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

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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

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

- 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

- Generalized Additive Model for Poisson Regression
- $Log(E[y_i]) = log(population_i) + \beta_0 + f(year_i) + \varepsilon_i$
 - Smooth $f(year_i) = \sum B_k(year_i)\beta_k$
 - $B_k(x) = B$ -spline basis function
 - Year (nx1 vector) $\rightarrow \mathbf{X}$ (nxk matrix)
 - Fit the model with basis functions as covariates
- $Log(E[y_{ij}]) =$ $log(population_{ij})+\beta_0+f_1(year_i)+f_2(month_j)+\varepsilon_{ij}$

- 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 Bspline basis functions for uniformly spaced knots
- In practice, need to impose identifiability constraint → k-1 orthogonal columns (QR decomposition)
- Smoothness controlled by penalty term, fit insensitive to basis dimension

- P-IRLS to obtain GLM likelihood maximization, s.t. smooth
- Given λ , min: $\left\|\sqrt{W}(z X\beta)\right\|^2 + \lambda\beta^T S\beta$
 - λ = 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 β coefficients
 - For D = second order difference matrix ~ $\int [f''(x)]^2 dx$
 - measure of total curvature

- Select degree of smoothness (λ) 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 $\rightarrow 1$ edf)

- 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

METHODS B-Spline Provides Flexibility



METHODS Penalized B-Spline Avoids Overfitting





Powell: P-Spline Regression



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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

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