Welcome to IFSAC's webinar

Please stand by - we will be starting the presentation soon.

IFSAC's Webinar – "Are Outbreak Illnesses Representative of Sporadic Illnesses?" Agenda Friday, January 10, 2014, 2:00 – 3:00 pm EST		
Time	**Speaker**	**Topic**
2:00 – 2:03 pm EST	Cary Parker (**FDA**) - *Moderator*	Welcome
2:03 – 2:10 pm EST	David Goldman (**USDA-FSIS**)	Introduction
2:10 – 2:50 pm EST	Eric Ebel & Mike Williams (**USDA-FSIS**)	IFSAC's outbreak and sporadic illness attribution project
2:50 – 2:55 pm EST	David Goldman (**USDA-FSIS**)	Closing Remarks
2:55 – 3:05 pm EST	Michael Bazaco (**FDA**) - *Moderator*	Q & A Session – Open to all attendees

NOTES

Name: Please log into the Adobe Connect software with your first and last name. If you did not log in with your full name, please close your internet browser, re-open it again, and log back in by entering your full name.

Q & A: Once the webinar begins, you can submit questions by typing text into the **Q & A Box**. Questions related to the content of the presentations can be submitted at any time; but they will be answered at the end of the presentation in the order they were received. We will attempt to answer as many questions as we can in the time allotted. However due to large number of registrants, any unaddressed questions should be directed to the IFSAC inbox: IFSAC@fda.hhs.gov

Recording: The entire webinar session will be recorded (audio & visual). A recording of this webinar will be posted online in the near future.

Technical Difficulties: If you experience problems with the Adobe Connect software, please submit your technical issue in the **Q & A Box** and someone will assist you.

The Interagency Food Safety Analytics Collaboration (IFSAC): Introduction

IFSAC Webinar Presented By:

David P. Goldman, MD, MPH

Assistant Administrator, Office of Public Health Science
Food Safety and Inspection Service (FSIS), United States Department of Agriculture (USDA)

January 10, 2014

Our Approach

An interagency collaboration that:

- Builds on a history of working together on source attribution
- Applies advances in source attribution methods
- Leverages knowledge, expertise and data among agencies
- Builds an efficient structure guided by strategy
- Prioritizes communications and stakeholder input

Apply Advances in Source Attribution Methods

- Improved food categories
- Statistical analysis of data from foodborne outbreak surveillance
- Hybrid analysis using outbreak surveillance data and sporadic case-control study data
- The Hald Bayesian model
- Estimates of uncertainty
- Expanded data sources

Leverage Knowledge, Expertise and Data Among Agencies

- Shared environment to develop methodology and conduct analyses
- Apply data from all applicable sources
- Shared results, interpretation and use
- Enhanced policy decisions

Build a Shared Structure and Strategy

Steering Committee

- 2 members from each agency able to commit resources
- Annual rotation of chair person among agencies
- Assess, approve and oversee IFSAC projects

Technical Workgroup

- Designated group of agency experts and analysts
- Understand the needs of each agency
- Develops proposals and plans for IFSAC projects
- Coordinates IFSAC activities within each agency

Project Teams

- Assigned agency experts performing specific projects

Communications and Stakeholder Input

Past:

- Series of public meetings, 2010
- Risk Communications Advisory Committee consultation, 2011
- CDC FSMA Surveillance Work Group
- IFSAC public meetings, 2012
- PEW/RWJ Food Safety Forum, 2012
- Web-based information and communications
  www.cdc.gov/foodborneburden/attribution.html
- Webinars, June 2013: “Improving the Categories Used to Classify Foods Implicated in Outbreaks”
- Stakeholder updates

Upcoming:

- New IFSAC webpage, Winter-Spring, 2014
- Planning Public Meeting, Fall-Winter, 2014

IFSAC Webinars

- Low-cost, easily accessible mode of communication with stakeholders
- Ability to expeditiously share project updates and results before publication in peer review journals
- Two webinars planned per year
- Today: “Are Outbreak Illnesses Representative of Sporadic Illnesses?”

Are Outbreak Illnesses Representative of Sporadic Illnesses?

An update on a project of the Interagency Food Safety Analytics Collaboration (IFSAC)

An IFSAC Webinar Presented By:

Eric D. Ebel, DVM, MS, DACVPM(Epi), ASA/CERA
Senior Veterinary Medical Officer
Food Safety and Inspection Service (FSIS), United States Department of Agriculture (USDA)

Michael S. Williams, PhD
Senior Risk Analyst
Food Safety and Inspection Service (FSIS), United States Department of Agriculture (USDA)

January 10, 2014

Purpose

- The purpose of this project is to:
  - Explore the question: are foodborne illnesses associated with outbreaks representative of the larger collection of all sporadic (non-outbreak) illnesses?
  - Prioritize pathogens for which outbreak data may be sufficient to draw conclusions about source attribution
  - Contribute to an analysis of uncertainty
- The purpose is *not* to estimate foodborne illness source attribution fractions

Outbreak-based attribution

- Source attribution generally requires two key pieces of illness information:
  1. the pathogen that caused the illness, and
  2. the contaminated food source responsible for the illness

- FDOSS, the Foodborne Disease Outbreak Surveillance System, includes both the pathogen and the implicated food
- So what are the limitations of focusing on outbreaks only?
  - FDOSS cases represent a fraction of all cases

FoodNet

- Surveillance system for enteric infections
- Collaboration between State Health Departments, CDC, FDA and FSIS
  - CT, GA, MD, MN, NM, OR, TN
  - Selected counties in CA, CO and NY
- Most FoodNet illnesses are sporadic
  - Cases do not identify most probable food source

Is Source Attribution from Outbreaks Representative of Sporadic Cases?

- Difficult to answer!
  - Source evidence for sporadic cases is needed
- Therefore, a key source of attribution uncertainty is
  - The validity of the assumption that the distribution of pathogens and their implicated food vehicles in outbreak reports reflects the relevant food exposure pathways in the general population

Objective

- H_0: Case characteristics are similar for outbreak and sporadic cases
  - If characteristics are reasonably similar between outbreak cases and sporadic cases, then there is no empiric evidence to reject the application of attribution inferences drawn from the population of outbreaks to the broader population of non-outbreak cases

- H_A: Characteristics are not similar
  - Alternatively, if characteristics are dissimilar, then empiric evidence suggests that the application of outbreak derived attribution estimates to non-outbreak cases may be problematic

Project Description - General

- Compare geographic, demographic, temporal and clinical characteristics of outbreak and non-outbreak cases for
  - *Salmonella*
  - *E. coli* O157:H7 (STEC)
  - *Campylobacter*
  - *Listeria monocytogenes*
- If outbreak cases look like sporadic cases across an array of epidemiologically-relevant factors, this would NOT REJECT the plausibility that causal food exposure pathways are similar in identity and degree of incidence

Data: FoodNet Surveillance System

- Only the FoodNet surveillance system provides data with identified outbreak and non-outbreak cases to compare directly across predictor variables
  - We used 2004-2011 FoodNet data in this analysis

Pathogen	Outbreak cases	Non-outbreak cases	Outbreak fraction
Campylobacter	201	47,887	0.4%
STEC	736	3,165	18.9%
Listeria	56	1,028	5.2%
Salmonella	3,273	53,810	5.7%

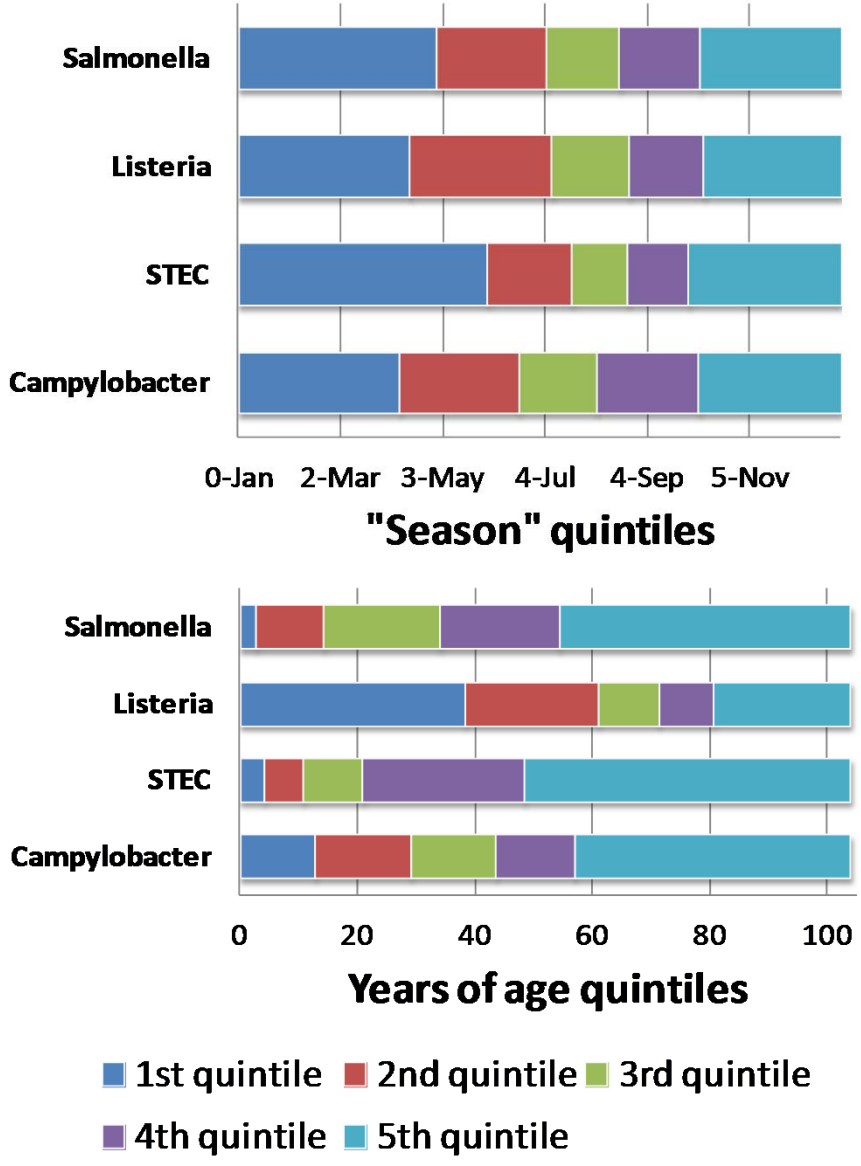
Predictor variables

- STATE – FoodNet location wherein case was identified
  - (CA, CO, CT, GA, MD, MN, NM, NY, OR, TN)
- YEAR – case year (2004 – 2011)
- SEASON – time of year case occurred
- AGE – of case individual
- GENDER
- HOSPITALIZATION – was the case hospitalized or not?

Classifications of predictors

- Structural (surveillance) factors
  - STATE, YEAR and SEASON
  - Not considered fundamental epidemiologic drivers of differences between outbreak and non-outbreak cases
  - Food source attribution estimates usually aggregated across these predictors
- Case factors
  - AGE, GENDER and HOSPITALIZATION
  - May indicate meaningful differences in epidemiology of outbreak and non-outbreak cases
  - Differences may indicate a potential bias from using outbreak data to estimate food sources

Simplifying SEASON and AGE



A two-step analytic approach

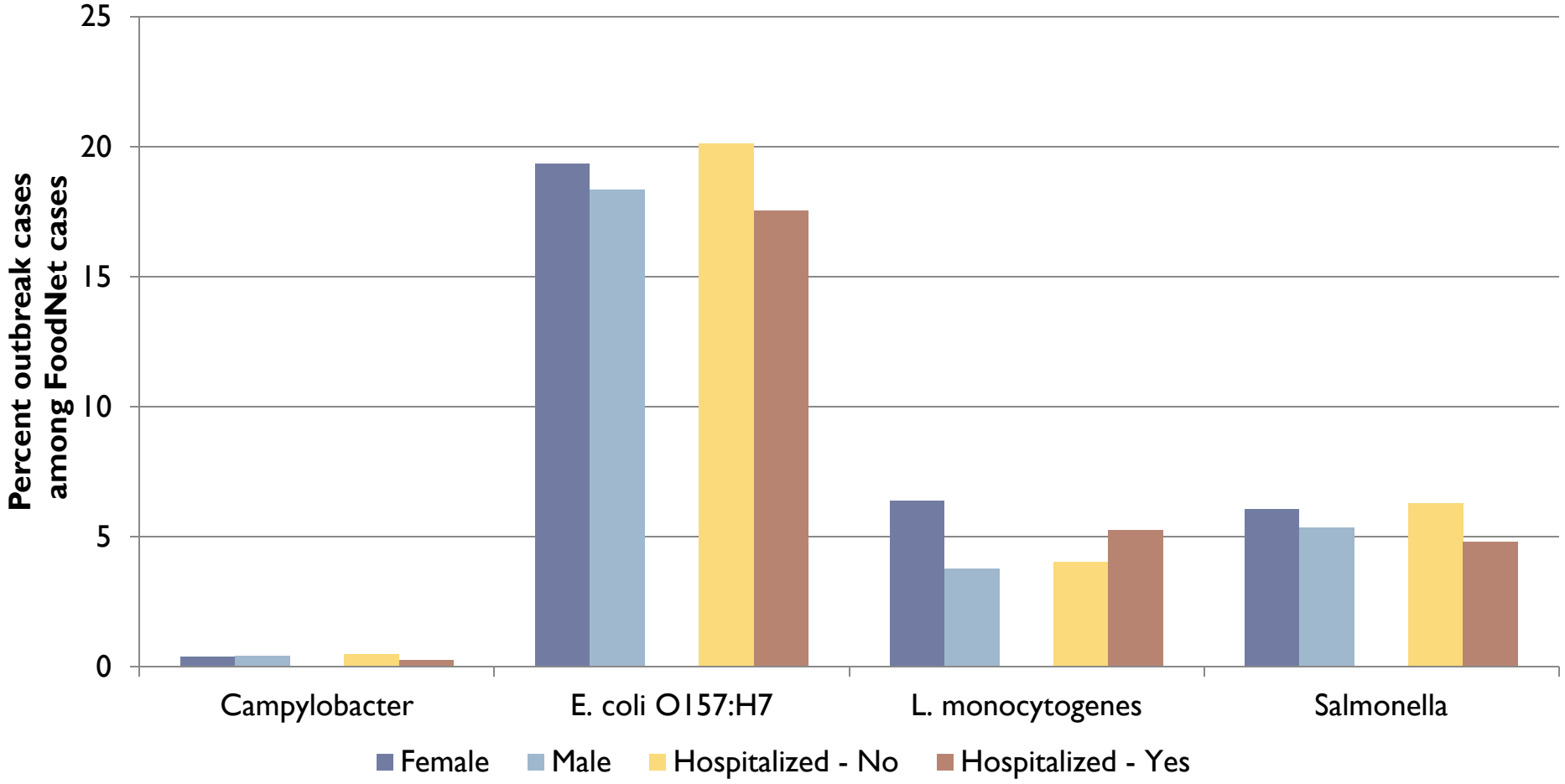
- Step 1 - Random Forest modeling conducted to gauge the importance of predictors
  - Tree-based models better account for interactions between predictors, and missing observations, than traditional regression models
  - Eliminates unimportant predictors for Step 2
- Step 2 – Logistic regression modeling conducted on remaining predictors

Results

Random Forest results

- Initially, full models included six predictor variables
  - YEAR, STATE, SEASON, AGE, GENDER and HOSPITALIZATION status
- GENDER and HOSPITALIZATION predictors were not significant for all pathogens – so these were dropped
  - Misclassification statistics suggested no substantial difference in models with or with out gender and hospitalization

Gender and Hospitalization predictors were not significant



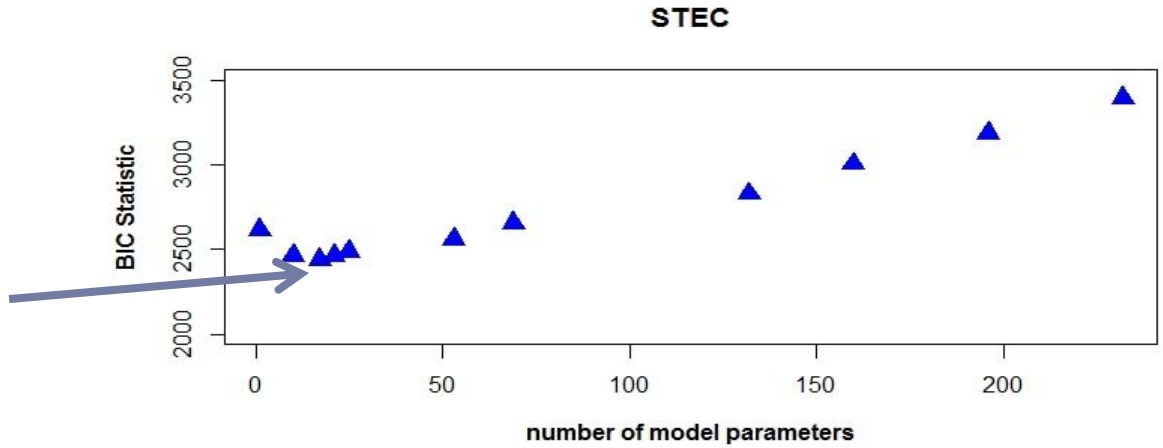
Logistic modeling

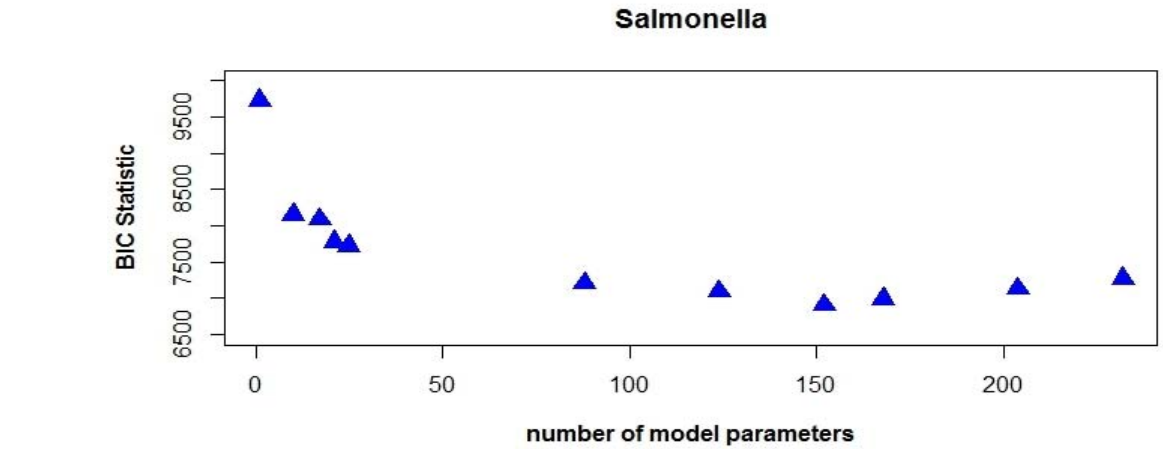
- Examined the remaining four predictors and their interactions in a step-wise fitting algorithm
- Used Bayesian Information Criteria (BIC) to select best model

Pathogen	Predictors in best model
Campylobacter	STATE
STEC	STATE+YEAR
Listeria	STATE+YEAR
Salmonella	STATE+YEAR+SEASON+AGE+ STATE*YEAR + YEAR*SEASON

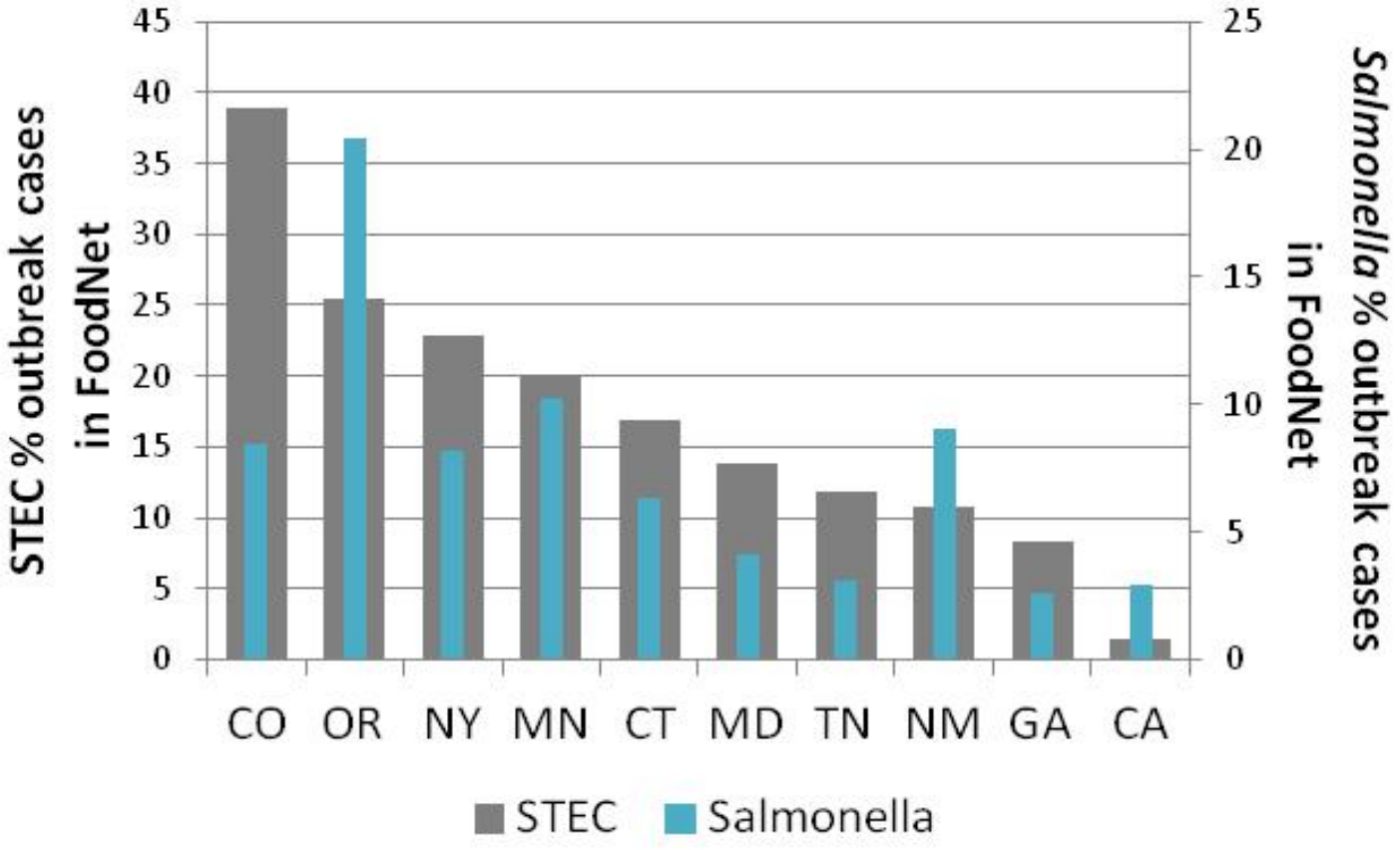
BIC for Selecting Significant Model Predictors

Best model is one with smallest BIC. For example, STEC model with 10 STATE parameters and 8 YEAR parameters has smallest BIC value.



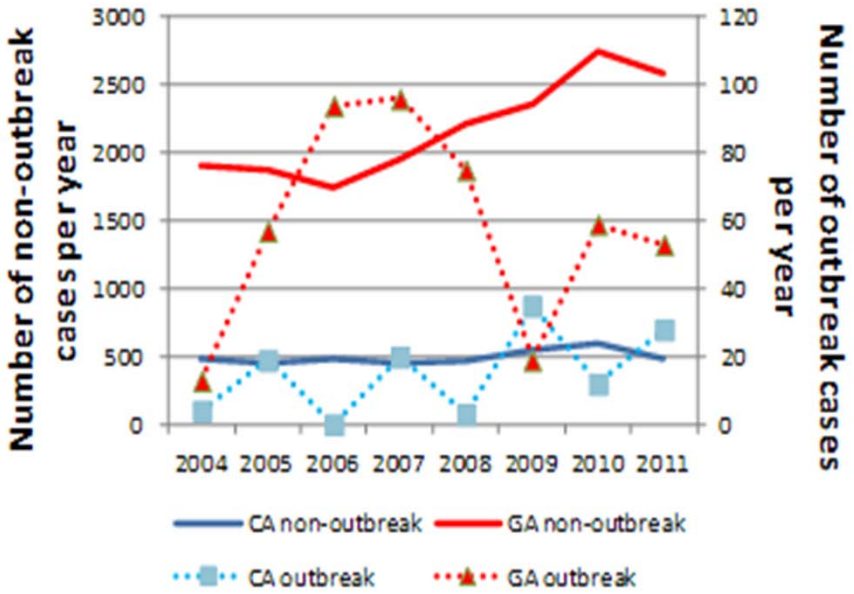


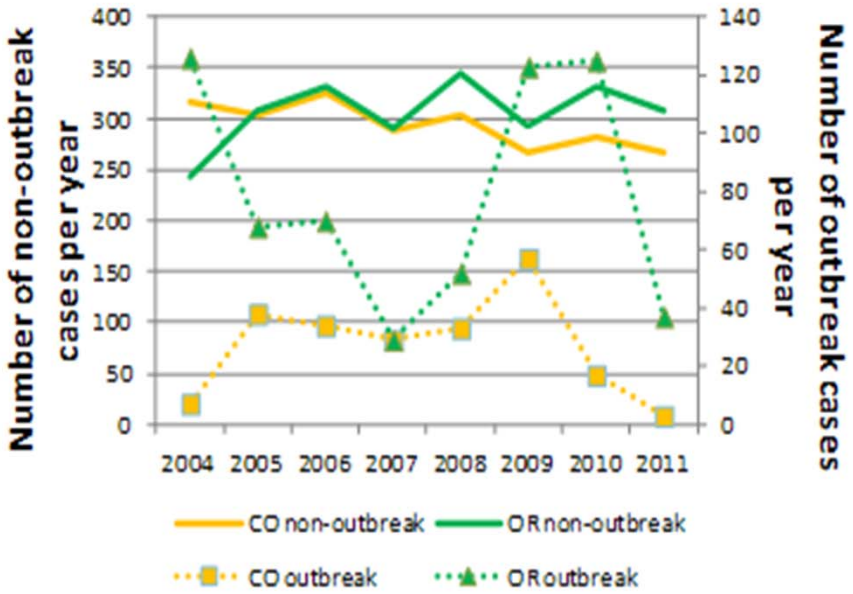
STATE effect – substantial variability in outbreak cases across FoodNet sites



STATE+YEAR effect – non-outbreak cases appear more stable than outbreak cases

Salmonella FoodNet data for two STATES with lower outbreak percents (left) and two STATES with higher outbreak percents (right)



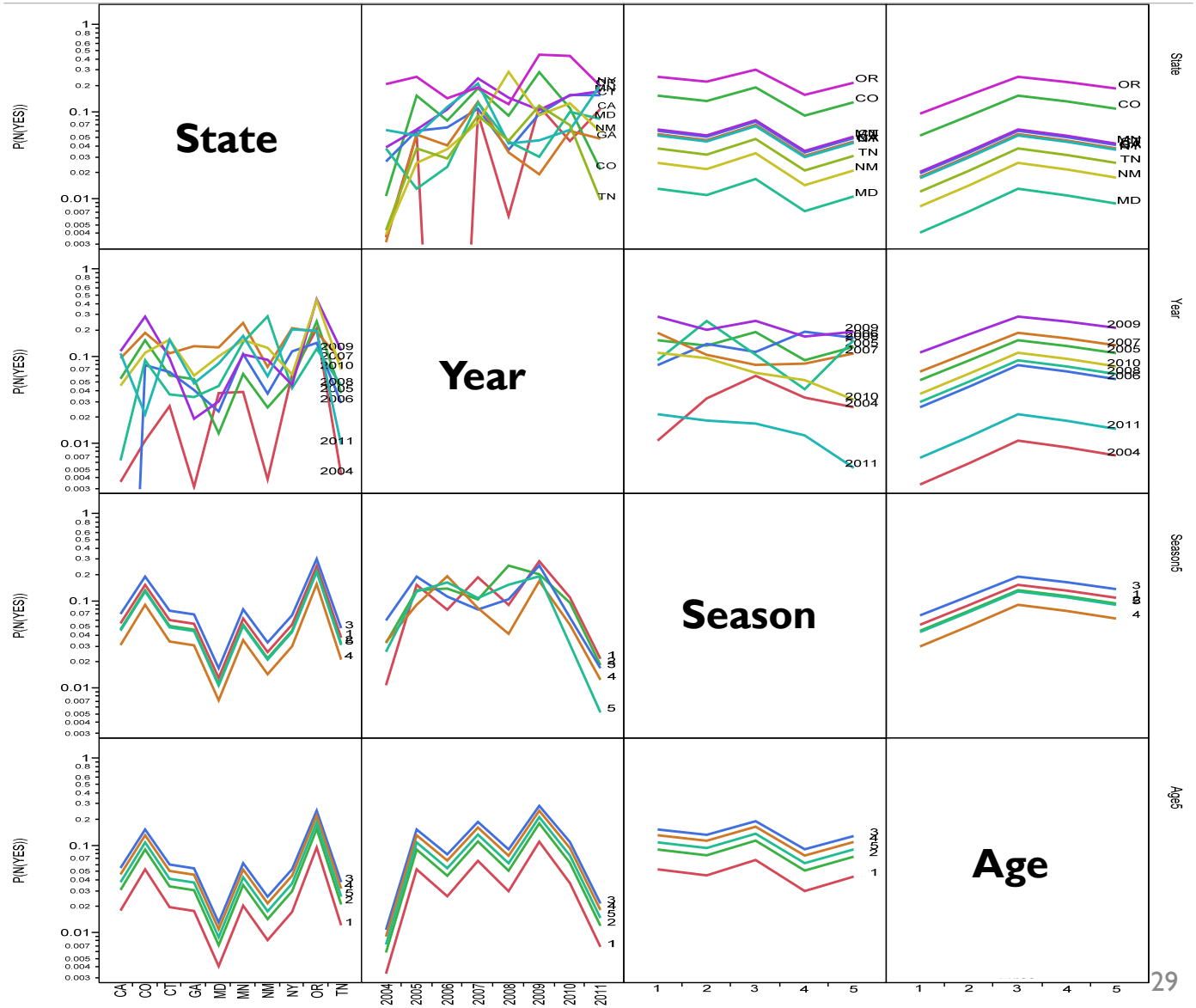


Interaction Profiles - Overview

- Interaction profiles were conducted to look at significant predictors of being outbreak associated
  - Crossed lines suggest "interactions" and could indicate different food exposure pathways
  - Parallel lines indicate no interactions and perhaps food exposure pathways are similar between outbreak and non-outbreak cases
- No interactions were found for *E. coli* O157:H7, *Campylobacter* spp., and *Listeria monocytogenes*

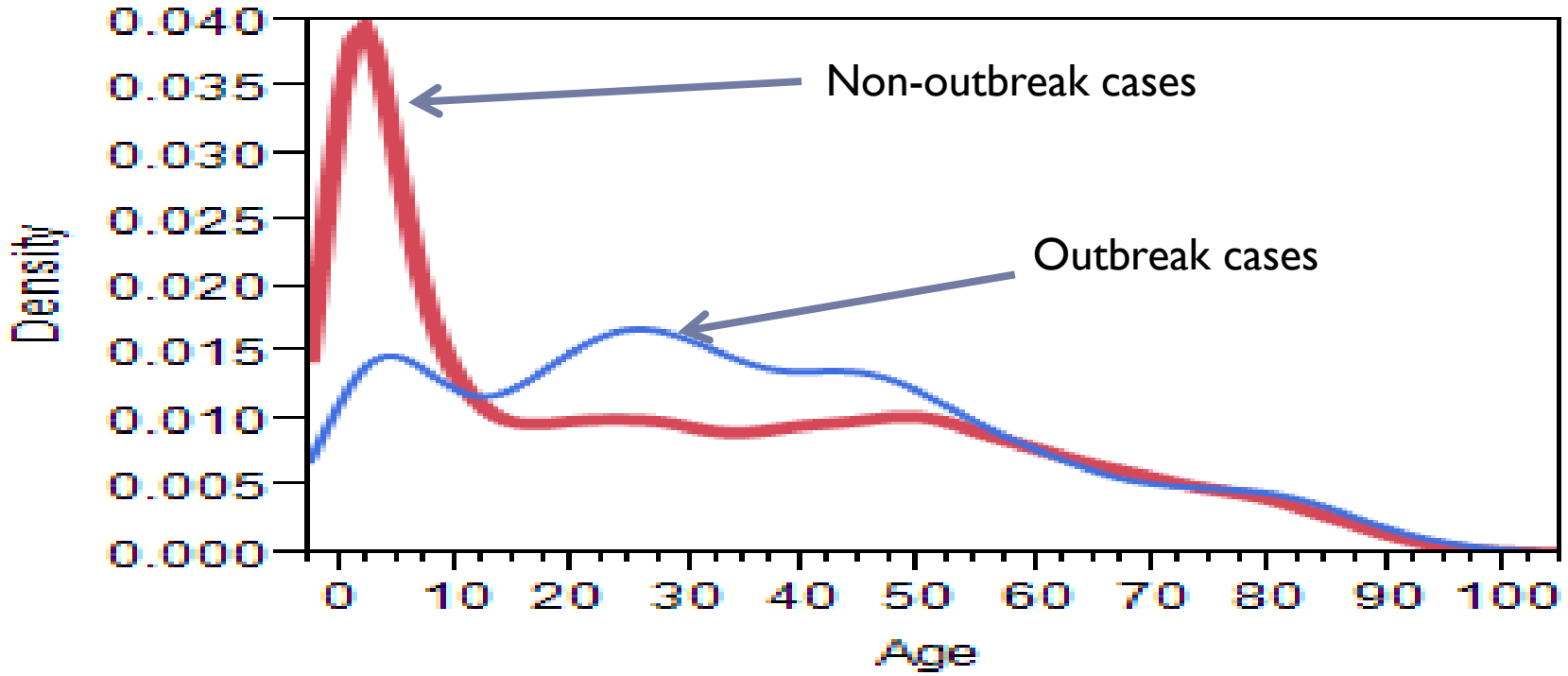
Salmonella Interaction Profile – State, Year, Season, Age

- Crossed lines for Year/State and Year/Season indicate interactions and perhaps exposure pathways may be different
- Some indication to refute H_0

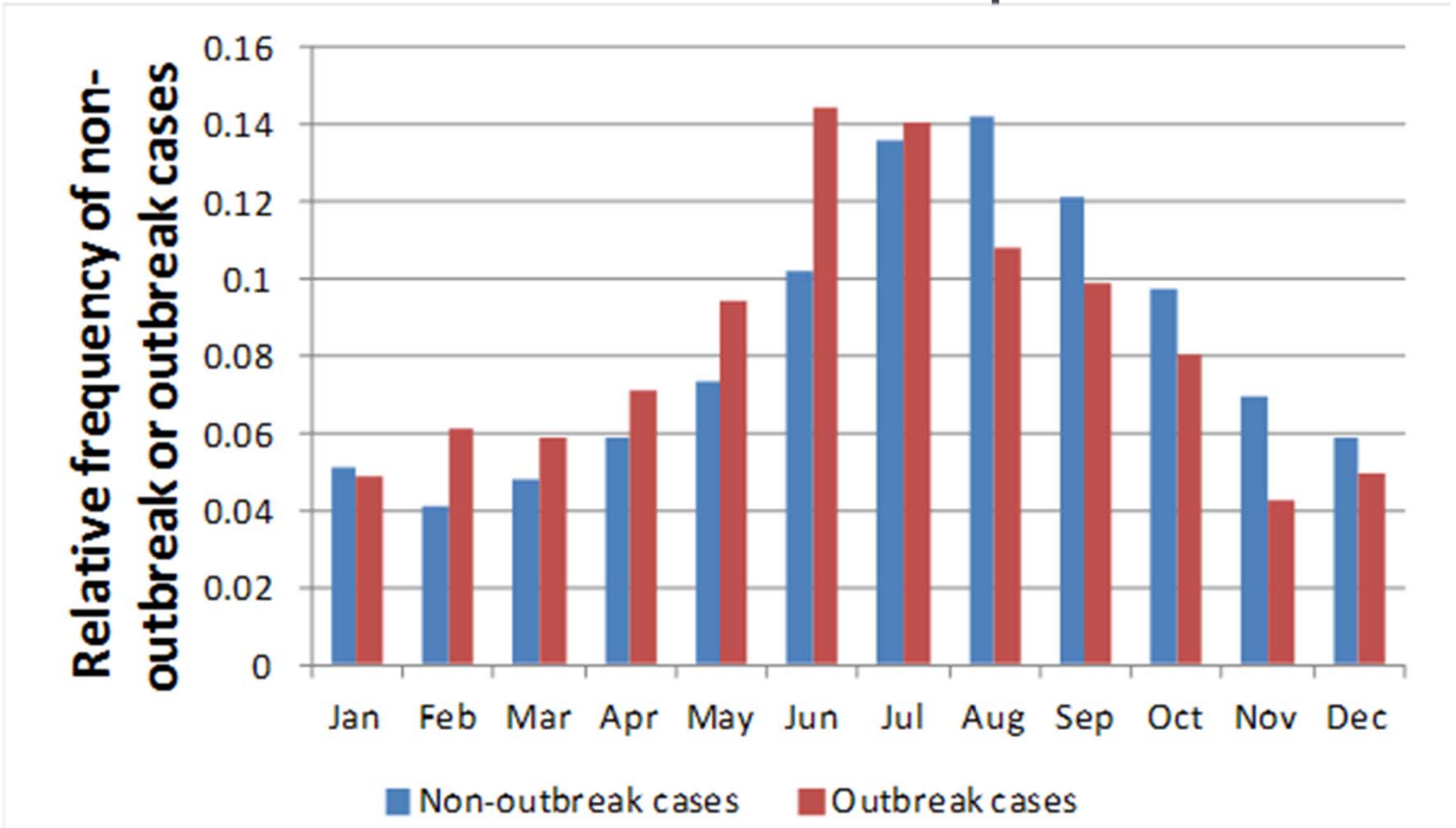


Age as a Predictor of *Salmonella* Outbreak Status

- The 0-3 years-old age range appears to be substantially over-represented among non-outbreak cases relative to outbreak cases



Season effect for *Salmonella:* outbreak peak occurs before non-outbreak peak



General Conclusions

- Outbreak cases "look like" non-outbreak cases with respect to case factors (age, gender, illness severity)
  - Therefore, source attribution from outbreak cases may be applicable to non-outbreak cases?
  - Exception: AGE factor for young *Salmonella* illnesses
- Outbreak cases occur differently from non-outbreak cases with respect to surveillance factors (geography, year and season)
  - Therefore, source attribution aggregated across space and time may not be applicable to a specific place or time?
  - Supports aggregating national outbreak evidence across multiple years AND applying these estimates to national sporadic illnesses

CENTERS FOR DISEASE CONTROL AND PREVENTION

Summary

- This work *cannot* answer if outbreak derived attribution is representative of sporadic cases
  - Data are not available for direct comparison
- However, the following statements can be made:
  - *Campylobacter* outbreak and non-outbreak cases are similar
    - However, too few data to draw conclusions
  - *L. monocytogenes* outbreak and non-outbreak cases are similar
  - *E. coli* O157:H7 outbreak and non-outbreak cases are similar
  - *Salmonella*: few outbreak cases among very young relative to non-outbreak cases
    - Possible that sporadic cases among the youngest quintile result from non-food sources
    - Source attribution estimates derived from aggregated outbreak information may not be applicable to young sporadic illnesses

IFSAC Project Team

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Thank you!

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Question & Answer Session

Thank you for attending IFSAC's webinar

- **More questions?** Please send an email to the IFSAC inbox: IFSAC@fda.hhs.gov
- **Recording:** A recording of this webinar will be posted online in the near future.
- **IFSAC Website:** We'll be launching an IFSAC website in Winter-Spring 2014. Please be on the lookout for an announcement soon.