Penalized B-Spline Regression to Analyze Trends in Reported Foodborne Illness

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Washington, DC

Society for Risk Analysis
6-10 December 2015
Arlington, VA
INTRODUCTION

• Objective: Analyze temporal patterns in reported U.S. foodborne illness without specifying model form

• Illustrative Case: Salmonella
  – Annual and seasonal patterns
  – All Salmonella serotypes, principal serotypes

Powell: P-Spline Regression
DATA

- FoodNet (Foodborne Diseases Active Surveillance Network)
- Reported illness counts by site, year, and month
- Population size by site and year
- Site composition stable since 2004

- All Salmonella Serotypes
- Principal Salmonella Serotypes
  - Typhimurium
  - Enteritidis
  - Newport
  - Account for over 40% of serotyped strains

Powell: P-Spline Regression
METHODS

• Penalized B-spline Regression
  – Semi-parametric method – no assumed trend model form
  – B-spline basis functions provide local control, local fit is insensitive to points far removed
  – Penalized form of B-spline regression is insensitive to number, placement of join-points (“knots”)

• Wide range of applications

Powell: P-Spline Regression
METHODS

• Generalized Additive Model for Poisson Regression

\[ \log(E[y_i]) = \log(\text{population}_i) + \beta_0 + f(\text{year}_i) + \varepsilon_i \]
  - Smooth \( f(\text{year}_i) = \sum B_k(\text{year}_i)\beta_k \)
    - \( B_k(x) = B\text{-spline basis function} \)
    - Year (nx1 vector) \( \rightarrow X \) (nxk matrix)
    - Fit the model with basis functions as covariates

• \( \log(E[y_{ij}]) = \log(\text{population}_{ij}) + \beta_0 + f_1(\text{year}_i) + f_2(\text{month}_j) + \varepsilon_{ij} \)
METHODS

- At any given point, \( q+1 \) B-splines are non-zero (local control)
  - \( q = \) B-spline degree (e.g., \( q=3 \) for cubic)
  - B-splines sum to 1
- Basis dimension \( (k) = q + n' \) (unconstrained)
  - \( n' = \) no. intervals along domain
  - e.g., 2 internal knots divides domain into \( n' = 3 \) intervals
- Eilers and Marx (1996) provides recursive algorithm for B-spline basis functions for uniformly spaced knots
- In practice, need to impose identifiability constraint \( \rightarrow k-1 \) orthogonal columns (QR decomposition)
- Smoothness controlled by penalty term, fit insensitive to basis dimension
METHODS

• P-IRLS to obtain GLM likelihood maximization, s.t. smooth
• Given $\lambda$, min: $\|\sqrt{W}(z - X\beta)\|^2 + \lambda \beta^T S \beta$
  - $\lambda =$ curvature penalty parameter
  - $w_i \propto [V(\mu_i)g'(\mu_i)^2]^{-1}$
  - $V[y_i] = \phi \mu_i$ (Generalized Poisson)
  - $z_i = g'(\mu_i)(y_i - \mu_i) + X_i \beta$
  - $X =$(constrained) design matrix
  - $g =$ link function (log)
  - $S$(penalty matrix) $= D^T D$
    • penalize differences among neighboring $\beta$ coefficients
  - For $D =$ second order difference matrix $\sim \int[f''(x)]^2 dx$
    • measure of total curvature

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METHODS

- Select degree of smoothness ($\lambda$) based on model selection criterion (GCV)
- Effective degrees of freedom (edf) = tr(A)
  - where $\hat{\mu} = Ay$
- With $\lambda = 0$, tr(A) = k-1
- As $\lambda \rightarrow \infty$, GAM $\rightarrow$ Log-Linear Model ($X \rightarrow 1 \text{ edf}$)
METHODS

• Uniform cubic B-spline basis with 2 internal knots
  – $k = q(3) + n'(3) = 6$ unconstrained basis functions
• S (penalty matrix): 2nd order difference matrix
• All Sites
  – Composition of FoodNet sites stable since 2004
• Original 5 Sites
  – Attempt to control for changes in FoodNet composition over time

Powell: P-Spline Regression
METHODS

B-Spline Provides Flexibility

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METHODS
Penalized B-Spline Avoids Overfitting

Data
Predicted
Upper conf limit
Lower conf limit
Slope = 0
x1
x2
x3
x4
x5
x6

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RESULTS

Salmonella All Serotypes All Sites

Incidence per 100,000 person-years

Powell: P-Spline Regression
RESULTS

Salmonella All Serotypes Original Sites

Incidence per 100,000 person-years

Powell: P-Spline Regression
RESULTS

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Limitations

• Serotype results are preliminary, work in progress
• Less smoothness is imposed at domain boundaries
• Reported illness is a proxy, not true incidence
• Not all FoodNet reported illness is foodborne
• Descriptive model, not infer causes
• Uncertainty about generalizing from FoodNet population to national level not quantified
Acknowledgements

• Data Provided by Foodborne Diseases Active Surveillance Network, CDC
  – Stacy Crim, CDC
  – Mike Hoekstra, CDC
  – Weidong Gu, CDC
  – Mike Williams, FSIS
Disclaimers

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