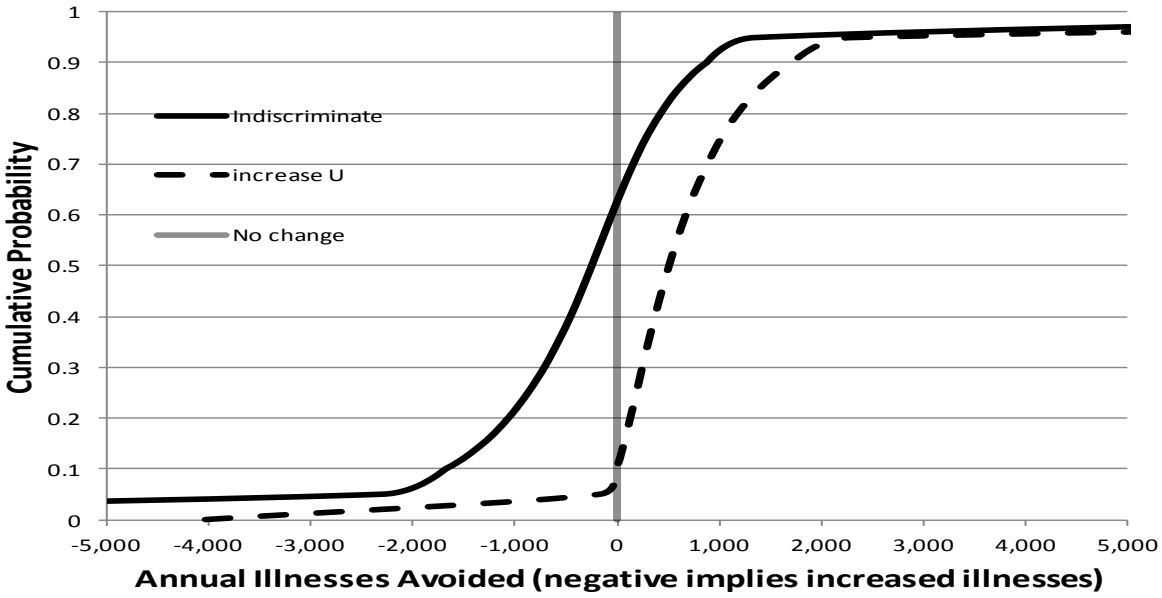

Figure 2. Estimated Change in the Annual *Campylobacter* Human Illness Rate when Off-line Inspection Procedures are Increased in Young Chicken Establishments**.**
Data depicted for the indiscriminate scenario and the discriminate scenario that increased unscheduled procedures (labeled above as "Increase U"). Note that the two distributions are distinguishable but that the model precision and data quality are not comparable to the young chicken-*Salmonella* model estimates.
Source: FSIS analysis of Agency generated data.

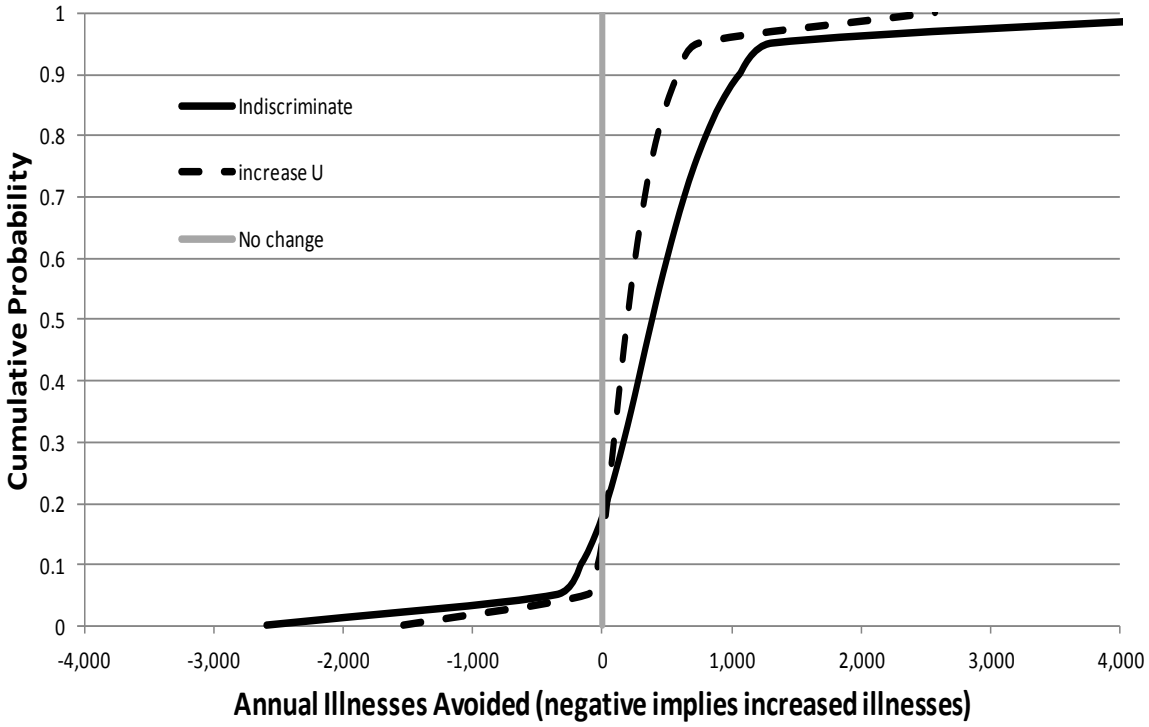

Figure 3. Uncertainty about the Change in the Annual *Salmonella* Human Illness Rate when Off-line Inspection Procedures are Increased in Young Turkey Establishments.
Data depicted for the indiscriminate scenario and the discriminate scenario that increased unscheduled procedures (labeled above as "Increase U"). Note that model uncertainty and data variability cannot statistically distinguish the two distributions.
Source: FSIS analysis of Agency generated data.

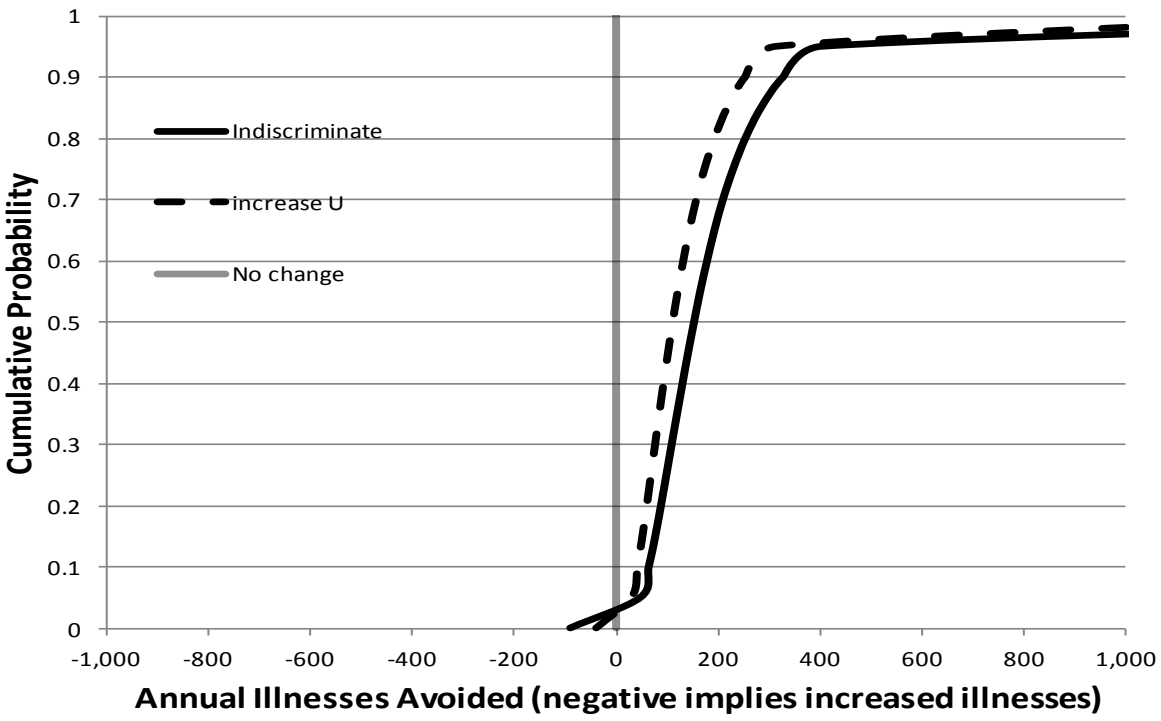

Figure 4. Estimated Change in the Annual *Campylobacter* Human Illness Rate when Off-line Iinspection Procedures are Increased in Young Turkey Establishments.

Data depicted for the indiscriminate scenario and the discriminate scenario that increased unscheduled procedures (labeled above as "Increase U"). Note that model uncertainty and data variability cannot statistically distinguish the two distributions.

Source: FSIS analysis of Agency generated data.

Sensitivity Analysis

This sensitivity analysis examined how the final model output ($\lambda_{avoided}$) is influenced by changes in the model inputs. First, the analysis examined the relative influence of the main stochastic inputs on the final uncertainty distribution for illnesses avoided. Second, the analysis examined the partial derivative of $\lambda_{avoided}$ for insight about the effect of alternative input values.

Three main stochastic inputs contribute uncertainty to the final distribution of $\lambda_{avoided}$: (i) λ_{ill} (lambda) that is modeled as a lognormal distribution; (ii) A_i that are modeled as Pert distributions; and (iii) β_i (beta) coefficients that are modeled in a multivariate Normal distribution. The analysis examined how each of these inputs influences uncertainty about $\lambda_{avoided}$ by simulating the model with only one stochastic input at a time. The variability from a simulation with just one stochastic input is compared to the simulation results when all inputs are stochastic.

Because the indiscriminate scenario model for chicken-*Salmonella* has the largest standard deviation for $\lambda_{avoided}$, this model was assessed for the relative influence of the main stochastic inputs on the uncertainty about $\lambda_{avoided}$ (Figure 5). These results demonstrate that the uncertainties about the A_i inputs are the largest contributor to uncertainty about $\lambda_{avoided}$. In other words, when the model only included the uncertainty about the A_i inputs – while inputs for λ_{ill} and β_i are fixed at their expected values – the resulting $\lambda_{avoided}$ distribution was only slightly less uncertain when compared to the $\lambda_{avoided}$ distribution where all inputs were stochastic ("All variability" distribution). The uncertainty about λ_{ill} was least influential as demonstrated by the narrowest $\lambda_{avoided}$ distribution resulting when that was the only stochastic input. The influence of uncertainty about the β_i inputs on the $\lambda_{avoided}$ distribution is in between that of the A_i and λ_{ill} inputs.

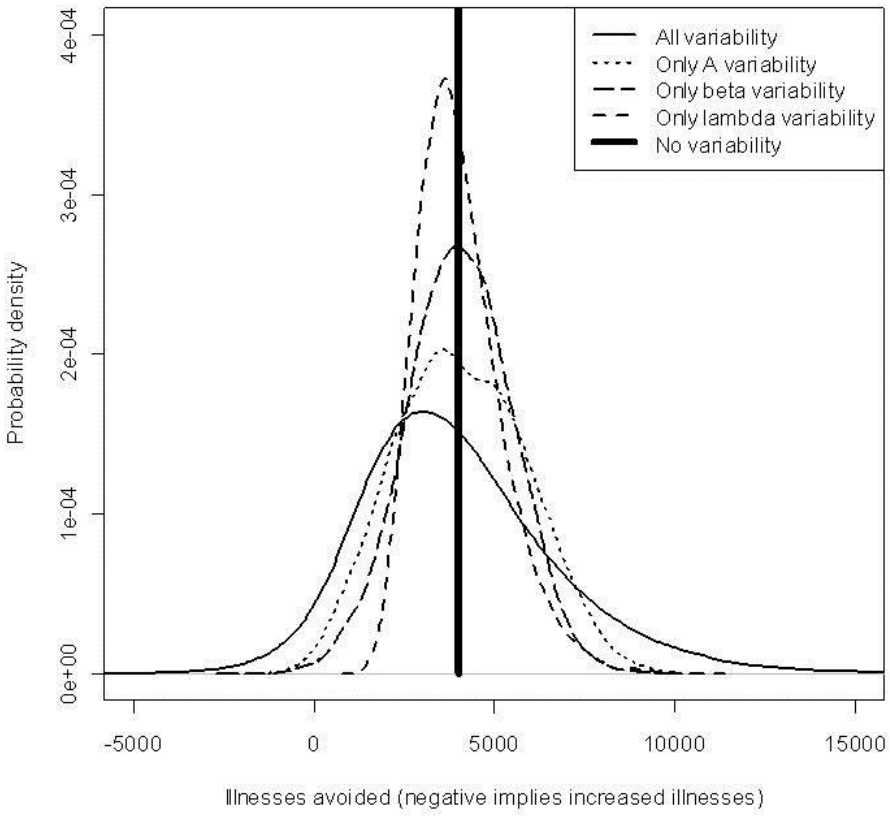

Figure 5. Relative Contributions to Uncertainty of Estimated Illnesses Avoided.
Source: FSIS analysis of Agency generated data.

Results of analysis of the relative contribution of uncertainty about $\lambda_{avoided}$ are shown in Figure 5. The indiscriminate scenario for chicken-*Salmonella* was simulated with all of the three main stochastic inputs (λ_{ill} [lambda], A_i and β_i [beta]); the uncertainty about $\lambda_{avoided}$ is shown as the "All variability" distribution. Alternatively, the same model was simulated with just one of these uncertain inputs (while holding the other two at their expected values); the resulting distributions for $\lambda_{avoided}$ are labeled as "Only A variability", "Only beta variability" and "Only lambda variability". These results demonstrate that the "Only A variability" distribution comes closest to replicating the "All variability" distribution. Therefore, uncertainty about A_i contributes most to total uncertainty about $\lambda_{avoided}$. Conversely, uncertainty about λ_{ill} contributes least to total uncertainty about $\lambda_{avoided}$. A simulation where all three inputs are fixed at their expected values ("No variability") is included to demonstrate that the model simply returns an expected value for $\lambda_{avoided}$.

To assess the effect of changing inputs on this model's output, the fundamental equation of the model is considered as

$$\lambda_{avoided} = \left(1 - \frac{1+e^{-\alpha+\beta_1 X_1+\ldots+\beta_i X_i+\ldots+\beta_n X_n}}{1+e^{-\alpha+\beta_1 X_1+\ldots+\beta_i A_i X_i+\ldots+\beta_n X_n}}\right) \times \lambda_{ill}$$

that takes advantage of the fact that $p = \frac{e^{\alpha+\beta_1 X_1+\ldots+\beta_i X_i+\ldots+\beta_n X_n}}{1+e^{\alpha+\beta_1 X_1+\ldots+\beta_i X_i+\ldots+\beta_n X_n}} = \frac{1}{1+e^{-\alpha+\beta_1 X_1+\ldots+\beta_i X_i+\ldots+\beta_n X_n}}$ and ignores the weighting of data used in the actual model. Note that $\lambda_{avoided}$ is simply a linear function of λ_{ill}, so any change in λ_{ill} would change $\lambda_{avoided}$ proportionally. Therefore, the main interest is how $\lambda_{avoided}$ changes with respect to the elements of the logistic regression. The partial derivative of the illnesses avoided function with respect to the logistic beta coefficients (while ignoring λ_{ill}) is determined as:

$$\frac{d\lambda_{avoided}}{d\beta_i} \propto -\left[\frac{AX_i\ e^{-\alpha+\beta_1 X_1+\ldots+\beta_i X_i+\ldots+\beta_n X_n}\ \left(1+e^{-\alpha+\beta_1 X_1+\ldots+\beta_i X_i+\ldots+\beta_n X_n}\right) - X_i\ e^{-\alpha+\beta_1 X_1+\ldots+\beta_i X_i+\ldots+\beta_n X_n}\ \left(1+e^{-\alpha+\beta_1 X_1+\ldots+\beta_i A_i X_i+\ldots+\beta_n X_n}\right)}{\left(1+e^{-\alpha+\beta_1 X_1+\ldots+\beta_i A_i X_i+\ldots+\beta_n X_n}\right)^2}\right]$$

From this partial derivative it is clear that if $A_i = 1$ (no change modeled, that is the traditional scenario), then there is no change in illnesses avoided (i.e., the partial derivative is zero). Therefore, the only coefficients in the illnesses avoided equation that would generate a change in illnesses are those influenced by the alternative scenario modeled.

The analysis calculates this partial derivative for each of the four decision variables (SP, SNP, U and NC), and for each of the four product-pathogen models (Figures 6-9). In the young chicken-*Salmonella* model, that determination of the number of illnesses avoided is most sensitive to the U decision variable (Figure 6). This variable is contributing to more illnesses avoided because the partial derivative implies that illnesses avoided would increase with an increase in the value of the U decision variable. A similar pattern is observed for the young chicken-*Campylobacter* model (Figure 7). In the young turkey-*Salmonella* model (Figure 8), the estimate of illnesses avoided is most sensitive to the SP decision variable, but the effect of increasing SP is to decrease illnesses avoided. In contrast, the effect of increasing SP in the young turkey-*Campylobacter* model is to increase illnesses avoided (Figure 9). For both young turkey models, the estimate of illnesses avoided is also sensitive to increasing U. Nevertheless, these partial derivatives are based on mean coefficient values and do not account for any uncertainty about those values. Consequently, the SP coefficient in the turkey-*Salmonella* model is highly influential based on its mean value, but its effect may be reversed if its value changes signs – and this can happen because of the large standard error associated with this coefficient (i.e., this coefficient is not statistically significant). Therefore, interpreting these partial derivatives *is only appropriate* when considering their mean values. These figures, which represent a standard sensitivity analysis, further substantiate focusing in the discriminate scenario on unscheduled inspection activities.

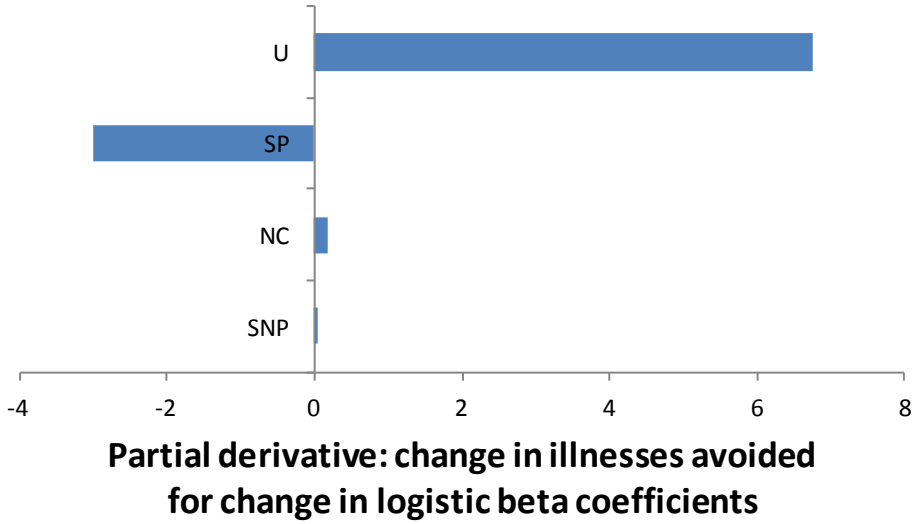

Figure 6. Sensitivity Analysis: Young Chicken-*Salmonella* Model.

This tornado graph illustrates the partial derivatives of $\lambda_{avoided}$ with respect to the non-compliance (NC), unscheduled procedures (U), scheduled not preformed procedures (SNP) and scheduled performed procedures (SP) logistic model coefficients.
Source: FSIS analysis of Agency generated data.

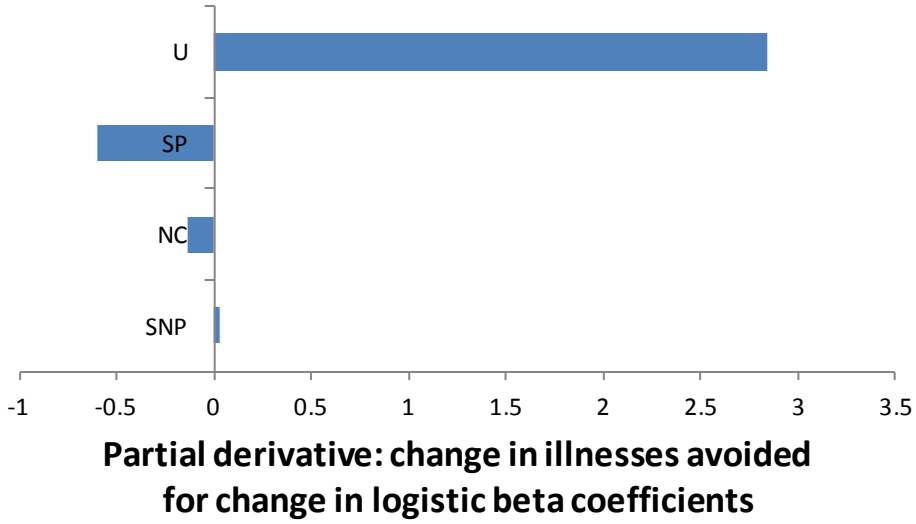

Figure 7. Sensitivity Analysis: Young Chicken-*Campylobacter* Model

This tornado graph illustrates the partial derivatives of $\lambda_{avoided}$ with respect to the non-compliance (NC), unscheduled procedures (U), scheduled not performed procedures (SNP) and scheduled performed procedures (SP) logistic model coefficients.
Source: FSIS analysis of Agency generated data.

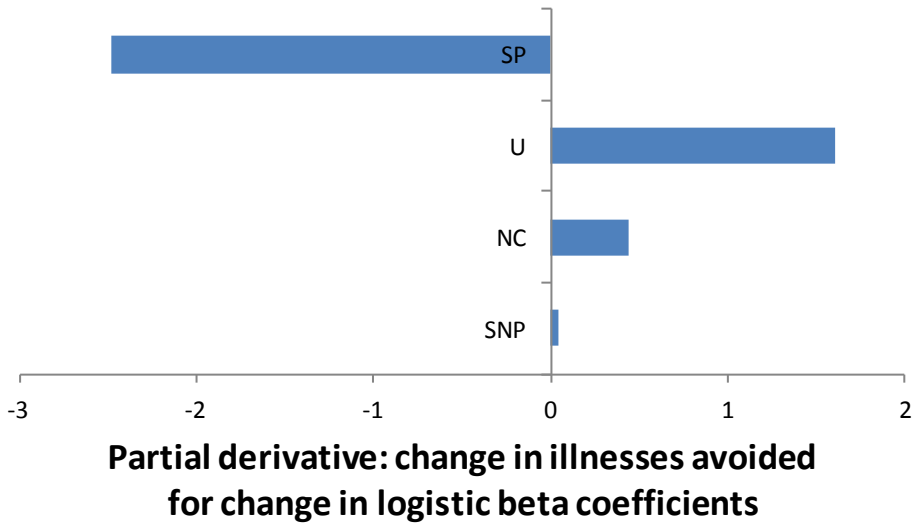

Figure 8. Sensitivity Analysis: Young Turkey-*Salmonella* Model.

This tornado graph illustrates the partial derivatives of $\lambda_{avoided}$ with respect to the non-compliance (NC), unscheduled procedures (U), scheduled not performed procedures (SNP) and scheduled performed procedures (SP) logistic model coefficients.
Source: FSIS analysis of Agency generated data.

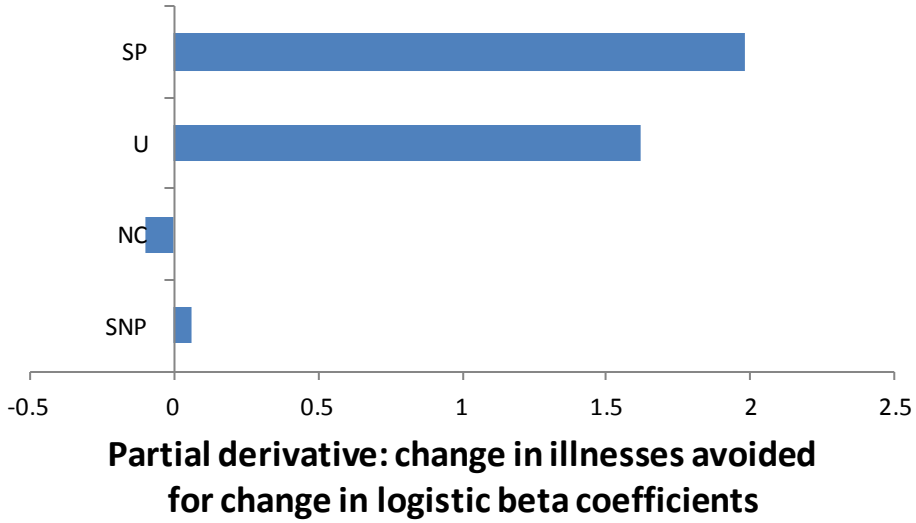

Figure 9. Sensitivity Analysis: Young Turkey-*Campylobacter* Model.

This tornado graph illustrates the partial derivatives of $\lambda_{avoided}$ with respect to the non-compliance (NC), unscheduled procedures (U), scheduled not performed procedures (SNP) and scheduled performed procedures (SP) logistic model coefficients.
Source: FSIS analysis of Agency generated data.

DISCUSSION

The model and analyses presented here examine available data to describe the quantitative relationship between observed *Salmonella*- and *Campylobacter*-positive samples and FSIS inspection activities taking place in young chicken and young turkey slaughter establishments. Each of the four product-pathogen pairs are modeled using the same decision variables with both an indiscriminate scenario and with a discriminate scenario. It is assumed that the association is predictive of the underlying relationship. It is further assumed that there is a probable relationship between observed *Salmonella* and *Campylobacter* positive samples in young chicken and young turkey slaughter establishments and attributable human illnesses from chicken and turkey consumption. A great deal of the quantitative portion of this risk assessment focuses on these two relationships.

Although more complicated models to relate occurrences of microbial pathogens to human illnesses might be conceived, the approach taken here makes the best use of available data to examine the potential public health effects of changes to inspection activities. It uses available inspection activity and pathogen testing data to assess the influence of those activities on the conditional likelihood of positive samples. This takes into account the differences in precision of the sampling data due to varying number of samples among the product-pathogen pairs for the data set available at the time of the assessment, and the complex empirical correlation structure between decision variable coefficients in the model's Stage 1 and their direct relationship to the estimated illnesses prevented in the model's Stage 2. It uses available human illness data to model the effect of changes in the likelihood of positive samples on numbers of human illnesses avoided. The methods used here have been applied extensively in other risk assessments (Bartholomew *et al*., 2005; Williams and Ebel 2012; Ebel *et al*., 2012; Withee *et al*., 2009). The risk assessment provides answers to each of the four risk management questions.

- *Can FSIS reallocate inspection activities in young chicken slaughter establishments without significant negative impact on microbial prevalence in the establishments?*

Depending on how reallocation of inspection activities is implemented, it is likely that changes in off-line inspection could result in a decrease in the numbers of positive microbial samples in FSIS-regulated young chicken and young turkey establishments. The results indicate that under some product-pathogen scenarios, the null hypothesis of no change in prevalence (or illness) would not be rejected at the 80% confidence level. In such cases, any purported public health benefits are dubious. Specifically, the ***discriminate scenario***, which only increases unscheduled inspection procedures, performs much better than the indiscriminate scenario, which does not target specific types of procedures, and the results suggest a reasonable degree of confidence that the ***discriminate scenario*** would do no harm.

The results reported for combined illnesses avoided are based on the assumption that the commodity-pathogen uncertainty distributions are independent. There is no empirical basis for accepting or rejecting this assumption. However, even if the uncertainty distributions were perfectly correlated (such that the percentiles simply summed), there would still be more than 90% confidence that the combined illnesses avoided under the scenario that increases unscheduled procedures exceeds zero (i.e., the 10th percentile of the combined *Campylobacter* illnesses avoided would be 30). The performance of both the HIMP and non-HIMP plants improved and converged over time.

This risk model results suggest that the ***discriminate scenario*** of increased off-line inspection could decrease the number of positive *Salmonella* and *Campylobacter* samples in young chicken and young turkey establishments with high probability.

Under the ***indiscriminate scenario*** in young chicken establishments, when off-line inspection procedures are increased, the model predicts an average decline of 2% in the proportion of samples testing *Salmonella* positive. However, when the substantially less robust *Campylobacter* data available at the time of the assessment are used, the model suggests a 0.2% increase in the proportion of samples testing *Campylobacter* positive. This very small increase is likely a function of the instability of this model, which is due to the combination of both small sample sizes and allowing the option of increasing off-line procedures that do not necessarily directly influence contamination rates. Under the ***discriminate scenario***, where only unscheduled inspection procedures are targeted for increase, the model in young chicken slaughter establishments predicts an average decline of 2% in the proportion of samples testing *Salmonella* positive, and an average decline of 0.44% in the proportion of samples testing *Campylobacter* positive. Removing the effect of this decision variable substantially reduces the probability that *Campylobacter* prevalence could increase.

Under the ***indiscriminate scenario*** in young turkey slaughter establishments, when off-line procedures are increased, the model predicts an average decline of 6% in the proportion of samples testing *Salmonella* positive, and an average decline of 26% in the proportion of samples testing *Campylobacter* positive. Under the ***discriminate scenario***, where only unscheduled inspection procedures are targeted for increase, the model in young turkey slaughter establishments predicts an average decline of 3% in the proportion of samples testing *Salmonella* positive, and an average decline of 19% in the proportion of samples testing *Campylobacter* positive.

However, the results under the discriminate scenario indicate that more than 90% confidence that the combined annual illnesses avoided under the scenario that increases unscheduled procedures exceeds zero (i.e., the 10th percentile of the combined *Campylobacter* illnesses avoided would be 30).

The results of the indiscriminant model suggest ambiguous effects of changes in the prevalence of inspection activities with respect to *Campylobacter* occurrence among young chicken establishments, with the possibility of increased illnesses occurring under some scenarios. Data supporting this model, however, was limited the smaller number of *Campylobacter* samples compared with *Salmonella* samples. Furthermore, this effect is primarily driven by the non-compliances decision variable. It is important to note that an increase in this variable might be expected to be associated with an increased prevalence of contamination, because when an inspector observes and records a non compliances in an establishment it is an indication that the establishment might not good food safety practices in place. That lack of good food safety practices could lead to an increase in positive results on product pathogen testing. Indeed the intended effect of changes in this category of procedures is arguable due to the diverse nature of potential reasons for non-compliances being issued in poultry slaughter establishments. Removing the effect of this decision variable in the alternative scenario substantially reduces the probability that *Campylobacter* prevalence could increase.

This latter conclusion is further supported by consideration of the HIMP structural variable in the young chicken-*Campylobacter* regression model (see Appendix). That model suggests that participation in HIMP was associated with a reduced prevalence of *Campylobacter*. Although *Campylobacter* occurrence was not considered in an analysis of HIMP establishments (FSIS, 2011a), these regression findings suggest that the positive *Salmonella* implications of that HIMP analysis also apply to *Campylobacter*.
In fact, the HIMP structural variable was (highly) statistically significant in all four regression models. In each case, that variable implied participation in HIMP was associated with reduced pathogen prevalence. While that regression model is not a focus of this risk assessment, the regression model's implication about HIMP establishments should provide some measure of confidence about the effects of the proposed rule – which intends to replicate HIMP across a wider swath of the poultry industry.

- *How will the relocation of on-line inspectors to off-line duties, or other areas within or outside the establishment, affect human illness?*

We assume that the total annual *Salmonella* and *Campylobacter* illnesses rates attributed to poultry are about 174,686 and 169,005, respectively (1).

Under the ***indiscriminate scenario***, where no specific category of procedures was targeted for increase, the model estimates an average decrease of 4,440 annual *Salmonella* illnesses attributable to young chicken and young turkey establishments combined, or an estimated prevention of 2.5% of those illnesses per year. The same scenario estimates an average increase

of 170 annual *Campylobacter* illnesses (0.1% of illnesses) attributable to young chicken and turkey establishments combined.

Under the ***discriminate scenario***, where only unscheduled procedures are targeted for increase, the model estimates an average decrease of 3,980 annual *Salmonella* illnesses (2.3%) attributable to young chicken and young turkey establishments, and an average decrease of 840 annual *Campylobacter* illnesses (0.5%) attributable to young chicken and turkey establishments combined.

- *Where within the establishment can relocated inspection activities have the most impact toward reducing microbial prevalence and corresponding human illness?*

The modeling results suggest that increasing unscheduled procedures would be most effective in reducing pathogen occurrence on carcasses. The other decision variables suggest ambiguous effects from their intended changes when those effects are considered across all four pathogen-product models. When targeting unscheduled inspection procedures in young chicken establishments, the estimated decrease in prevalence was 2% for *Salmonella* and 0.5% for *Campylobacter*. For young turkey establishments, the corresponding decrease in prevalence was 3% and 19% respectively.

- *What is the uncertainty about these effects?*

Our modeling approach includes the inherent uncertainty about the relationship between the frequency of inspection activities and pathogen prevalence, about the actual change in future inspection activities that would likely be observed, and about the representativeness of the rates of human *Salmonella* and *Campylobacter* illness attributable to poultry.

It is also advisable when encountering the results of the models might appear counterintuitive or inconsistent, when interpreting those results it is important to consider how model uncertainty, variability in the number of samples among the product-pathogen pairs, and the number of instances of a decision variable might affect the results. For example, among the product-pathogen pairs, there are more sample results for *Salmonella* than for *Campylobacter*, and more for chicken than turkey. The model's precision and correlation estimates and predicted illness reductions are highly dependent on variable sample size and assumptions of uniform data quality.

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APPENDIX

Regression Modeling Methods and Observational Datasets

This appendix explains the results of regression modeling that are the foundation of this risk assessment. It is here that evidence about the occurrence of pathogens on poultry carcasses is statistically linked to evidence about possible explanatory variables. Based on these findings, the body of this report estimates human illnesses avoided following implementation of the poultry slaughter rule.

The proposed rule intends to shift some on-line inspectors to off-line inspection duties. It is assumed that the increased off-line inspection work force would– because of apparent correlations between performance of inspection procedures and occurrence of pathogens on carcasses – influence public health exposures to these foodborne pathogens.

Regression models were developed to assess the strength of relationships between the performance of off-line inspection procedures and the prevalence of *Salmonella* and *Campylobacter* on young chicken and young turkey carcasses. A binary logistic regression with coefficients that are weighted by slaughter volume were estimated.

Previously, the basic modeling approach was peer reviewed and revised in the 2008 version of this risk assessment. In this version, the number of samples and variables evaluated were increased. Prior experience with the logistic regression modeling of FSIS poultry slaughter sampling verification methods – and inspector procedure data – were used to update the model. Also, this version included modifications in response to comments from the National Advisory Committee on Meat and Poultry Inspection (NACMPI) after release of the 2008 FSIS Risk Assessment (FSIS, 2008a).

Regression Model Approach

Four basic regression models are estimated to account for the two target pathogens (*Salmonella* and *Campylobacter*) and two major poultry classes (young chickens and young turkeys). For each product-pathogen pair, a multivariate logistic model is fit. Each model accounts for slaughter volume and the clustered (and correlated) nature of the data available from slaughter establishments. Each model uses pseudo-likelihood estimation and employs a correction for over-dispersion.

Each model evaluates pathogen prevalence in relation to four off-line inspection procedure categories: (i) scheduled and performed; (ii) scheduled but not performed; (iii) unscheduled; and

(iv) non-compliances. These four categories of inspection procedures encompass the totality of procedure elements across six classes of standard off-line procedures completed by FSIS personnel: (i) sanitation; (ii) HACCP; (iii) wholesomeness/economic consumer protection; (iv) sampling; (v) sanitation performance standards; and (vi) emergency procedures.
The four defined categories were chosen because the expected/intended effect of the modeled alternative scenario was consistent for procedures within each category. For example, the proposed increase in off-line inspectors is expected to increase scheduled and performed procedures. Similarly, increased availability of off-line inspectors should increase unscheduled procedures while reducing scheduled but not performed procedures. It is also assumed that – in the long-run – reported non-compliances would decrease with more off-line inspectors in slaughter establishments because such establishments would attain appropriate process control. Although an alternative approach was explored that collapsed decision variables according to the six classes of off-line procedures, this approach created confusion about the intended effect of the alternative scenario modeled within each class. For example, a random variable that summarized all HACCP procedures would need to increase scheduled and performed procedures (and unscheduled procedures) but also decrease scheduled but not performed procedures (and non-compliances). Thus, some components of the aggregate HACCP procedures variable would be going up (positive signs) while others would be going down (negative signs) – leaving any interpretation of effects on pathogen prevalence in establishments as, at the least complex, and most likely intractable.

Because of the observational nature of the data, a set of structural variables were used to control confounding. These structural variables pertained to non-inspection activities but included consideration of establishment size, temporal, spatial and other establishment factors.
The regressions are estimated using SAS Proc Logistic version 9.1 software. The logit link function is used for the dependent variable and quasi-maximum likelihood estimates of the structural and decision variable regression coefficients are obtained using the Fisher scoring algorithm. Wald statistics are calculated for assessing the significance of regression coefficients. The general form of the binary model relating unconditional probabilities (p) to the regression coefficients (b_i) in standardized form with X_i's as the regressors is:

$$p = \exp(b_0 + b_1 X_1 + b_2 X_2 + \ldots + b_n X_n) / (1 + \exp(b_0 + b_1 X_1 + b_2 X_2 + \ldots + b_n X_n))$$

The logit link function relating the natural log of the odds ratio (p/(1-p)) to the standardized regression coefficients is:

$$\log(p/(1-p)) = b_0 + b_1 X_1 + b_2 X_2 + \ldots + b_n X_n$$

A single estimate of the linear component in the prevalence prediction equations is η which is equal to the logit or $\log((p)/(1-p))$.

$$\eta = b_0 + b_1 X_1 + b_2 X_2 + \ldots + b_p X_p ,$$

The scalar quantity, η, is simplified to:

$$\eta = BX$$

in the tables below where B and X are vectors of the b coefficients and the X means combined as a linear composition

The estimate of the **η** vector over all data points is a vector equation. Each vector element represents a data point from the **X** matrix of n data points and p variables plus the intercept.

$$\boldsymbol{\eta}(n,1) = \mathbf{X}(n,p+1)\mathbf{b}(p+1,1)$$

At each iteration of the multivariate normal distribution of regression coefficients in the simulation model first stage a **b*** vector is produced.

$$\mathbf{b^*}(n,1) = \mathbf{b} + \mathbf{z}\ C,$$

where C'C = S, the variance-covariance matrix taken from the SAS model output and C is the upper triangular Cholesky factor of S. The result is that for each iteration of **b*** a new set of multivariate normal regression coefficients is estimated. The coefficient vector, **b**, has the initial quasi-likelihood regression coefficient estimates and **z** is a vector of random normal deviates. So, at each iteration the vector, **η*** is produced.

$$\boldsymbol{\eta^*}(n,1) = \mathbf{X}(n,p+1)\mathbf{b^*}(p+1,1)$$

The equation for estimating a single prevalence for a single η estimate is the inverse logistic equation.

$$p = 1/(1+\exp(-\eta))$$

The equation for estimating the prevalence vector over all data points is the vectorized inverse logistic equation.

$$\mathbf{p}(n,1) = 1/(1+\exp(-\boldsymbol{\eta}(n,1)))$$

At each of the 100,000 iterations of the model the weighted average of the **p** vector is taken and then divided by the baseline prevalence. The weighted prevalence of the **p** vector is the weighted average.

$$p_{ave} = \sum_1^n w_i p_i / \sum_1^n w_i$$

The ratio of the average weighted prevalence to the baseline prevalence is the simple ratio of p_{ave} to $p_{baseline}$. The baseline prevalence is estimated from the single prevalence estimating equation where η is calculated with the b's taken at their maximum quasi-likelihood estimates. Because multiple variables were identified as possible contributors to each logistic regression model the SAS forward selection procedure in proc logistic was used to include structural variables in the model with the largest data set (chicken-*Salmonella* with n=22,761). This method proved adequate for identifying structural variables to include in the model except for the time variable which was problematic. The selection of the appropriate time variable as a categorical variable representing each month of the time series represented by each of the four models was decided by the matrix of AIC, BIC, R-squared (Nagelkerke corrected), Hosmer-Lemeshow test p-value, AUC (area under the curve) as the c coefficient, and the validation statistic. Each of these statistics was captured from the SAS proc logistic output. This same matrix is used below for the evaluation of the final four models. The best categorical time variable combination is identified by the smallest AIC and BIC, the largest R-squared, a p-value for the Hosmer-Lemeshow test greater than 0.05, a significant c coefficient representing the area under the ROC curve, and a decreasing validation statistic. The validation statistic, v, is calculated as the average sum of squares of the predicted prevalence minus the cross-validated prevalence (using N-1 deletion in proc logistic) divided by (1-leverage(h)).

$$v = \sum_1^n ((p_i - pcv_i) / (1 - h_i))^2 / N$$

The relationship between the validation statistic and R-squared provide evidence that the model is not over-parameterized if the Nagelkerke parameter corrected R-squared is increasing but the validation statistic is not increasing which means for the sample size the increasing R-squared that naturally increases with increasing parameters in the model is balanced by increasing information in the model. The point at which R-squared and v increase together is where too many parameters have been added to the model even though they may be significant. The categorical time selection matrix is shown in Table A-1a for the chicken *Salmonella* model.

Since it is well known that *Salmonella* prevalence is seasonal several categorical time variable groups were evaluated that encompassed broad and narrow seasonal definitions. These groups were four quarters, 12 months, and the total months of the study which varied among models. Because of the unusual data structure that required rehang and post-chill prevalence from the baselines in the first 12 months and only post-chill prevalence in the last three 12-month cycles,

categorical time variables with interaction components were added as additional categorical variables for the quarterly (8 components) and 12 month variables (24 components). Due to the unusual data structure for a binary logistic model the 39 monthly component variable was selected on the basis of the smallest AIC and BIC and the largest R-squared, Hosmer-Lemeshow p-value, and c statistic. The validation statistics were all similar in magnitude. This same analysis was carried out for each of the four prevalence models. The selection matrix for the four final regression models is shown in Table A-1b.

Each binary logistic regression model was evaluated for lack of fit to the data using the standard Hosmer-Lemeshow test. All models are required to pass this test for fit to the logistic distribution. Model over-dispersion was evaluated with the Pearson chi-square divided by the degrees of freedom. The dispersion parameter statistic indicating over-dispersion requires multiplication of the covariance matrix to correct for the over-dispersion when greater than 1.05. This adjustment converts the regression coefficient estimates to quasi-likelihoods and appropriately decreases the regression coefficient significance by increasing the standard errors of the estimates effectively converting the model dispersion parameter to unity. Unconditional maximum likelihood estimates are used because the total sample size in the data structure is sufficiently large. A conditional analysis was assessed, but offered no advantage. The conditional analysis shows an advantage when the total sample size is small (in the hundreds or less). The expected requirements for a valid unconditional maximum likelihood analysis are met for both the *Salmonella* and *Campylobacter* datasets.

Data Sets

The core data come from the FSIS "Young Chicken Baseline" (July 2007 through September 2008) and the FSIS "Young Turkey Baseline" (August 2008 through July 2009). Both baselines provide data for *Salmonella* and *Campylobacter* sampling at rehang and post-chill locations. These data are supplemented with young chicken and young turkey data from the FSIS PR/HACCP *Salmonella* verification program (July 2007 through September 2010).

Data from 189 young chicken slaughter establishments provided 6,558 Baseline results for *Salmonella* and *Campylobacter,* with an additional 16,115 PR/HACCP post chill results added to the *Salmonella* dataset. In the Baseline data there were 3,379 samples taken at rehang and 3,278 taken at post chill. There are 2,790 positive *Salmonella* results out of 22,671 total results, and 4,809 positive *Campylobacter* results out of 6,558 total results.

For young turkeys, there were 65 establishments in the *Salmonella* dataset and 58 establishments in the *Campylobacter* dataset. The *Salmonella* dataset had 8,749 samples (2,884 baseline and 5,865 regulatory) of which 638 (7.29%) were positive and the *Campylobacter* dataset had 2,884 samples of which 343 (11.89%) were positive.

Decision variables: Inspection procedures

There are six general inspection system procedure (ISP) code activity categories captured in the FSIS database (Table A-3). Sums of daily scheduled and unscheduled procedures performed – as well as unperformed procedures and non-compliance reports – for individual establishments were matched with same-day positive and negative *Salmonella* or *Campylobacter* results.

The ISP codes from the FSIS database were tabulated daily for all scheduled procedures, unscheduled procedures, uncompleted procedures, non-compliances, and total procedures performed for each establishment. Scheduled procedures are assigned to each establishment's shift according to a systematic process by an automated Performance-Based Inspection System. Unscheduled procedures are performed according to in-establishment inspector availability that goes beyond the time allocated for performing scheduled procedures; they typically involve regulatory inspection activities such as fecal checks for zero-tolerance beyond the requirement of twice per line per shift or other procedures not regularly scheduled or performed. Unscheduled procedures are also performed in response to unforeseen hazards such as metal or plastic in product which are identified during operations and were not previously seen at this stage in operations, or unsanitary conditions arising from Sanitation Standard Operating Procedures (SSOP) failures, and PR/HACCP corrective actions.

Among the six general ISP procedure activities, 47 specific ISP procedure codes were used. These included five Sanitation (01) codes, 17 PR/HACCP (03) codes, 11 Wholesomeness/Economic Consumer Protection (04) codes, six Sampling (05) codes, four Other Inspection Requirements (06) codes and four Emergency Activity (08) codes (Table A-3). Ultimately, these specific codes were designated in the database as scheduled and performed (SP), scheduled and not performed (SNP), unscheduled (U) and non-compliance (NC). The inspection procedures used in the model are shown in Table A-3. The code sum variable denotes the summed procedure elements on each sample day while the detail sum variable gives specific details of each inspection procedure element included in the daily sums.

The total activity for each of these four categories was calculated as the sum across all codes for that category. The categories are repetitive such that all are the same except for unscheduled procedure which include the extra emergency procedures (08) elements. The four categories are sub-categorized with the common name for the procedure followed in parenthesis by the procedure element code:

SP = scheduled and performed procedures for sanitation(01), HACCP(03), wholesomeness/economic consumer protection(04), sampling(05), other inspection requirements(06), sanitation performance standards (06D01), raw ground (03B), raw not ground (03C), fecal check (03J), economic poultry kill (04C04)

SNP = scheduled not performed procedures for sanitation(01), HACCP (03), wholesomeness/economic consumer protection(04), sampling (05), other inspection requirements (06), sanitation performance standards(06D01), raw ground (03B), raw not ground (03C), fecal check(03J), economic poultry kill (04C04)

U = unscheduled procedures performed for sanitation(01), HACCP(03), wholesomeness/economic consumer protection(04), sampling(05), other inspection requirements(06), sanitation performance standards(06D01), raw ground(03B), raw not ground(03C), fecal check (03J), economic poultry kill (04C04), emergency procedures (08)

NC = non-compliant procedures for sanitation(01), HACCP(03), wholesomeness/economic consumer protection(04), sampling(05), other inspection requirements(06), sanitation performance standards(06D01), raw ground(03B), raw not ground(03C), fecal check(03J), economic poultry kill(04C04).

Structural variables: Non-inspection procedures

A minimal set of structural variables were found to contribute most to reducing the model deviance, controlling confounding and providing the best overall model fit to the data as assessed by the Hosmer-Lemeshow test. Structural variables were selected using forward regression in the SAS logistic procedure with the probability to enter the model taken as 0.05. Twelve of nineteen tested structural variables provided the best model[10] (i.e., the inclusion of these structural variables significantly reduces the model deviance). These structural variables are:

1. The **re-hang** variable distinguishes between locations of sample collection (where 1 signifies post-chill samples and 0 signifies re-hang samples).

[10] Variables that were considered but are excluded because of less contribution or overlapping contribution to the model fit to the data are HACCP size (Large, Small, and Very Small according to the Small Business Administration definition), production area, inspector positions (numbers of supervisors, on-line inspectors, and off-line inspectors), time in weeks (52), time in months (12), time in quarters (4 and 12), time in years (4), and time from grant of inspection date.

[8] Line speed is defined as the maximum rated speed allowable by regulation for the establishment inspection/evisceration system(s) in use at the time of sampling. The units are "birds per minute" or "bpm" and refers to the maximum number of carcasses that passes a given point on the line every minute. FSIS does not record ongoing line speed in poultry establishments, but is allowed to evaluate line speed with a stop watch. It is evaluated as a fixed categorical variable in the models because there is no day-to-day data available.

[9] Number of establishment inspectors is specific for each establishment. Therefore it is not an average and varies by establishment depending on the number of slaughter lines and the size of the establishment. The larger the establishment and the more processing activities the greater the size of the inspection staff required

[10] Line count is the number of slaughter lines in the establishment.

2. The **categorical month** variable breaks down the time dependency into 39 consecutive months. The last study month in 2010 is used as reference. In the case of *Campylobacter* this variable was shortened to 12 months due to only one year of data being available.
3. The **categorical district** variable differentiates the 15 districts. District 90 is used as the reference.
4. **Linespeed[8] (carcasses per minute)** - the maximum rated speed allowable by regulation for the establishment inspection/evisceration system(s) in use at the time of sampling.
5. **Number of establishment inspectors[9]**,
6. **Linecount[10] (number of processing lines)**
7. The **categorical inspection system** variable identifies 22 inspection type combinations (Table A-7) from the eight basic types (MAESTRO, NELS, Nu-Tech, Nuova, SIS, HIMP, Traditional, and Religious Slaughter). Traditional inspection is used as the reference. (Table A-4 shows these categories for young chicken while Table A-5 shows the shorter list for young turkey)
8. The binary **HACCP Inspection Models Project (HIMP) variable** appears separately in the young chicken models and examines the HIMP establishment model contribution. Non-HIMP establishments are used as the reference.
9. **Septicemia-toxemia** the number of condemnations of carcasses as the daily total,
10. **Contamination** the number of contaminated carcasses condemned for contamination (fecal, ingesta, body fluids, etc.) as the daily total
11. **Air sacculitis** the number of cases among carcasses as the daily total
12. **Synovitis** the number of cases among carcasses as the daily total (only a relevant disease to the turkey slaughter).

Final Models

Tables A-6 and A-7 list the estimated regression coefficients, standard errors, the means and the standard deviations for all decision and structural variables in the young chicken models. Tables A-8 and A-9 show these estimates for young turkey. The same structural variables were used in each of the models to compensate for confounding. Some coefficients have non-significant contributions according to a 0.05 significance assumption but were retained in the model for consistency across all four models.

Among the four decision variables, a common finding across all four models was that the coefficient for unscheduled procedures was consistently negative. This finding suggests that increasing these procedures (while holding other variables constant) would decrease the prevalence of *Salmonella* and *Campylobacter*. Nevertheless, the unscheduled procedures U variable is only statistically significant in the chicken-*Salmonella* and turkey-*Campylobacter* models.

Among structural variables, a common finding was the (statistically significant) negative coefficient for HIMP participation across all four models. The HIMP participation variable is a separate structural variable in the chicken models, but it is incorporated into an inspection system variable in the turkey models. This finding suggests that when this variable is assigned a value of one (indicating participation in HIMP), the prevalence of *Salmonella* and *Campylobacter* predicted by the model is lower than when the alternative (non-HIMP) participation value is assigned[11].

The baseline post-chill prevalence predictions from each model are derived by setting the rehang structural variable to one. Comparing these predictions to production-volume weighted prevalence values from the data suggests that the model reasonably reflects the empiric evidence. For example, the chicken-*Salmonella* model predicts a post-chill prevalence of 0.058 versus a weighted average of 0.053 from the raw data. The chicken-*Campylobacter* model predicts a post-chill prevalence of 0.63 versus a weighted average of 0.61 from the raw data. The turkey-*Salmonella* model predicts a post-chill prevalence of 0.046 versus a weighted average of 0.069 from the raw data. The turkey-*Campylobacter* model predicts a post-chill prevalence of 0.009 versus a weighted average of 0.008 from the raw data. Differences between predicted and raw values generally reflect the additional weighting for other structural factors (e.g., temporal factors, spatial factors, line speed, HIMP participation, etc.) included in the predicted values (but not included in the simple weighting of the raw data prevalence levels).

[11] This alternative value is -1 for the chicken-*Salmonella* model and zero for the other models.

Alternative models were assessed by using 43 and 21 decision variables. Models were compared with respect to three statistics: the Akaike Information Criterion (AIC); the Bayesian Information Criterion (BIC-Schwartz); and the coefficient of determination (R-squared). For the young chicken-*Salmonella* model, the four decision variable model was best according to all statistics (Table A-2). For the young chicken-*Campylobacter* model, the BIC and R-squared statistics indicated the four decision variable model was best, although the AIC suggested the 21-variable model was preferred. For the young turkey models (*Salmonella* and *Campylobacter*), only the BIC statistic supported the four variable model while the other models were each preferred by different statistics. Nevertheless, to maintain consistency when estimating effects of the expected model scenarios, the four decision variable model for each product-pathogen pairing was selected. The R-square values for these chicken-*Salmonella*, chicken-*Campylobacter*, turkey-*Salmonella* and turkey-*Campylobacte*r models are 0.2707, 0.4124, 0.0966, and 0.3328 respectively.

For model evaluation and validation, the datasets used in model development were randomly split, the regression coefficients for each subset of data were re-estimated and the stability of the prevalence estimates were assessed (Picard *et al*. 1990).

Tables A-10 and A-11 show the results of splitting the young chicken datasets for *Salmonella*. Table A-8 shows the parameter estimates for the un-split data model estimates and also for the two split halves of data. Table A-11 shows the prevalence estimates from each of the models compared to the unadjusted prevalence estimates from the full dataset. The model appears to be stable when splitting the data since all estimates for the mean, rehang, and post-chill prevalence are in close agreement. Also, the post-chill prevalence is within the sampling error of the post-chill prevalence found in the FSIS HIMP report (FSIS 2011a). The only matter of concern is the estimation of the mean prevalence which is lower than the unweighted overall prevalence. This is likely due to the model weighting compensating from the relatively high prevalence at re-hang and the low prevalence at post-chill.

Similarly, the results for splitting the young chicken *Campylobacte*r dataset are shown in Tables A-12 and A-13. The parameter estimates from Table A-10 are used to calculate the prevalence estimates in Table A-13. The BX element as described above equal to η in Table A-11 is the sum of cross products of the B regression parameter and the mean variable components in the model. By back transforming BX through the inverse logit function the estimated prevalence is obtained. The prevalence estimates for the mean, rehang, and post-chill are consistent within the sampling error across the dataset splits. There is no external comparison data for *Campylobacte*r.

Tables A-14 and A-15 show the dataset splitting results for young turkey *Salmonella*. All the prevalence estimates are consistent with sampling error across the splits of data and agree with

the full dataset estimates. The estimates are in agreement with the high unweighted *Salmonella* prevalence.

Tables A-16 and A-17 show the dataset splitting results for young turkey *Campylobacte*r. This model has the smallest number of observations and the expectation with split datasets is that there would be some variability not seen with the larger datasets. This is in fact the case. For although the rehang and post-chill estimates are in relatively close agreement there is variation with the mean estimates which tend to be lower than the unweighted prevalence estimate. Since this is a concern further model evaluation is warranted.

Figures A-1through A-4 show the Receiver Operating Characteristic (ROC) plots for the four models. The interpretation of these plots is that the model is more predictive the greater the distance the curve is away from the imaginary diagonal dividing the figure in halves. The best predictors are the closest to the 100% sensitivity and 0% 1-Specifity corner point. Sensitivity is defined as the number of positives (taken as the number of positives with a given cut point) divided by the total positives (taken as the number of FSIS positive tests) . The false positive rate is defined as 1 – Specificity. Where the specificity is the number of negatives (taken as the number of negatives with the same cut point) divided by the total negatives (taken as the number of FSIS negative tests). The curve described by ROC plot follows the various cut points dividing the positives and negatives from the total positives and total negatives thus producing corresponding pairs of sensitivity and 1-specificity on the ROC curve. A standard method for ROC curve evaluation is to estimate the area under the curve (AUC). This can be done using the SAS logistic procedure output for binary response models. The c-statistic is equivalent to the area under the curve (AUC). Each c-statistic was evaluated for significance against the c=0.5 non-significant alternative and passed the z-test with $p<0.05$ (Hosmer and Lemeshow, 2000). The predictive order of c coefficients across the four models is 0.702, 0.710, 0.792, and 0.852, making the young chicken *Campylobacter* the least predictive, young turkey *Salmonella* somewhat more predictive, young chicken *Salmonella* still more predictive, and the young turkey *Campylobacter* model the most predictive. However, all models are sufficiently predictive with areas under the curve all greater than 0.7.

Because the analysis so far shows that the unscheduled procedures regression coefficients are consistent in sign and generally significant across all four models, curiosity about what the four model sets expanded for only unscheduled procedures might look like was undertaken. Because the turkey-*Salmonella* model does not have a significant aggregate coefficient only the three remaining models were considered. Therefore, the previously aggregated sets of sanitation, HACCP, wholesomeness/economic consumer protection, sampling, other inspection requirements, and emergency procedures were disaggregated and put into each of the models with their respective structural variables. Table A-18 shows the results for the four models. The results are mixed between significant negative coefficient signs for decreased prevalence and

significant positive coefficient signs for increased prevalence. Because of the aggregate significant negative sign coefficients for two of the four models, focusing on the same type of significant negative coefficient in the disaggregated models seemed justified. The HACCP(03), wholesomeness/economic consumer protection (04), and other inspection requirements (06) procedure elements have this characteristic in the chicken-*Salmonella* model and the wholesomeness/economic consumer protection (04) and sampling(05) procedures elements behave similarly in the chicken-*Campylobacter* model with the HACCP(03) element almost significant. The turkey-*Campylobacter* model has the HACCP(03) and other inspection requirements (06) elements significant. It is not clear why the sampling(05) and other inspection requirements (06) coefficients have significant positive signs in the chicken models. Table A-19 shows the results for further disaggregated models. It becomes clear that the fecal check(03J) procedures are the drivers decreasing prevalence for HACCP in the chicken-*Campylobacter* model and the sanitation performance standards (06D01) procedures are drivers for other inspection requirements in the chicken-*Salmonella* and turkey-*Campylobacter* models. The prevalence estimates from these models shown in Table A-20 indicate the same consistent predictability and validity associated with the subset models that was verified with the same collinearity analysis.

PRIA Dataset Evaluation

Because the original observational dataset used to develop the four models for scenario analysis excluded some of the establishments that are expected to adopt the proposed inspection system a presumptive dataset including all poultry slaughter establishments was created. The over-arching assumption required a shift of the majority of on-line inspectors to off-line inspection duties while leaving one inspector on-line for final carcass inspection according to the Preliminary Regulatory Impact Analysis (PRIA) of the proposed poultry slaughter rule. A simulated dataset corresponding to all establishments expected to adopt the proposed inspection system was created. Looking at the establishment breakdown by the small business administration (SBA) size classification of large, small, and very small establishments (L, S, V) it was noticed that there is an imperfect match between the observed establishment size and the total number of establishments available. Additionally none of the very small establishments in the observational dataset are expected to adopt the proposed inspection system. This is an assumption taken from the PRIA where very small establishments are not expected to accept the proposed system due to economic burden. Table A-21 shows the breakdown for SBA size for the observational study and Table A-22 shows the expected size breakdown for establishments that would adopt the proposed inspection system according to the PRIA. Therefore, four simulated datasets were constructed based on the known characteristics studied in the observational analysis and using substituted known values according to matched establishment characteristics based on the list of establishments expected to adopt the proposed inspection system. Repeated random selection of establishments with matching characteristics created an averaged (expected

value) dataset corresponding to the characteristics of the establishment distribution of establishments expected to adopt the proposed inspection system.

It was found that each of the four observed datasets could be recast to resemble the distribution of establishments expected to adopt the proposed inspection system as shown in Table A-23. The 19 establishments in the "other" category were placed in either the young chicken or the young turkey datasets according to size and predominant production characteristics. The 19 "other" establishments accounted for all the very small establishments in the expected datasets. However, upon further inspection it became apparent that all but the small establishments in the *Salmonella and Campylobacter* young chicken datasets were subsets of the original four observed datasets. This meant that 4% and 10% of the small plants from these two datasets would have to be reused in recasting the expected distributions for the young chicken *Salmonella and Campylobacter* models. This was not a problem when all four datasets were recast as expected datasets for logistic regression analysis and the four expected dataset prevalence estimates were found to be within the prevalence error of each the observed datasets (Table A-24). It is therefore assumed that the results of the four observed dataset models contain the results of the four expected dataset models and that no further analysis is required because the conclusions of the risk assessment contain the same conclusions that can be drawn from the expected datasets.

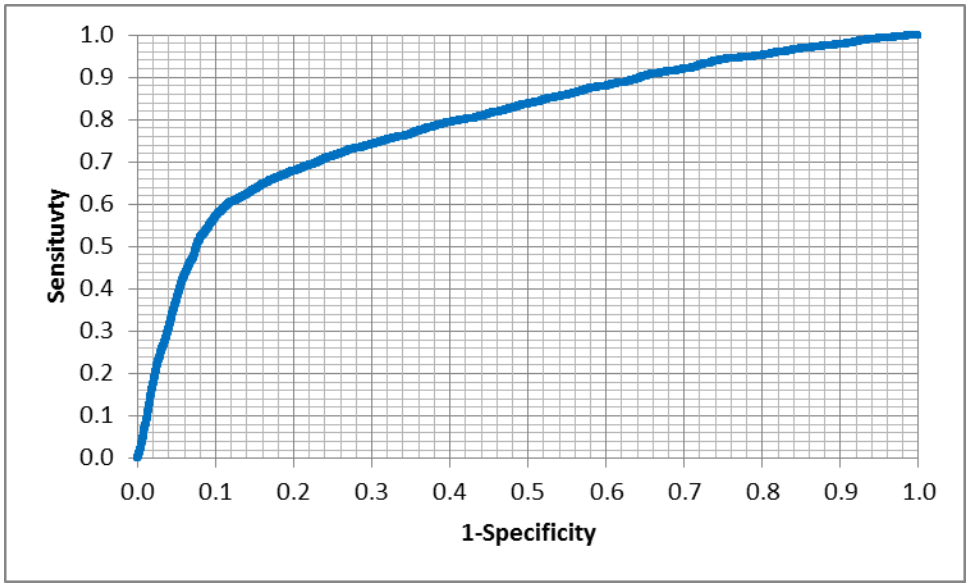

Figure A-1. ROC Plot of Sensitivity against 1-Specificity with an AUC of 0.792 for the Young Chicken *Salmonella* Predictive Model

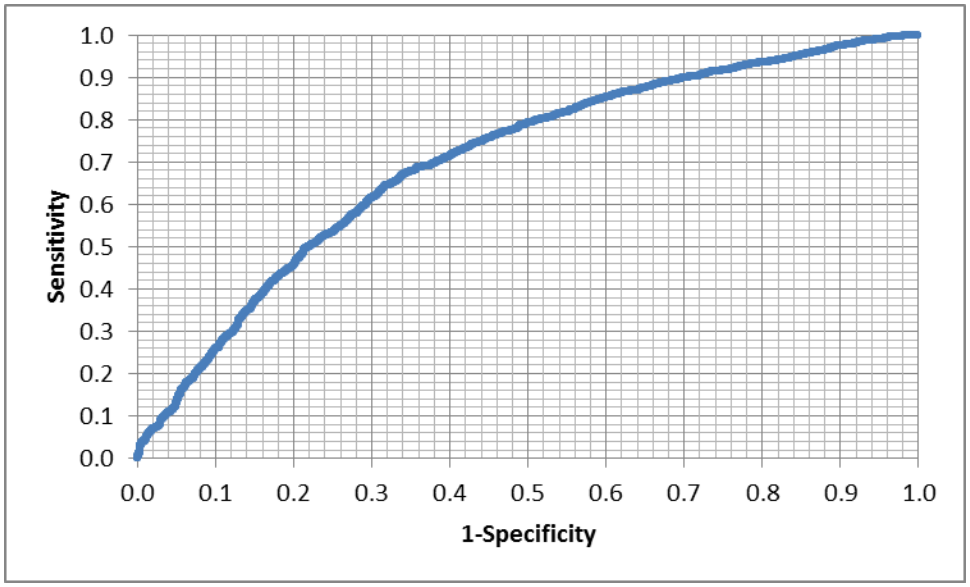

Figure A-2. ROC Plot of Sensitivity against 1-Specificity with an AUC of 0.702 for the Young Chicken *Campylobacter* Predictive Model

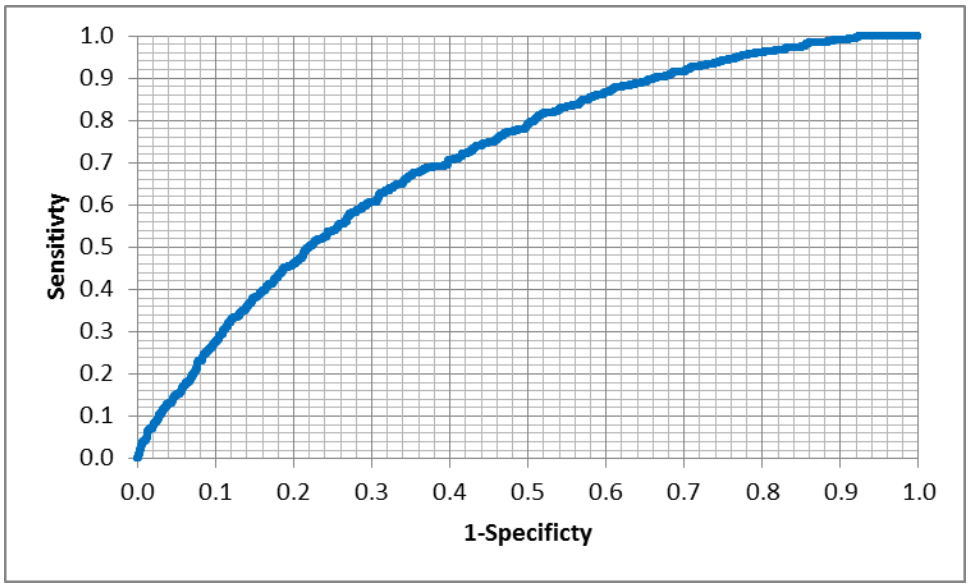

Figure A-3. ROC Plot of Sensitivity against 1-Specificity with an AUC of 0.710 for the Young Turkey *Salmonella* Predictive Model

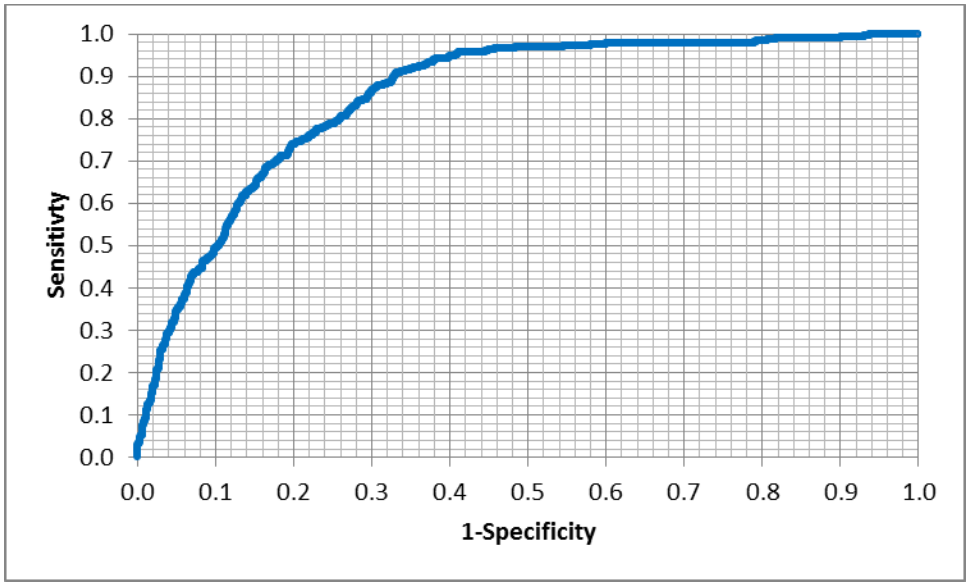

Figure A-4. ROC Plot of Sensitivity against 1-Specificity with an AUC of 0.852 for the Young Turkey *Campylobacter* Predictive Model

APPENDIX TABLES

Table A-1a. Categorical Time Selection Matrix for Chicken *Salmonella* Model

Statistic	month39[1]	quarter4[2]	month12[3]	quarter8[4]	month24[5]
AIC[6]	68,942.52	69,317.84	69,124.08	69,312.80	69,090.97
BIC[7]	69,633.00	69,727.31	69,597.78	69,746.36	69,652.99
R-Sq[8]	0.2707	0.2645	0.2674	0.2645	0.5535
p(H-L)[9]	0.4537	0.0065	0.0005	0.0034	0.2137
c[10]	0.792	0.784	0.787	0.784	0.787
Validation[11]	0.0002	0.0002	0.0011	0.0002	0.0002
Parameters[12]	85	50	58	53	69
N	22,671	22,671	22,671	22,671	22,671

[1] *Model with 39 month categorical time scale*
[2] *Model with 4 quarter categorical time scale*
[3] *Model with 12 month categorical time scale*
[4] *Model with 4 quarters and 4 interactions*
[5] *Model with 12 months and 12 interactions*
[6] *Akaike information criterion- smaller is better*
[7] *Bayesian information criterion (Schwarz) – smaller is better*
[8] *Adjusted R-Square (Nagelkerke) – larger is better*
[9] *p-value for Hosmer-Lemeshow test – greater than 0.05 is better*
[10] *c-statistic – greater than 0.7 is better*
[11] *Validation statistic- smaller is better*
[12] *Number of parameters in model minus intercept*

Table A-1b. Selection Matrix Variables for the Final Four Prevalence Models

Statistic	CS[1]	CC[2]	TS[3]	TC[4]
AIC[5]	68,942.52	36,661.69	4,438.87	1,283.20
BIC[6]	69,633.00	37,055.42	4,913.01	1,521.88
R-Sq[7]	0.2707	0.4124	0.0966	0.3328
p(H-L)[8]	0.4537	0.7585	0.981	0.5631
c[9]	0.792	0.702	0.71	0.852
Validation[10]	0.0002	0.0003	0.0002	0.0011
Parameters[11]	85	57	66	39
N	22,671	6,558	8,749	2,884

[1] Chicken *Salmonella* Model
[2] Chicken *Campylobacter* Model
[3] Turkey *Salmonella* Model
[4] Turkey *Campylobacter* Model
[5] Akaike information criterion- smaller is better
[6] Bayesian information criterion (Schwarz) – smaller is better
[7] Adjusted R-Square (Nagelkerke) – larger is better
[8] p-value for Hosmer-Lemeshow test – greater than 0.05 is better
[9] c-statistic – greater than 0.7 is better
[10] Validation statistic- smaller is better
[11] Number of parameters in model minus intercept

Table A-2. Selection Matrix Variables for Prevalence Model Comparison

Model	Criterion	Value	model	Criterion	Value
CS-43[1]	AIC[7]	13730.6	CC-43[4]	AIC	38935.89
CS-43	SC[8]	14734.2	CC-43	SC	39354.04
CS-43	-2 Log L[9]	13480.6	CC-43	-2 Log L	38812.69
CS-43	R-Square[10]	0.2673	CC-43	R-Square	0.4380
CS-21[2]	AIC	13719.5	CC-21[5]	AIC	37681.16
CS-21	SC	14538.4	CC-21	SC	38085.84
CS-21	-2 Log L	13515.5	CC-21	-2 Log L	37561.93
CS-21	R-Square	0.2645	CC-21	R-Square	0.4239
CS-4[3]	AIC	13535.3	CC-4[6]	AIC	36661.69
CS-4	SC	14225.8	CC-4	SC	37055.42
CS-4	-2 Log L	13363.3	CC-4	-2 Log L	36545.69
CS-4	R-Square	0.2707	CC-4	R-Square	0.4124

[1] *Chicken Salmonella model- 43 decision parameters*
[2] *Chicken Salmonella model- 21 decision parameters*
[3] *Chicken Salmonella model- 4 decision parameters*
[4] *Chicken Campylobacter model- 43 decision parameters*
[5] *Chicken Campylobacter model- 21 decision parameters*
[6] *Chicken Campylobacter model- 4 decision parameters*
[7] *Akaike information criterion – smaller is better*
[8] *Bayesian information criterion (Schwartz) – smaller is better*
[9] *-2 Log Likelihood – smaller is better*
[10] *R-Square (Nagelkerke) – larger is better*

Table A-2. (continued)

Model	Criterion	Value	model	Criterion	Value
TS-43[11]	AIC[7]	5141.39	TC-43[14]	AIC	3576.64
TS-43	SC[8]	6022.06	TC-43	SC	4755.80
TS-43	-2 Log L[9]	4892.52	TC-43	-2 Log L	3243.41
TS-43	R-Square[10]	0.1134	TC-43	R-Square	0.5407
TS-21[12]	AIC	4679.51	TC-21[15]	AIC	1282.97
TS-21	SC	5295.49	TC-21	SC	1628.31
TS-21	-2 Log L	4505.44	TC-21	-2 Log L	1167.20
TS-21	R-Square	0.1013	TC-21	R-Square	0.3440
TS-4[13]	AIC	4438.87	TC-4[16]	AIC	1283.20
TS-4	SC	4913.01	TC-4	SC	1521.88
TS-4	-2 Log L	4304.87	TC-4	-2 Log L	1203.20
TS-4	R-Square	0.0966	TC-4	R-Square	0.3328

[7] *Akaike information criterion – smaller is better*
[8] *Bayesian information criterion (Schwartz) – smaller is better*
[9] *-2 Log Likelihood – smaller is better*
[10] *R-Square (Nagelkerke) – larger is better*
[11] *Turkey Salmonella model- 43 decision parameters*
[12] *Turkey Salmonella model- 21 decision parameters*
[13] *Turkey Salmonella model- 4 decision parameters*
[14] *Turkey Campylobacter model- 43 decision parameters*
[15] *Turkey Campylobacter model- 21 decision parameters*
[16] *Turkey Campylobacter model- 4 decision parameters*

Table A-3. Inspection System Procedure (ISP) Code Listing of Individual and Summed Codes, used as Independent Variable Identifiers for Daily Sums of Procedures Scheduled, Performed, Unscheduled, and Non-Compliant in the Binary Logistic Regression Model

No.	**Code Sum***	**Activity**	**Detail Sum****	**Elements**	**No.**	**ISP Code**	**Procedures**
1	sum01	sanitation	sum01A	verification	24	01A01	sanitation SOP
2	sum01	sanitation	sum01B	preoperational	25	01B01	m/v/r/ca/fu[4]
3	sum01	sanitation	sum01B	preoperational	26	01B02	01B01 verification
4	sum01	sanitation	sum01C	operational	27	01C01	m/v/r/ca/fu[4]
5	sum01	sanitation	sum01C	operational	28	01C02	01C01 verification
6	sum03	HACCP	sum03A	verification	29	03A01	HACCP plan
7	sum03	HACCP	sum03B	raw ground	30	03B01	m/v/r/ca/fu[4]
8	sum03	HACCP	sum03B	raw ground	31	03B02	03B01 verification
9	sum03	HACCP	sum03C	raw not ground	32	03C01	m/v/r/ca/fu[4]

Table A-3. (continued)

No.	Code Sum*	Activity	Detail Sum**	Elements	No.	ISP Code	Procedures
10	sum03	HACCP	sum03C	raw not ground	33	03C02	03C01 verification
11	sum03	HACCP	sum03E	not heat treated-shelf stable	34	‘03E01	m/v/r/ca/fu[4]
12	sum03	HACCP	sum03F	not heat treated-shelf stable	35	‘03E02	03E01 verification
13	sum03	HACCP	sum03F	heat treated-shelf stable	36	03F01	m/v/r/ca/fu[4]
14	sum03	HACCP	sum03F	heat treated-shelf stable	37	03F02	03F01 verification
15	sum03	HACCP	sum03G	fully cooked-not shelf stable	38	03G01	m/v/r/ca/fu[4]
16	sum03	HACCP	sum03G	fully cooked-not shelf stable	39	03G02	03G01 verification
17	sum03	HACCP	sum03H	heat treated-not fully cooked	40	03H01	m/v/r/ca/fu[4]
18	sum03	HACCP	sum03H	heat treated-not fully cooked	41	03H02	03H01 verification
19	sum03	HACCP	sum03I	secondary inhibitors-not shelf stable	42	03I01	m/v/r/ca/fu[4]
20	sum03	HACCP	sum03I	secondary inhibitors-not shelf stable	43	03I02	03I01 verification
21	sum03	HACCP	sum03J	slaughter/fecal check	44	03J01	m/v/r/ca/fu[4]
22	sum03	HACCP	sum03J	slaughter/fecal check	45	03J02	03J01 verification
23	sum04	W/ECP[1]	sum04A01	yield/shrink	46	04A01	m/v/r/ca/fu[4]
47	sum04	W/ECP[1]	sum04A02	product solution formulation	71	04A02	m/v/r/ca/fu[4]
48	sum04	W/ECP[1]	sum04A03	comminuted/mechanically separated	72	04A03	m/v/r/ca/fu[4]
49	sum04	W/ECP[1]	sum04A04	battered products	73	04A04	m/v/r/ca/fu[4]
50	sum04	W/ECP[1]	sum04B01	product meets standard	74	04B01	m/v/r/ca/fu[4]
51	sum04	W/ECP[1]	sum04B02	packaging/labeling standards	75	04B02	m/v/r/ca/fu[4]
52	sum04	W/ECP[1]	sum04B03	stated label net weight	76	04B03	m/v/r/ca/fu[4]
53	sum04	W/ECP[1]	sum04B04	product identification	77	04B04	m/v/r/ca/fu[4]
54	sum04	W/ECP[1]	sum04C02	humane slaughter requirements	78	04C02	m/v/r/ca/fu[4]
55	sum04	W/ECP[1]	sum04C03	non-food safety product req.	79	04C03	m/v/r/ca/fu[4]
56	sum04	W/ECP[1]	sum04C04	poultry humane slaughter (economic)	80	04C04	m/v/r/ca/fu[4]
57	sum05	sampling	sum05A01	generic *E. coli* record plan	81	05A01	verification
58	sum05	sampling	sum05A02	generic *E. coli* record review	82	05A02	m/v/r/ca/fu[4]
59	sum05	sampling	sum05A03	*Salmonella* in raw products	83	05A03	sample collection

Table A-3. (continued)

No.	Code Sum*	Activity	Detail Sum**	Elements	No.	ISP Code	Procedures
60	sum05	sampling	sum05B01	random product sample	84	05B01	sample collection
61	sum05	sampling	sum05B02	CS/DO/headquarters request[5]	85	05B02	sample collection
62	sum05	sampling	sum05C01	random residue sample	86	05C01	sample collection
63	sum06	OIR/SPS[2]	sum06A01	export regulation compliance	87	06A01	m/v/r/ca/fu[4]
64	sum06	OIR/SPS[2]	sum06B01	custom exempt retail compliance	88	06B01	m/v/r/ca/fu[4]
65	sum06	OIR/SPS[2]	sum06D01	sanit. performance standards	89	06D01	m/v/r/ca/fu[4]
66	sum06	OIR/SPS[2]	sum06D02	facility sanitation compliance	90	06D02	m/v/r/ca/fu[4]
67	sum08	emergency[3]	sum08S14	water systems	91	08S14	unscheduled check
68	sum08	emergency[3]	sum08S15	processing/manufacture	92	08S15	unscheduled check
69	sum08	emergency[3]	sum08S16	storage areas	93	08S16	unscheduled check
70	sum08	emergency[3]	sum08S17	shipping/receiving	94	08S17	unscheduled check

** Code Sum refers to the ISP code summation variable that contains the Detail Sum elements*

*** Detail Sum refers to the procedure summed within given code summed ISP elements with their descriptions*

[1] *W/ECP = wholesomeness/economic consumer protection*

[2] *OIR/SPS = other inspection requirements/sanitation performance standards*

[3] *emergency procedures performed under homeland security requirements*

[4] *m/v/r/ca/fu = monitoring/verification/records checks/corrective action to non-compliance/follow up reassessment to corrective action*

[5] *Circuit supervisor, district office, or headquarters request*

Table A-4. Combinations of Eight Basic Inspection Systems Used in FSIS Inspected Chicken Establishments

number	Inspection System	line speed[1]
1	MAESTRO.[2]	140 bpm
2	MAESTRO, Nu-Tech	140 bpm, 140 bpm
3	MAESTRO, Religious	140 bpm, 14-35 bpm
4	MAESTRO, SIS	140 bpm
5	NELS[3]	91 bpm
6	NELS, MAESTRO	91 bpm, 140 bpm
7	NELS, Nu-Tech, MAESTRO	91 bpm, 140 bpm, 140 bpm
8	NELS, Nu-Tech	91 bpm, 140 bpm
9	NELS, Nu-Tech, Religious	91 bpm, 140 bpm, 14-35 bpm
10	NELS, Religious	91 bpm, 14-35 bpm
11	NELS, SIS	91 bpm, 70 bpm
12	NELS, SIS, Religious	91 bpm, 70 bpm, 14-35 bpm
13	Nuova[4]	140 bpm
14	Nu-Tech[5]	142 bpm
15	Nu-Tech, Religious	142 bpm, 14-35 bpm
16	SIS[6]	70 bpm
17	SIS, MAESTRO	70 bpm, 140 bpm
18	SIS, MAESTRO, Religious	70bpm, 140 bpm, 14-35 bpm
19	SIS, Religious	70 bpm, 14-35 bpm
20	SIS- NuOva	70 bpm, 140 bpm
21	SIS, Nu-Tech	70 bpm, 142 bpm
22	Traditional[7]	35 bpm
23	Religious Slaughter[8]	14-35 bpm
24	HIMP[9]	170 bpm[10]

[1] *maximum regulatory line speed in birds per minute (bpm) for each inspection type taken as the average over the number of lines per establishment*

[2] *MAESTRO (Meyn Poultry, Gainesville, GA)*

[3] *New Enhanced Line Speed (NELS) various manufacturers*

[4] *Nuova (Marel Stork Poultry Processing, Gainesville, Ga)*

[5] *Nu_Tech (Stork Gamco, Gainesville, Ga)*

[6] *Streamlined Inspection System (SIS) various manufacturers*

[7] *Traditional Inspection System*

[8] *Religious Slaughter (Buddhist, Kosher, Islamic)*

[9] *HACCP Inspection Models Project (HIMP)*

[10] *HIMP establishments can exceed this limit*

Table A-5. Basic Inspection Systems Used in FSIS Inspected Turkey Establishments

number	**Inspection System**	**line speed**[1]
1	HIMP, NTIS	no maximum
2	NTIS-1 or 2	J or Bar-Type[1]
3	NTIS-1 or 2 (modified)	Bar-Type[2]
4	NTIS - Other	not specific

[1] *J-type - one inspector 32 bpm (<16#), 30 bpm (>16#)*
J-type - two inspectors 51 bpm (<16#), 41 bpm (>16#)
Bar-type - one inspector 25 bpm (<16#), 21 bpm (>16#)
Bar-type two inspectors 45 bpm (<16#), 35 bpm (>16#)

[2] *Bar-type one inspector 32 bpm (<16#), 30 bpm (>16#)*

Table A-6. Parameter Estimates for Young Chicken *Salmonella* Model Used in Scenario Analysis

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
Intercept	-1.9647	0.3123	<0.0001*	1	0
rehang	-1.1699	0.0162	<0.0001*	0.7107	0.7035
loglinespeed	0.4675	0.1553	0.0013*	2.0266	0.1786
logInspectors	-0.2878	0.0823	0.0002*	1.2820	0.2675
lines	-0.0866	0.0184	<0.0001*	2.1464	1.0877
Himp	-0.068	0.0267	0.0054*	0.7518	0.6594
month1	0.3558	0.0846	<0.0001*	-0.0110	0.1598
month2	0.0076	0.0537	0.4437	0.0047	0.2035
month3	0.4576	0.0473	<0.0001*	0.0090	0.2137
month4	0.2492	0.0493	<0.0001*	0.0076	0.2103
month5	0.302	0.0479	<0.0001*	0.0094	0.2145
month6	0.2414	0.0502	<0.0001*	0.0067	0.2082
month7	0.6349	0.0485	<0.0001*	0.0063	0.2073
month8	0.0956	0.0522	0.0335*	0.0056	0.2057
month9	0.1752	0.0499	0.0002*	0.0078	0.2107
month10	0.2302	0.0494	<0.0001*	0.0080	0.2112
month11	-0.1409	0.0525	0.0036*	0.0075	0.2102
month12	0.1534	0.0504	0.0012*	0.0073	0.2097
month13	0.0988	0.0704	0.0803	0.0100	0.2159
month14	0.0228	0.0669	0.3666	0.0152	0.2273
month15	0.0969	0.0753	0.0991	0.0049	0.2040
month16	-0.2017	0.1055	0.0280*	-0.0043	0.1799
month17	-0.7525	0.1801	<0.0001*	-0.0108	0.1606
month18	0.0571	0.0707	0.2097	0.0082	0.2116
month19	0.3435	0.059	<0.0001*	0.0133	0.2232
month20	0.2108	0.0685	0.0010*	0.0075	0.2100
month21	-0.5773	0.1134	<0.0001*	0.0000	0.1916
month22	-0.4173	0.0776	<0.0001*	0.0157	0.2285
month23	-0.4668	0.0770	<0.0001*	0.0184	0.2341
month24	-0.3467	0.0821	<0.0001*	0.0099	0.2156
month25	0.0985	0.0731	0.0889	0.0065	0.2077
month26	-0.1432	0.0748	0.0278*	0.0105	0.2169
month27	-0.2187	0.0751	0.0018*	0.0113	0.2189

Table A-6. (continued)

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
month28	-0.0124	0.0846	0.4417	0.0014	0.1952
month29	0.2626	0.0865	0.0012*	-0.0026	0.1845
month30	0.0750	0.1045	0.2365	-0.0056	0.1763
month31	0.6006	0.1286	<0.0001*	-0.0130	0.1535
month32	-0.2403	0.1991	0.1137	-0.0142	0.1492
month33	-0.2092	0.0766	0.0032*	0.0095	0.2147
month34	-0.1156	0.0544	0.0168*	0.0363	0.2678
month35	-0.5026	0.0634	<0.0001*	0.0380	0.2706
month36	-0.3344	0.064	<0.0001*	0.0298	0.2562
month37	-0.0387	0.0698	0.2896	0.0134	0.2235
month38	0.0351	0.0775	0.3253	0.0061	0.2069
District1	-0.3544	0.1256	0.0024*	-0.2177	0.4311
District2	-0.5096	0.0977	<0.0001*	-0.2097	0.4440
District3	0.3047	0.0815	<0.0001*	-0.2113	0.4416
District4	0.3918	0.1251	0.0009*	-0.2174	0.4315
District5	-0.1139	0.0561	0.0212*	-0.1793	0.4894
District6	-0.0603	0.0388	0.0601	-0.0857	0.5982
District7	-0.0185	0.0491	0.3532	-0.1513	0.5260
District8	-1.2824	0.2123	<0.0001*	-0.2219	0.4240
District9	0.5377	0.0469	<0.0001*	-0.1615	0.5131
District10	0.2689	0.056	<0.0001*	-0.1828	0.4845
District11	0.5986	0.1054	<0.0001*	-0.2130	0.4388
District12	0.3913	0.0449	<0.0001*	-0.1440	0.5350
District13	-0.0510	0.0381	0.0904	-0.0781	0.6056
District14	0.0505	0.0392	0.0988	-0.1080	0.5756
InspSysMAESTRO	-0.1228	0.0392	0.0008*	0.3088	0.5336
InspSysMAESTRO,Nu-Tech	-0.1219	0.0777	0.0583	-0.0144	0.2381
InspSysMAESTRO,Religio	0.0269	0.0716	0.3536	-0.0106	0.2461
InspSysMAESTRO-SIS	-0.5622	0.1875	0.0014*	-0.0315	0.1968
InspSysNELS	0.0633	0.0414	0.0631	0.0670	0.3658
InspSysNELS,MAESTRO	0.5052	0.0851	<0.0001*	-0.0236	0.2171
InspSysNELS,NTIS,MAEST	0.7756	0.1451	<0.0001*	-0.0325	0.1942
InspSysNELS,Nu-Tech	-0.3414	0.1383	0.0068	-0.0267	0.2095

Table A-6. (continued)

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
InspSysNELS,Nu-Tech,Re	0.6381	0.1179	<0.0001*	-0.0304	0.1998
InspSysNELS,Religious	0.3605	0.0696	<0.0001*	-0.0080	0.2515
InspSysNELS,SIS	0.2929	0.0967	0.0013*	-0.0220	0.2209
InspSysNELS,SIS,Religi	-0.2293	0.1551	0.0697	-0.0296	0.2020
InspSysNu-Ova	-0.8808	0.3005	0.0017*	-0.0333	0.1919
InspSysNu-Tech	-0.1878	0.0477	<0.0001*	0.0886	0.3899
InspSysNu-Tech,Religio	-0.4308	0.1088	<0.0001*	-0.0286	0.2047
InspSysSIS	-0.0361	0.0401	0.1840	0.1452	0.4420
InspSysSIS,MAESTRO	0.3542	0.0586	<0.0001*	0.0011	0.2690
InspSysSIS,MAESTRO,Rel	0.2889	0.1318	0.0142*	-0.0292	0.2031
InspSysSIS,Religious S	-0.3865	0.1259	0.0011*	-0.0255	0.2123
InspSysSIS-Nu-Tech	0.066	0.0898	0.2312	-0.0198	0.2260
InspSysSIS-NuOva	-0.8173	0.1442	<0.0001*	-0.0289	0.2037
Sep_Tox	0.0001	0.000001	<0.0001*	258.0830	282.0689
Contam	0.0005	0.0001	<0.0001*	34.1020	84.5970
AirSac	0.0000	0.0001	0.496	134.3891	1101.8910
sum_SP	0.0021	0.0021	0.1587	12.9624	6.0291
sum_SNP	0.0461	0.0093	<0.0001*	0.5536	1.0524
sum_U	-0.0032	0.0009	0.0002*	29.1353	20.5648
sum_NC	0.0091	0.0096	0.1716	0.7834	1.1422

**Significant difference for two-sided t-test on the regression coefficient*

Table A-7. Parameter Estimates for Young Chicken *Campylobacter* Model Used in Scenario Analysis

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
Intercept	0.3286	5.8184	0.4775	1	0
Rehang	-0.6359	0.0134	<0.0001*	-0.0003	1.0001
loglinespeed	1.2788	0.2047	<0.0001*	2.0428	0.1626
logInspectors	-0.9754	0.1212	<0.0001*	1.3214	0.2366
lines	0.0497	0.0237	0.0180*	2.1751	1.0420
Himp	-0.4332	0.0689	<0.0001*	0.1327	0.3392
month1	-0.1895	0.0713	0.0039*	-0.063	0.3316
month2	-0.0734	0.0429	0.0436*	-0.0085	0.4102
month3	0.5022	0.0444	<0.0001*	0.0063	0.4279
month4	0.2178	0.0427	<0.0001*	0.0012	0.4221
month5	0.2193	0.0418	<0.0001*	0.0075	0.4293
month6	0.1160	0.0430	0.0035*	-0.0018	0.4184
month7	-0.1053	0.0416	0.0057*	-0.0032	0.4168
month8	-0.0817	0.0424	0.0270*	-0.0055	0.4140
month9	0.1315	0.0423	0.0009*	0.0018	0.4228
month10	-0.3165	0.0392	<0.0001*	0.0026	0.4237
month11	-0.2484	0.0400	<0.0001*	0.0014	0.4222
District1	-0.3553	0.1548	0.0109*	-0.2318	0.4404
District2	-0.3201	0.1995	0.0543	-0.2353	0.4345
District3	-0.5514	0.1431	<0.0001*	-0.2315	0.4409
District4	-0.3275	0.2135	0.0625	-0.2351	0.4348
District5	0.1098	0.0755	0.0730	-0.1991	0.4906
District6	-0.0589	0.0505	0.1218	-0.0820	0.6251
District7	0.2839	0.0656	<0.0001*	-0.1700	0.5296
District8	-0.6106	0.1520	<0.0001*	-0.2336	0.4373
District9	0.4256	0.0920	<0.0001*	-0.2052	0.4817
District10	0.1869	0.0889	0.0178*	-0.2072	0.4788
District11	1.5979	0.2689	<0.0001*	-0.2321	0.4399
District12	-0.2427	0.0589	<0.0001*	-0.1475	0.5570
District13	-0.3898	0.0510	<0.0001*	-0.0907	0.6169
District14	0.3007	0.0520	<0.0001*	-0.0944	0.6133
InspSysMAESTRO	-0.8593	5.8054	0.4412	0.3385	0.5116
InspSysMAESTRO,Nu-Tech	-0.4422	5.8058	0.4696	0.0127	0.2243

Table A-7. (continued)

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
InspSysMAESTRO,Religio	-0.0386	5.8061	0.4973	0.0041	0.2048
InspSysMAESTRO-SIS	-0.5936	5.8080	0.4593	-0.0131	0.1566
InspSysNELS	-0.7700	5.8054	0.4472	0.0718	0.3233
InspSysNELS,MAESTRO	-0.4104	5.8060	0.4718	0.0008	0.1964
InspSysNELS,NTIS,MAEST	-1.8641	5.8112	0.3742	-0.0168	0.1441
InspSysNELS,Nu-Tech	10.621	116.1000	0.4636	-0.0177	0.1408
InspSysNELS,Nu-Tech,Re	-0.7159	5.8065	0.4509	-0.0087	0.1705
InspSysNELS,Religious	-0.9813	5.8061	0.4329	0.0035	0.2033
InspSysNELS,SIS	-0.4999	5.8065	0.4657	-0.0055	0.1797
InspSysNELS,SIS,Religi	-0.1027	5.8079	0.4929	-0.0128	0.1576
InspSysNu-Tech	-0.8998	5.8055	0.4384	0.1136	0.3722
InspSysNu-Tech,Religio	-0.2656	5.8062	0.4818	-0.0029	0.1869
InspSysSIS	-0.5426	5.8054	0.4628	0.1629	0.4173
InspSysSIS,MAESTRO	-0.8898	5.8056	0.4391	0.0178	0.2353
InspSysSIS,MAESTRO,Rel	0.4083	5.8089	0.4720	-0.0134	0.1556
InspSysSIS,Religious S	-1.1934	5.8100	0.4186	-0.0131	0.1566
InspSysSIS-Nu-Tech	-0.0369	5.8069	0.4975	-0.0069	0.1758
InspSysSIS-NuOva	-0.1944	5.8075	0.4866	-0.0119	0.1606
Sep_Tox	0.0005	0.0001	<0.0001*	295.9538	265.3369
Contam	-0.0003	0.0001	0.0014*	49.3667	98.6220
AirSac	0.0000	0.0000	0.1587	237.9061	2006.1750
sum_SP	0.0076	0.0065	0.1212	6.5629	0.8762
sum_SNP	0.0198	0.0107	0.0321*	0.6929	0.2600
sum_U	-0.0014	0.0011	0.1016	31.0927	7.3283
sum_NC	-0.0157	0.0074	0.0170*	1.3634	0.3212

**Significant difference for two-sided t-test on the regression coefficient*

Table A-8. Parameter Estimates for Young Turkey *Salmonella* Model Used in Scenario Analysis

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
Intercept	-3.5814	1.0534	0.0003*	1	0
rehang	-0.4599	0.0622	<0.0001*	0.6704	0.7421
loglinespeed	-0.2945	0.8881	0.3701	1.4698	0.1246
logInspectors	1.5612	0.5439	0.0020*	0.9141	0.1980
lines	-0.1717	0.2275	0.2252	1.2725	0.4453
month1	0.7670	0.2418	0.0008*	0.0025	0.2149
month2	0.8158	0.2844	0.0021*	-0.0057	0.1947
month3	0.9719	0.3408	0.0022*	-0.0129	0.1749
month4	0.4361	0.3146	0.0829	-0.0064	0.1929
month5	0.6889	0.3059	0.0121*	-0.0081	0.1884
month6	1.1158	0.2472	<0.0001*	-0.0048	0.1971
month7	0.0318	0.3150	0.4598	-0.0053	0.1959
month8	-0.2106	0.3494	0.2733	-0.0077	0.1896
month9	0.0922	0.3317	0.3905	-0.0071	0.1911
month10	0.4242	0.3176	0.0909	-0.0082	0.1881
month11	0.3148	0.3469	0.1821	-0.0119	0.1779
month12	0.5751	0.4077	0.0792	-0.0154	0.1673
month13	-0.0699	0.5346	0.4480	-0.017	0.1623
month14	0.1461	0.2439	0.2746	0.0066	0.2242
month15	0.1761	0.2183	0.2099	0.0186	0.2489
month16	-0.0216	0.2318	0.4629	0.0200	0.2515
month17	-0.5254	0.2975	0.0387*	0.0134	0.2385
month18	-0.4990	0.2798	0.0373*	0.0158	0.2433
month19	-0.1435	0.2746	0.3006	0.0117	0.2349
month20	0.0301	0.2551	0.4530	0.0114	0.2345
month21	-0.2562	0.2700	0.1714	0.0121	0.2359
month22	-0.1792	0.2304	0.2184	0.0369	0.2815
month23	-0.3559	0.2287	0.0599	0.0554	0.3099
month24	0.3405	0.1880	0.0351*	0.0610	0.3178
month25	0.2955	0.2031	0.0729	0.0395	0.2858
month26	0.5999	0.3965	0.0652	-0.0122	0.1769
month27	-3.2689	2.8210	0.1233	-0.0138	0.1722
month28	-0.6259	0.6202	0.1565	-0.0090	0.1859

Table A-8. (continued)

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
month29	-3.4238	2.8103	0.1116	-0.0117	0.1785
month30	-0.0102	0.5741	0.4929	-0.0128	0.1752
month31	0.0199	0.4202	0.4811	-0.0086	0.1871
month32	0.5131	0.3604	0.0773	-0.0099	0.1834
month33	-1.4332	0.6777	0.0172*	-0.0046	0.1977
month34	0.1280	0.3056	0.3377	0.0053	0.2211
month35	-0.4092	0.3445	0.1175	0.0142	0.2401
month36	0.0642	0.2774	0.4085	0.0184	0.2485
month37	0.5597	0.2781	0.0221*	0.0033	0.2167
month38	0.9966	0.2835	0.0002	-0.0045	0.198
district1	-0.0841	0.1910	0.3299	0.1021	0.3295
district2	0.1486	0.2300	0.2591	0.0354	0.2261
district3	0.5899	0.1464	<0.0001*	0.1605	0.3894
district4	0.3528	0.1979	0.0373*	0.0794	0.3001
district5	-1.3221	0.4326	0.0011*	0.0350	0.2251
district6	0.0284	0.1970	0.4427	0.0769	0.2965
district7	-1.3599	0.6720	0.0215*	0.0158	0.1801
district8	0.3582	0.2027	0.0386*	0.0552	0.2628
district9	0.5694	0.1552	0.0001*	0.1005	0.3276
district10	-0.1438	0.2189	0.2556	0.0655	0.2795
district11	0.4412	0.8227	0.2959	-0.0046	0.1110
district12	-0.0660	0.2531	0.3971	0.0501	0.2539
district13	0.5190	0.1709	0.0012*	0.1098	0.3387
InspSysHIMP	-0.4680	0.2356	0.0235*	0.0507	0.3450
InspSysNTIS	-0.1056	0.1150	0.1793	0.7058	0.5278
InspSysOtherNTIS	0.7860	0.2182	0.0002*	0.1017	0.4028
sep_tox	0.0011	0.0005	0.0139*	60.1749	75.9333
contam	0.0053	0.0034	0.0595	3.7394	9.3027
airsac	0.0016	0.0009	0.0377*	8.5823	30.7198
synovitis	0.0012	0.0019	0.2638	5.5832	21.0532
sum_SP	0.0054	0.0121	0.3277	10.7622	6.3381
sum_SNP	-0.0805	0.0408	0.0243*	0.4945	1.0889
sum_U	-0.0208	0.0190	0.1368	6.9431	3.1892
sum_NC	0.0581	0.0223	0.0046*	1.8542	3.6883

**Significant difference for two-sided t-test on the regression coefficient*

Table A-9. Parameter Estimates for Young Turkey *Campylobacter* Model Used in Scenario Analysis

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
Intercept	-13.1301	3.2288	<0.0001*	1	0
rehang	-1.7619	0.1523	<0.0001*	-0.6770	1.0002
loglinespeed	7.4946	2.6152	0.0021*	1.4706	0.1266
logemployees	3.6115	1.0235	0.0002*	0.9212	0.1865
lines	-2.7200	0.6853	<0.0001*	1.2420	0.4284
month14	-0.3209	0.4314	0.2285	0.0583	0.2372
month15	0.7339	0.3665	0.0227*	0.0943	0.2947
month16	0.6898	0.3639	0.0291*	0.1040	0.3076
month17	0.3507	0.3764	0.1758	0.0929	0.2928
month18	0.2939	0.3756	0.2170	0.0874	0.2849
month19	0.5901	0.3813	0.0609	0.0693	0.2568
month20	0.5215	0.3819	0.0861	0.0721	0.2614
month21	0.1840	0.3819	0.3150	0.0818	0.2767
month22	-1.5164	0.4950	0.0011*	0.0867	0.2839
month23	-0.8771	0.4473	0.0250*	0.0777	0.2703
month24	-0.5709	0.4238	0.0890	0.0798	0.2735
month25	-0.2184	0.3940	0.2897	0.0867	0.2839
district1	0.4785	0.3196	0.0672	-0.0576	0.4639
district2	-0.6647	1.0543	0.2642	-0.1290	0.3611
district3	0.3415	0.2636	0.0976	0.0069	0.5320
district4	0.9143	0.3496	0.0045*	-0.0596	0.4614
district5	0.0481	0.3594	0.4468	-0.0673	0.4520
district6	0.3492	0.2922	0.1161	-0.0368	0.4878
district7	-1.5516	0.6421	0.0079*	-0.1047	0.4005
district8	-0.6302	0.3867	0.0516	-0.077	0.4395
district9	-0.2110	0.2587	0.2074	-0.0132	0.5126
district10	0.8127	0.2975	0.0032*	-0.0617	0.4589
district11	-0.9561	1.2489	0.2220	-0.1269	0.3647
district12	1.0358	0.4560	0.0116*	-0.0673	0.4520
InspSysHIMP	-1.6265	0.5348	0.0012*	0.1179	0.4359
InspSysNTIS	0.1801	0.1804	0.1591	0.6845	0.5496
InspSysOtherNTIS	0.7410	0.3786	0.0252*	0.0257	0.3332
sep_tox	0.0015	0.0011	0.0864	63.1945	81.9786

Table A-9. (continued)

Parameter	Estimate	Std Error	p-value	Mean	Std Dev
contam	0.0023	0.0046	0.3086	3.3797	10.4619
airsac	0.0011	0.0015	0.2317	9.9397	47.0573
synovitis	-0.0067	0.0065	0.1514	4.8176	23.6373
sum_SP	-0.0344	0.0203	0.0451*	10.8187	4.2699
sum_SNP	0.0444	0.0573	0.2192	0.9022	1.3254
sum_U	-0.1027	0.0303	0.0004*	8.8464	3.1642
sum_NC	-0.0548	0.0801	0.2470	0.5374	1.0612

**Significant difference for two-sided t-test on the regression coefficient*

Table A-10. Parameter Estimates from the Young Chicken *Salmonella* Split Datasets

Parameter	B	mean	B split1	mean	B split2	mean
Intercept	-1.8967	1.0000	-3.0788	1.0000	-0.8715	1.0000
rehang	-1.1699	0.7107	-1.2067	0.7105	-1.1434	0.7110
loglinespeed	0.4675	2.0266	1.1160	2.0265	-0.1595	2.0266
logemployees	-0.2878	1.2820	-0.3838	1.2809	-0.1754	1.2830
lines	-0.0866	2.1464	-0.1059	2.1380	-0.0753	2.1549
Himp	-0.0680	0.7518	-0.0001	0.7532	-0.1444	0.7505
month1	0.3558	-0.0110	0.4367	-0.0129	0.2887	-0.0092
month2	0.0076	0.0047	-0.0618	0.0034	0.0957	0.0060
month3	0.4576	0.0090	0.5183	0.0081	0.4234	0.0100
month4	0.2492	0.0076	0.0373	0.0055	0.4472	0.0097
month5	0.3020	0.0094	0.2938	0.0067	0.3088	0.0121
month6	0.2414	0.0067	0.0869	0.0049	0.4057	0.0085
month7	0.6349	0.0063	0.6008	0.0044	0.6795	0.0082
month8	0.0956	0.0056	-0.0525	0.0043	0.2246	0.0070
month9	0.1752	0.0078	0.0918	0.0083	0.2367	0.0072
month10	0.2302	0.0080	0.1706	0.0086	0.3204	0.0073
month11	-0.1409	0.0075	-0.1608	0.0064	-0.0815	0.0086
month12	0.1534	0.0073	0.1047	0.0068	0.2069	0.0079
month13	0.0988	0.0100	0.2928	0.0075	-0.0415	0.0125
month14	0.0228	0.0152	-0.1733	0.0143	0.2070	0.0161
month15	0.0969	0.0049	0.0846	0.0023	0.1151	0.0076
month16	-0.2017	-0.0043	-0.4168	-0.0056	-0.0051	-0.0030
month17	-0.7525	-0.0108	-0.5376	-0.0114	-0.9929	-0.0102
month18	0.0571	0.0082	0.0748	0.0052	0.0803	0.0111
month19	0.3435	0.0133	0.3778	0.0144	0.2915	0.0122
month20	0.2108	0.0075	0.4840	0.0073	-0.1315	0.0076
month21	-0.5773	0.0000	-0.5580	-0.0020	-0.5348	0.0020
month22	-0.4173	0.0157	-0.2626	0.0149	-0.5369	0.0166
month23	-0.4668	0.0184	-0.4863	0.0160	-0.4385	0.0209
month24	-0.3467	0.0099	-0.1900	0.0102	-0.5007	0.0095
month25	0.0985	0.0065	-0.0428	0.0055	0.2650	0.0075
month26	-0.1432	0.0105	-0.1998	0.0099	-0.0297	0.0110
month27	-0.2187	0.0113	-0.2753	0.0100	-0.1581	0.0127

Table A-10. (continued)

Parameter	B	mean	B split1	mean	B split2	mean
month28	-0.0124	0.0014	-0.2503	0.0005	0.1983	0.0023
month29	0.2626	-0.0026	0.5159	-0.0040	0.0380	-0.0013
month30	0.0750	-0.0056	-0.6091	-0.0061	0.5400	-0.0051
month31	0.6006	-0.0130	0.7536	-0.0136	0.4727	-0.0124
month32	-0.2403	-0.0142	0.0421	-0.0154	-0.4760	-0.0131
month33	-0.2092	0.0095	-0.4207	0.0077	-0.0174	0.0113
month34	-0.1156	0.0363	0.0468	0.0352	-0.2828	0.0375
month35	-0.5026	0.0380	-0.5960	0.0376	-0.3811	0.0384
month36	-0.3344	0.0298	-0.2227	0.0296	-0.4242	0.0300
month37	-0.0387	0.0134	0.3686	0.0123	-0.6047	0.0146
month38	0.0351	0.0061	0.0119	0.0061	0.1033	0.0062
District1	-0.3544	-0.2177	-0.2458	-0.2149	-0.5112	-0.2204
District2	-0.5096	-0.2097	-0.4804	-0.2083	-0.5441	-0.2112
District3	0.3047	-0.2113	0.5023	-0.2088	0.1484	-0.2137
District4	0.3918	-0.2174	0.2477	-0.2156	0.4641	-0.2192
District5	-0.1139	-0.1793	0.0366	-0.1758	-0.2511	-0.1827
District6	-0.0603	-0.0857	-0.0672	-0.0814	-0.0422	-0.0900
District7	-0.0185	-0.1513	0.0342	-0.1479	-0.0494	-0.1548
District8	-1.2824	-0.2219	-1.2668	-0.2199	-1.2299	-0.2238
District9	0.5377	-0.1615	0.4967	-0.1577	0.5982	-0.1653
District10	0.2689	-0.1828	0.2931	-0.1808	0.2465	-0.1848
District11	0.5986	-0.2130	0.2874	-0.2102	0.8852	-0.2158
District12	0.3913	-0.1440	0.4247	-0.1444	0.3592	-0.1435
District13	-0.0510	-0.0781	-0.1031	-0.0783	-0.0033	-0.0779
District14	0.0505	-0.1080	0.1461	-0.1052	-0.0654	-0.1107
InspSysMAESTRO	-0.1228	0.3088	-0.1436	0.3079	-0.0138	0.3096
InspSysMAESTRO,Nu-Tech	-0.1219	-0.0144	-0.0504	-0.0150	-0.0640	-0.0138
InspSysMAESTRO,Religio	0.0269	-0.0106	-0.1947	-0.0126	0.2813	-0.0086
InspSysMAESTRO-SIS	-0.5622	-0.0315	-1.8466	-0.0330	0.1943	-0.0301
InspSysNELS	0.0633	0.0670	-0.0188	0.0656	0.2369	0.0684
InspSysNELS,MAESTRO	0.5052	-0.0236	0.6424	-0.0248	0.4402	-0.0224
InspSysNELS,NTIS,MAEST	0.7756	-0.0325	0.8684	-0.0335	0.8551	-0.0315
InspSysNELS,Nu-Tech	-0.3414	-0.0267	0.1567	-0.0279	-0.7383	-0.0255

Table A-10. (continued)

Parameter	B	mean	B split1	mean	B split2	mean
InspSysNELS,Nu-Tech,Re	0.6381	-0.0304	0.7337	-0.0311	0.7066	-0.0297
InspSysNELS,Religious	0.3605	-0.0080	0.5837	-0.0108	0.2934	-0.0052
InspSysNELS,SIS	0.2929	-0.0220	0.1642	-0.0227	0.5175	-0.0213
InspSysNELS,SIS,Religi	-0.2293	-0.0296	0.0992	-0.0310	-0.4378	-0.0282
InspSysNu-Ova	-0.8808	-0.0333	-0.3615	-0.0342	-3.0147	-0.0325
InspSysNu-Tech	-0.1878	0.0886	-0.3631	0.0903	0.0876	0.0870
InspSysNu-Tech,Religio	-0.4308	-0.0286	-0.3161	-0.0291	-0.4191	-0.0281
InspSysSIS	-0.0361	0.1452	0.0259	0.1401	0.0137	0.1502
InspSysSIS,MAESTRO	0.3542	0.0011	0.2914	0.0007	0.5088	0.0015
InspSysSIS,MAESTRO,Rel	0.2889	-0.0292	0.2840	-0.0311	0.3791	-0.0273
InspSysSIS,Religious S	-0.3865	-0.0255	-0.4129	-0.027	-0.2581	-0.0241
InspSysSIS-Nu-Tech	0.0660	-0.0198	-0.0234	-0.0218	0.2237	-0.0178
InspSysSIS-NuOva	-0.8173	-0.0289	-0.9757	-0.0303	-0.5229	-0.0276
Sep_Tox	0.0001	258.0830	0.0000	257.031	0.0002	259.1350
Contam	0.0005	34.102	0.0005	33.4667	0.0006	34.7371
AirSac	0.0000	134.389	0.0000	142.77	0.0001	126.009
sum_SP	0.0021	12.9624	0.0024	12.9508	0.0019	12.9740
sum_SNP	0.0461	0.5536	0.0451	0.5580	0.0491	0.5493
sum_U	-0.0032	29.1353	-0.001	29.0843	-0.0056	29.1864
sum_NC	0.0091	0.7834	0.0025	0.7869	0.0196	0.7798

Table A-11. Prevalence Estimates from the Young Chicken *Salmonella* Model for the Mean, Rehang, and Post-chill Sample Collection Locations

Estimates	unsplit	split1	split2
BX (rehang= mean)[1]	-2.3905	-2.4041	-2.4069
BX (rehang= 1) post-chill[2]	-2.7290	-2.7535	-2.7373
BX (rehang= -1) rehang[3]	0.3376	1.5320	-0.7224
Prevalence (rehang= mean)[4]	0.0839	0.0829	0.0826
Prevalence (rehang= 1) post-chill[5]	0.0613	0.0599	0.0608
Prevalence (rehang= -1) rehang[6]	0.4039	0.4158	0.3892
Prevalence unweighted[7]	0.1231	0.1226	0.1235

[1] *BX is the linear combination equal to η where the rehang variable for x equals the mean*

[2] *BX is the liner combination equal to η where the rehang variable for x equals +1*

[3] *BX is the liner combination equal to η where the rehang variable for x equals -1*

[4] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at the mean*

[5] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at +1*

[6] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at -1*

[7] *Crude Prevalence*

Table A-12. Parameter Estimates from the Young Chicken *Campylobacter* Split Datasets

Parameter	B unsplit	mean	B split1	mean	B split2	mean
Intercept	0.3286	1	0.2875	1	0.4175	1
Rehang	-0.6359	-0.0003	-0.6443	0.0259	-0.6463	-0.0265
loglinespeed	1.2788	2.0428	1.2441	2.0428	1.2848	2.0429
logInspectors	-0.9754	1.3214	-0.8820	1.3222	-1.0994	1.3206
lines	0.0497	2.1751	0.0694	2.1799	0.0305	2.1702
Himp	-0.4332	0.1327	-0.4044	0.1330	-0.4538	0.1324
month1	-0.1895	-0.0630	-0.6428	-0.0403	1.5155	-0.0857
month2	-0.0734	-0.0085	-0.071	0.0021	-0.0911	-0.0192
month3	0.5022	0.0063	0.4724	0.0162	0.5727	-0.0037
month4	0.2178	0.0012	0.1247	0.0088	0.4277	-0.0064
month5	0.2193	0.0075	0.0787	0.0195	0.4805	-0.0046
month6	0.1160	-0.0018	-0.1132	0.0052	0.1816	-0.0088
month7	-0.1053	-0.0032	-0.1489	0.0095	-0.0387	-0.0159
month8	-0.0817	-0.0055	-0.1046	0.0037	-0.0457	-0.0146
month9	0.1315	0.0018	-0.2289	0.0091	-0.2282	-0.0055
month10	-0.3165	0.0026	-0.3073	0.0113	-0.2962	-0.0061
month11	-0.2484	0.0014	-0.2782	0.0107	-0.1985	-0.0079
District1	-0.3553	-0.2318	-0.3006	-0.2315	-0.4227	-0.2321
District2	-0.3201	-0.2353	-0.369	-0.2339	-0.3255	-0.2367
District3	-0.5514	-0.2315	-0.7509	-0.2306	-0.3496	-0.2324
District4	-0.3275	-0.2351	-0.4915	-0.2339	-0.1427	-0.2364
District5	0.1098	-0.1991	0.1810	-0.1979	0.0378	-0.2004
District6	-0.0589	-0.082	0.0159	-0.0808	-0.1348	-0.0833
District7	0.2839	-0.1700	0.3628	-0.1677	0.2042	-0.1723
District8	-0.6106	-0.2336	-0.6771	-0.233	-0.5854	-0.2342
District9	0.4256	-0.2052	0.5492	-0.2025	0.3060	-0.2080
District10	0.1869	-0.2072	0.2304	-0.2059	0.1410	-0.2086
District11	1.5979	-0.2321	1.3490	-0.2309	1.9126	-0.2333
District12	-0.2427	-0.1475	-0.1381	-0.1464	-0.3443	-0.1485
District13	-0.3898	-0.0907	-0.3474	-0.0887	-0.4343	-0.0927
District14	0.3007	-0.0944	0.2965	-0.0936	0.3164	-0.0952
InspSysMAESTRO	-0.8593	0.3385	-0.9787	0.3388	-0.7395	0.3382
InspSysMAESTRO,Nu-Tech	-0.4422	0.0127	-0.6049	0.0128	-0.2462	0.0125

Table A-12. (continued)

Parameter	B unsplit	mean	B split1	mean	B split2	mean
InspSysMAESTRO,Religio	-0.0386	0.0041	0.0216	0.0046	-0.1066	0.0037
InspSysMAESTRO-SIS	-0.5936	-0.0131	-0.5830	-0.0128	-0.5870	-0.0134
InspSysNELS	-0.7700	0.0718	-0.8675	0.0717	-0.6704	0.0720
InspSysNELS,MAESTRO	-0.4104	0.0008	-0.6552	0.0006	-0.1678	0.0009
InspSysNELS,NTIS,MAEST	-1.8641	-0.0168	-1.8537	-0.0165	-1.9102	-0.0171
InspSysNELS,Nu-Tech	10.6210	-0.0177	10.7515	-0.0168	9.9638	-0.0186
InspSysNELS,Nu-Tech,Re	-0.7159	-0.0087	-0.9883	-0.0082	-0.4274	-0.0091
InspSysNELS,Religious	-0.9813	0.0035	-0.8961	0.0040	-1.0827	0.0030
InspSysNELS,SIS	-0.4999	-0.0055	-0.7386	-0.0052	-0.2767	-0.0058
InspSysNELS,SIS,Religi	-0.1027	-0.0128	-0.1361	-0.0128	-0.0791	-0.0128
InspSysNu-Tech	-0.8998	0.1136	-0.9766	0.1134	-0.8265	0.1138
InspSysNu-Tech,Religio	-0.2656	-0.0029	-1.2466	-0.0024	0.7596	-0.0034
InspSysSIS	-0.5426	0.1629	-0.6646	0.1641	-0.4284	0.1616
InspSysSIS,MAESTRO	-0.8898	0.0178	-0.9271	0.0186	-0.8542	0.0171
InspSysSIS,MAESTRO,Rel	0.4083	-0.0134	0.8663	-0.0131	0.2159	-0.0137
InspSysSIS,Religious S	-1.1934	-0.0131	-1.0458	-0.0128	-1.4245	-0.0134
InspSysSIS-Nu-Tech	-0.0369	-0.0069	-0.0588	-0.0067	-0.0235	-0.0070
InspSysSIS-NuOva	-0.1944	-0.0119	1.4957	-0.0119	-2.0137	-0.0119
Sep_Tox	0.0005	295.953	0.0005	297.638	0.0006	294.260
Contam	-0.0003	49.3667	-0.0005	48.8615	-0.0001	49.872
AirSac	-1E-5	237.906	-3E-5	229.711	1.3E-5	246.1000
sum_SP	0.0076	6.5629	0.0118	6.5784	0.0039	6.5474
sum_SNP	0.0198	0.6929	0.0183	0.6879	0.0210	0.6979
sum_U	-0.0014	31.092	-0.0022	31.1031	-0.0006	31.0820
sum_NC	-0.0157	1.3634	-0.0078	1.3617	-0.0220	1.3652

Table A-13. Prevalence Estimates from the Young Chicken *Campylobacter* Model for the Mean, Rehang, and Post-chill Sample Collection Locations

Estimates	unsplit	split1	split2
BX (rehang= mean)[1]	1.1615	1.1755	0.9760
BX (rehang= 1) post-chill[2]	0.5254	0.5479	0.3125
BX (rehang= -1) rehang[3]	1.7972	1.8365	1.6052
Prevalence (rehang= mean)[4]	0.7616	0.7641	0.7263
Prevalence (rehang= 1) post-chill[5]	0.6284	0.6336	0.5775
Prevalence (rehang= -1) rehang[6]	0.8578	0.8625	0.8327
Prevalence Unweighted[7]	0.7333	0.7310	0.7356

[1] *BX is the linear combination equal to η where the rehang variable for x equals the mean*

[2] *BX is the liner combination equal to η where the rehang variable for x equals +1*

[3] *BX is the liner combination equal to η where the rehang variable for x equals -1*

[4] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at the mean*

[5] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at +1*

[6] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at -1*

[7] *Crude Prevalence*

Table A-14. Parameter Estimates from the Young Turkey *Salmonella* Split Datasets

Parameter	B unsplit	mean	B split1	mean	B split2	mean
Intercept	-13.1301	1	-13.7398	1	-11.0424	1
rehang	-1.7619	-0.6770	-1.7406	-0.1678	-1.7728	0.1678
loglinespeed	7.4946	1.4706	8.1873	1.4706	5.4553	1.4706
logemployees	3.6115	0.9212	3.0640	0.9212	5.0195	0.9212
lines	-2.7200	1.2420	-2.8184	1.242	-2.502	1.2420
month14	-0.3209	0.0583	-0.1256	0.0583	-0.7948	0.0583
month15	0.7339	0.0943	0.6582	0.0943	0.7898	0.0943
month16	0.6898	0.1040	0.7230	0.1040	0.6085	0.1040
month17	0.3507	0.0929	0.2723	0.0929	0.4151	0.0929
month18	0.2939	0.0874	0.1584	0.0874	0.4748	0.0874
month19	0.5901	0.0693	0.4681	0.0693	0.6994	0.0693
month20	0.5215	0.0721	0.4142	0.0721	0.5889	0.0721
month21	0.184	0.0818	0.0628	0.0818	0.2895	0.0818
month22	-1.5164	0.0867	-1.0174	0.0867	-5.0329	0.0867
month23	-0.8771	0.0777	-0.8407	0.0777	-1.0566	0.0777
month24	-0.5709	0.0798	-0.9067	0.0798	-0.3064	0.0798
month25	-0.2184	0.0867	-0.4303	0.0867	-0.0354	0.0867
district1	0.4785	-0.0576	0.7216	-0.0576	0.0289	-0.0576
district2	-0.6647	-0.1290	-0.6636	-0.1290	-0.4711	-0.129
district3	0.3415	0.0069	0.6031	0.0069	-0.0099	0.0069
district4	0.9143	-0.0596	0.9601	-0.0596	1.1142	-0.0596
district5	0.0481	-0.0673	0.4158	-0.0673	-0.0823	-0.0673
district6	0.3492	-0.0368	0.5643	-0.0368	0.1535	-0.0368
district7	-1.5516	-0.1047	-1.2849	-0.1047	-1.8853	-0.1047
district8	-0.6302	-0.0770	-0.3543	-0.0770	-0.8661	-0.0770

Table A-14. (continued)

Parameter	B unsplit	mean	B split1	mean	B split2	mean
district9	-0.2110	-0.0132	-0.1346	-0.0132	-0.4063	-0.0132
district10	0.8127	-0.0617	0.8419	-0.0617	0.8601	-0.0617
district11	-0.9561	-0.1269	-2.7293	-0.1269	0.6884	-0.1269
district12	1.0358	-0.0673	1.1407	-0.0673	0.7464	-0.0673
InspSysHIMP	-1.6265	0.1179	-1.5988	0.1158	-1.4969	0.1200
InspSysNTIS	0.1801	0.6845	0.1829	0.6803	0.2115	0.6886
InspSysOtherNTIS	0.7410	0.0257	0.8485	0.0236	0.6748	0.0277
sep_tox	0.0015	63.1945	0.0007	63.3731	0.0036	63.0160
contam	0.0023	3.3797	0.0026	3.9619	-0.0791	2.7975
airsac	0.0011	9.9397	0.0015	10.7621	-0.0026	9.1172
synovitis	-0.0067	4.8176	-0.0022	4.8904	-0.0118	4.7448
sum_SP	-0.0344	10.8187	-0.0268	10.8308	-0.0445	10.8065
sum_SNP	0.0444	0.9022	0.0681	0.8988	0.0182	0.9057
sum_U	-0.1027	8.8464	-0.0894	8.8405	-0.1056	8.8523
sum_NC	-0.0548	0.5374	-0.0479	0.5270	-0.0589	0.5479

Table A-15. Prevalence Estimates from the Young Turkey *Salmonella* Model for the Mean, Rehang, and Post-chill Sample Collection Locations

Estimates	unsplit	split1	split2
BX (rehang= mean)[1]	-2.8464	-2.8534	-2.8557
BX (rehang= 1) post-chill[2]	-2.9980	-2.9823	-2.9792
BX (rehang= -1) rehang[3]	-2.0782	-2.2187	-2.2496
Prevalence (rehang= mean)[4]	0.0549	0.0545	0.0544
Prevalence (rehang= 1) post-chill[5]	0.0475	0.0482	0.0484
Prevalence (rehang= -1) rehang[6]	0.1112	0.0981	0.0954
Prevalence Unweighted[7]	0.0729	0.0729	0.0715

[1] *BX is the linear combination equal to η where the rehang variable for x equals the mean*

[2] *BX is the liner combination equal to η where the rehang variable for x equals +1*

[3] *BX is the liner combination equal to η where the rehang variable for x equals -1*

[4] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at the mean*

[5] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at +1*

[6] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at -1*

[7] *Crude Prevalence*

Table A-16. Parameter Estimates from the Young Turkey *Campylobacter* Split Datasets

Parameter	B unsplit	mean	B split1	mean	B split2	mean
Intercept	-13.1300	1	-13.7400	1	-11.0420	1
rehang	-1.7619	-0.6770	-1.7406	-0.1678	-1.7728	0.1678
loglinespeed	7.4946	1.4706	8.1873	1.4706	5.4553	1.4706
logemployees	3.6115	0.9212	3.064	0.9212	5.0195	0.9212
lines	-2.7200	1.2420	-2.8184	1.2420	-2.5020	1.2420
month14	-0.3209	0.0583	-0.1256	0.0583	-0.7948	0.0583
month15	0.7339	0.0943	0.6582	0.0943	0.7898	0.0943
month16	0.6898	0.1040	0.7230	0.1040	0.6085	0.1040
month17	0.3507	0.0929	0.2723	0.0929	0.4151	0.0929
month18	0.2939	0.0874	0.1584	0.0874	0.4748	0.0874
month19	0.5901	0.0693	0.4681	0.0693	0.6994	0.0693
month20	0.5215	0.0721	0.4142	0.0721	0.5889	0.0721
month21	0.1840	0.0818	0.0628	0.0818	0.2895	0.0818
month22	-1.5164	0.0867	-1.0174	0.0867	-5.0329	0.0867
month23	-0.8771	0.0777	-0.8407	0.0777	-1.0566	0.0777
month24	-0.5709	0.0798	-0.9067	0.0798	-0.3064	0.0798
month25	-0.2184	0.0867	-0.4303	0.0867	-0.0354	0.0867
district1	0.4785	-0.0576	0.7216	-0.0576	0.0289	-0.0576
district2	-0.6647	-0.1290	-0.6636	-0.1290	-0.4711	-0.129
district3	0.3415	0.0069	0.6031	0.0069	-0.0099	0.0069
district4	0.9143	-0.0596	0.9601	-0.0596	1.1142	-0.0596
district5	0.0481	-0.0673	0.4158	-0.0673	-0.0823	-0.0673
district6	0.3492	-0.0368	0.5643	-0.0368	0.1535	-0.0368
district7	-1.5516	-0.1047	-1.2849	-0.1047	-1.8853	-0.1047
district8	-0.6302	-0.077	-0.3543	-0.0770	-0.8661	-0.077
district9	-0.211	-0.0132	-0.1346	-0.0132	-0.4063	-0.0132
district10	0.8127	-0.0617	0.8419	-0.0617	0.8601	-0.0617
district11	-0.9561	-0.1269	-2.7293	-0.1269	0.6884	-0.1269
district12	1.0358	-0.0673	1.1407	-0.0673	0.7464	-0.0673
InspSysHIMP	-1.6265	0.1179	-1.5988	0.1158	-1.4969	0.1200
InspSysNTIS	0.1801	0.6845	0.1829	0.6803	0.2115	0.6886
InspSysOtherNTIS	0.7410	0.0257	0.8485	0.0236	0.6748	0.0277
sep_tox	0.0015	63.1945	0.0007	63.3731	0.0036	63.016

Table A-16. (continued)

Parameter	B unsplit	mean	B split1	mean	B split2	mean
contam	0.0023	3.3797	0.0026	3.9619	-0.0791	2.7975
airsac	0.0011	9.9397	0.0015	10.7621	-0.0026	9.1172
synovitis	-0.0067	4.8176	-0.0022	4.8904	-0.0118	4.7448
sum_SP	-0.0344	10.8187	-0.0268	10.8308	-0.0445	10.8065
sum_SNP	0.0444	0.9022	0.0681	0.8988	0.0182	0.9057
sum_U	-0.1027	8.8464	-0.0894	8.8405	-0.1056	8.8523
sum_NC	-0.0548	0.5374	-0.0479	0.5270	-0.0589	0.5479

Table A-17. Prevalence Estimates from the Young Turkey *Campylobacter* Model for the Mean, Rehang, and Post-chill Sample Collection Locations

Estimates	unsplit	split1	split2
BX (rehang= mean)[1]	-1.9928	-2.8116	-3.5105
BX (rehang= 1) post-chill[2]	-4.9475	-4.8444	-4.9858
BX (rehang= -1) rehang[3]	-1.4237	-1.3632	-1.4402
Prevalence (rehang= mean)[4]	0.1200	0.0567	0.0290
Prevalence (rehang= 1) post-chill[5]	0.0071	0.0078	0.0068
Prevalence (rehang= -1) rehang[6]	0.1941	0.2037	0.1915
Prevalence Unweighted[7]	0.1189	0.1401	0.0978

[1] *BX is the linear combination equal to η where the rehang variable for x equals the mean*

[2] *BX is the liner combination equal to η where the rehang variable for x equals +1*

[3] *BX is the liner combination equal to η where the rehang variable for x equals -1*

[4] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at the mean*

[5] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at +1*

[6] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at -1*

[7] *Crude Prevalence*

Table A-18. Regression Coefficients for Unscheduled Procedures (U) by Inspection Element

	Young Chicken - *Salmonella*				
ISP Element	B	sB	p-value	Mean	Std Dev
sum01_U[1]	-0.0020	0.0150	0.8966	0.3741	0.7482
sum03_U[2]	-0.0030	0.0016	0.0500*	13.2204	14.3555
sum04_U[3]	-0.0035	0.0015	0.0237*	12.1161	10.3950
sum05_U[4]	0.0845	0.0159	<.0001*	0.8947	0.6132
sum06_U[5]	-0.0146	0.0053	0.0058*	1.7249	2.6899
sum08_U[6]	0.0059	0.0212	0.7813	0.8051	0.6211

[1] *Unscheduled sanitation procedures*

[2] *Unscheduled HACCP procedures*

[3] *Unscheduled wholesomeness/other consumer protection procedures*

[4] *Unscheduled sampling procedures*

[5] *Unscheduled sanitation performance standard procedures*

[6] *Emergency procedures are always unscheduled*

Table A-18. (continued)

	Young Chicken - *Campylobacter*				
ISP Element	B	sB	p-value	Mean	Std Dev
sum01_U[1]	0.0065	0.0205	0.7528	0.3741	0.7482
sum03_U[2]	-0.0264	0.0146	0.0715	13.2204	14.3555
sum04_U[3]	-0.0780	0.0280	0.0053*	12.1161	10.395
sum05_U[4]	-0.1099	0.0183	<.0001*	0.8947	0.6132
sum06_U[5]	0.0128	0.0063	0.0435*	1.7249	2.6899
sum08_U[6]	0.0043	0.0277	0.8775	0.8051	0.6211

[1] *Unscheduled sanitation procedures*
[2] *Unscheduled HACCP procedures*
[3] *Unscheduled wholesomeness/other consumer protection procedures*
[4] *Unscheduled sampling procedures*
[5] *Unscheduled sanitation performance standard procedures*
[6] *Emergency procedures are always unscheduled*

Table A-18. (continued)

	Young Turkey - *Salmonella*				
ISP Element	B	sB	p-value	Mean	Std Dev
sum01_U[1]	-0.1060	0.1077	0.3252	0.1845	0.4483
sum03_U[2]	0.0283	0.0285	0.3213	2.4450	1.8068
sum04_U[3]	-0.0169	0.0731	0.8166	1.6907	0.8603
sum05_U[4]	-0.1286	0.0785	0.1015	0.9444	0.6137
sum06_U[5]	-0.0638	0.0690	0.3555	0.8843	0.8492
sum08_U[6]	0.0557	0.0992	0.5744	0.7939	0.5501

[1] *Unscheduled sanitation procedures*
[2] *Unscheduled HACCP procedures*
[3] *Unscheduled wholesomeness/other consumer protection procedures*
[4] *Unscheduled sampling procedures*
[5] *Unscheduled sanitation performance standard procedures*
[6] *Emergency procedures are always unscheduled*

Table A-18. (continued)

	Young Turkey - *Campylobacter*				
ISP Element	B	sB	p-value	Mean	Std Dev
sum01_U[1]	-0.0994	0.1244	0.4242	0.2510251	0.6869
sum03_U[2]	-0.1031	0.0492	0.0363*	2.6741	1.7617
sum04_U[3]	-0.0818	0.0860	0.3412	2.8266	1.0534
sum05_U[4]	-0.0559	0.1252	0.6556	0.9917	0.6807
sum06_U[5]	-0.1675	0.0808	0.0381*	1.1390	1.1582
sum08_U[6]	-0.2074	0.2018	0.3040304	0.9639	0.3763

[1] *Unscheduled sanitation procedures*

[2] *Unscheduled HACCP procedures*

[3] *Unscheduled wholesomeness/other consumer protection procedures*

[4] *Unscheduled sampling procedures*

[5] *Unscheduled sanitation performance standard procedures*

[6] *Emergency procedures are always unscheduled*

Table A-19. Regression Coefficient for Unscheduled Procedures (U) by ISP Code

	Chicken-*Salmonella*				
ISP Code	B	sB	p-value	Mean	Std Dev
sum01B_U[1]	0.0143	0.0468	0.7596	0.0768	0.2763
sum01C_U[2]	0.0022	0.0184	0.9055	0.2886	0.6435
sum01_Uother[3]	-0.2239	0.1081	0.0383*	0.0087	0.1038
sum03B_U[4]	0.0200	0.0561	0.7216	0.0356	0.2071
sum03C_U[5]	-0.1036	0.0294	0.0004*	0.3627	1.2117
sum03J_U[6]	-0.0026	0.0017	0.1133	12.3816	13.8886
sum03_Uother[7]	0.1119	0.0272	<.0001*	0.4405	1.3024
sum04_U[8]	-0.0034	0.0015	0.028*	12.1161	10.395
sum05_U[9]	0.0799	0.0159	<.0001*	0.8947	0.6132
sum06D01_U[10]	-0.1247	0.0181	<.0001*	0.3250	0.621
sum06_Uother[11]	-0.0076	0.0055	0.1652	1.400	2.6579
sum08_U[12]	0.0036	0.0212	0.8644	0.8051	0.6211

[1] *Preoperational sanitation*
[2] *Operational sanitation*
[3] *Other 01 sanitation*
[4] *HACCP raw not ground product inspection*
[5] *HACCP raw ground product inspection*
[6] *HACCP fecal checks in slaughter area*
[7] *Other HACCP procedures*
[8] *Wholesomeness/other consumer protection inspection*
[9] *Sampling*
[10] *Sanitation performance standard inspection*
[11] *Other 06 sanitation inspection*
[12] *Emergency inspection*

Table A-19. (continued)

	Chicken-*Campylobacter*				
ISP Code	B	sB	p-value	Mean	Std Dev
sum01B_U[1]	0.0259	0.0551	0.6383	0.0627	0.2522
sum01C_U[2]	-0.0015	0.0240	0.9501	0.2849	0.6290
sum03B_U[3]	0.1078	0.0459	0.0190*	0.0610	0.3019
sum03C_U[4]	0.0771	0.0402	0.0554	0.3054	0.9130
sum03J_U[5]	-0.0097	0.0020	<.0001*	13.8051	15.3436
sum03_Uother[6]	-0.0940	0.0357	0.0085*	0.3814	1.0212
sum04_U[7]	0.0060	0.0019	0.0020*	11.6642	9.6596
sum05_U[8]	-0.1072	0.0184	<.0001*	0.7620	0.7275
sum06D01_U[9]	0.0488	0.0223	0.0286*	0.3667	0.6456
sum06_Uother[10]	0.0065	0.0066	0.3249	1.8606	2.8507
sum08_U[11]	0.0145	0.0281	0.6066	1.1757	0.5389

[1] *Preoperational sanitation*
[2] *Operational sanitation*
[3] *Other 01 sanitation*
[4] *HACCP raw not ground product inspection*
[5] *HACCP raw ground product inspection*
[6] *HACCP fecal checks in slaughter area*
[7] *Other HACCP procedures*
[8] *Wholesomeness/other consumer protection inspection*
[9] *Sampling*
[10] *Sanitation performance standard inspection*
[11] *Other 06 sanitation inspection*
[12] *Emergency inspection*

Table A-19. (continued)

	Turkey-*Salmonella*				
ISP Code	B	sB	p-value	mean	Std Dev
sum01B_U[1]	0.1305	0.1787	0.4653	0.0664	0.2558
sum01C_U[2]	-0.2639	0.1534	0.0854	0.1106	0.3188
sum01_Uother[3]	-0.7034	0.6871	0.3059	0.0075	0.0865
sum03B_U[4]	0.0697	0.2012	0.7290	0.1193	0.3758
sum03C_U[5]	-0.3255	0.1997	0.1030	0.1437	0.4072
sum03J_U[6]	-0.5469	0.1918	0.0043*	0.9244	0.4632
sum03_Uother[7]	0.2725	0.1411	0.0535	1.2576	0.9609
sum04_U[8]	0.0292	0.0757	0.6996	1.6907	0.8603
sum05_U[9]	-0.1134	0.0801	0.1567	0.9445	0.6137
sum06D01_U[10]	-0.0686	0.1396	0.6232	0.1589	0.3712
sum06_Uother[11]	-0.0521	0.0849	0.5391	0.7255	0.7601
sum08_U[12]	0.0866	0.1013	0.3926	0.7939	0.5501

[1] *Preoperational sanitation*
[2] *Operational sanitation*
[3] *Other 01 sanitation*
[4] *HACCP raw not ground product inspection*
[5] *HACCP raw ground product inspection*
[6] *HACCP fecal checks in slaughter area*
[7] *Other HACCP procedures*
[8] *Wholesomeness/other consumer protection inspection*
[9] *Sampling*
[10] *Sanitation performance standard inspection*
[11] *Other 06 sanitation inspection*
[12] *Emergency inspection*

Table A-19. (continued)

	Turkey-*Campylobacter*				
ISP Code	B	sB	p-value	Mean	Std Dev
sum01B_U[1]	0.1405	0.3308	0.6709	0.0659	0.2591
sum01C_U[2]	-0.4178	0.2833	0.1403	0.1342	0.3480
sum01_Uother[3]	0.0636	0.3130	0.8390	0.0510	0.3136
sum03B_U[4]	-0.2212	0.4389	0.6143	0.1120	0.3701
sum03C_U[5]	-0.0018	0.4102	0.9965	0.1449	0.4170
sum03J_U[6]	0.2225	0.3607	0.5372	1.0482	0.4321
sum03_Uother[7]	-0.1558	0.3077	0.6127	1.3689	0.9374
sum04_U[8]	-0.1010	0.0905	0.2643	2.8266	1.0534
sum05_U[9]	-0.0678	0.1306	0.6036	0.9917	0.6807

[1] *Preoperational sanitation*
[2] *Operational sanitation*
[3] *Other 01 sanitation*
[4] *HACCP raw not ground product inspection*
[5] *HACCP raw ground product inspection*
[6] *HACCP fecal checks in slaughter area*
[7] *Other HACCP procedures*
[8] *Wholesomeness/other consumer protection inspection*
[9] *Sampling*

Table A-20. Prevalence Estimates for Models Disaggregated by Unscheduled Procedures

Variable (6)	CS[a]	CC[b]	TS[c]	TC[d]
BX (rehang= mean)[1]	-2.3906	1.1632	-2.8368	-3.1793
BX (rehang= 1) post-chill[2]	-2.7291	0.5257	-2.9746	-4.9373
BX (rehang= -1) rehang[3]	-0.3889	1.8003	-2.1386	-1.4213
Prevalence (rehang= mean)[4]	0.0839	0.7619	0.0554	0.0400
Prevalence (rehang= 1) post-chill[5]	0.0613	0.6285	0.0486	0.0071
Prevalence (rehang= -1) rehang[6]	0.4040	0.8582	0.1054	0.1945
Variable (10-12)	CS[a]	CC[b]	TS[c]	TC[d]
BX (rehang= mean)[1]	-2.3928	1.1645	-2.8510	-3.2059
BX (rehang= 1) post-chill[2]	-2.7317	0.5267	-2.9934	-4.9695
BX (rehang= -1) rehang[3]	-0.3885	1.8019	-2.1292	-1.4423
Prevalence (rehang= mean)[4]	0.0837	0.7622	0.0546	0.0389
Prevalence (rehang= 1) post-chill[5]	0.0611	0.6287	0.0477	0.0069
Prevalence (rehang= -1) rehang[6]	0.4041	0.8584	0.1063	0.1912

[a] *CS chicken-Salmonella model*

[b] *CC chicken-Campylobacter model*

[c] *TS turkey-Salmonella model*

[d] *TC turkey-Campylobacter model*

[1] *BX is the linear combination equal to η where the rehang variable for x equals the mean*

[2] *BX is the liner combination equal to η where the rehang variable for x equals +1*

[3] *BX is the liner combination equal to η where the rehang variable for x equals -1*

[4] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at the mean*

[5] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at +1*

[6] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at -1*

[6] *Crude Prevalence*

Table A-21. Number of Establishments in the Four Observed Datasets by SBA Size

Pathogen	Species	L	S	V	total
Salmonella	chicken	133	48	8	189
Campylobacter	chicken	130	45	5	180
Salmonella	turkey	26	26	13	65
Campylobacter	turkey	24	22	12	58
total		313	141	38	492

Table A-22. Number of Establishments Expected to adopt the Proposed Inspection System by SBA Size according to Preliminary Regulatory Impact Analysis (PRIA)

Species	Switch[1]	L	S	V	total
chicken	170	127	43	0	170
turkey	30	20	10	0	30
subtotal	200	147	53	0	200
other	19	2	14	3	19
total	219	147	72	3	219

[1] Switch indicates the number of establishments expected to adopt the proposed inspection system according to the PRIA

Table A-23. Number of Observed Establishments Expected to adopt the Proposed Inspection System by SBA Size

Pathogen	Species	L	S	V	total
Salmonella[1]	chicken	128	50	2	180
Campylobacter[2]	chicken	128	50	2	180
Salmonella[3]	turkey	21	17	1	39
Campylobacter[4]	turkey	21	17	1	39
Total[5]		298	134	6	438

[1] *Expected values for chicken slaughter Salmonella dataset establishments*

[2] *Expected values for chicken slaughter Campylobacter dataset establishments*

[3] *Expected values for turkey slaughter Salmonella dataset establishments*

[4] *Expected values for turkey slaughter Campylobacter dataset establishments*

[5] *Summed totals reflect pathogen sampling overlap in the same establishments*

Table A-24. Observed Baseline Datasets and Expected to Shift Baseline Datasets Prevalence Estimates

Dataset Prevalence Estimates	Young Chicken			
	Salmonella		*Campylobacter*	
Estimates	observed	expected	observed	expected
BX (rehang= mean)[1]	-2.3905	-2.3940	1.1615	1.1657
BX (rehang= 1) post-chill[2]	-2.7290	-2.7289	0.5254	0.5351
BX (rehang= -1) rehang[3]	0.3376	-0.4119	1.7972	1.7961
Prevalence (rehang= mean)[4]	0.0839	0.08363	0.7616	0.7623
Prevalence (rehang= 1) post-chill[5]	0.0613	0.0612	0.6284	0.6306
Prevalence (rehang= -1) rehang[6]	0.4039	0.3984	0.8578	0.8576
Prevalence Unweighted[7]	0.1231		0.7333	
Dataset Prevalence Estimates	Young Turkey			
	Salmonella		*Campylobacter*	
Estimates	observed	expected	observed	expected
BX (rehang= mean)	-2.8464	-2.8625	-1.9928	-2.0155
BX (rehang= 1) post-chill	-2.998	-3.0221	-4.9475	-5.1080
BX (rehang= -1) rehang	-2.0782	-2.0233	-1.4237	-1.3690
Prevalence (rehang= mean)	0.0549	0.05404	0.1200	0.11759
Prevalence (rehang= 1) post-chill	0.0475	0.04644	0.0071	0.00601
Prevalence (rehang= -1) rehang	0.1112	0.11678	0.1941	0.20278
Prevalence Unweighted	0.0729		0.1189	

[1] *BX is the linear combination equal to η where the rehang variable for x equals the mean*

[2] *BX is the liner combination equal to η where the rehang variable for x equals +1*

[3] *BX is the liner combination equal to η where the rehang variable for x equals -1*

[4] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at the mean*

[5] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at +1*

[6] *Prevalence equals the inverse logistic function with the exponent BX equal to rehang at -1*

[7] *Crude Prevalence for observed data*