Spatial Survival Analysis via Copulas

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International Conference on Survival Analysis in Memory of John P. Klein Medical College of Wisconsin

June 2014





2 II: Frog extinction, point-referenced nonparametric survival

SCCCR data set on prostate cancer survival

- Large dataset on prostate cancer survival that does not follow proportional hazards.
- n = 20599 patients from South Carolina Central Cancer Registry (SCCCR) for the period 1996–2004; each recorded with county, race, marital status, grade of tumor, and SEER summary stage; 72.3% are censored.
- Need to allow for non-proportional hazards and accommodate correlation of survival times within county.
- Joint work with Li Li and Jiajia Zhang.

Model Analysis of SCCCR prostate cancer survival

Extended hazards model

• Etezadi-Amoli and Ciampi (1987) propose EH model

$$\lambda_{\mathbf{x}}(t) = \lambda_0(t e^{\mathbf{x}' \boldsymbol{\beta}}) e^{\mathbf{x}' \boldsymbol{\gamma}}.$$

• Say $\mathbf{x} = (x_1, x_2)$, then EH is

$$\lambda_{\mathbf{x}}(t) = \lambda_0(t e^{\beta_1 x_1 + \beta_2 x_2}) e^{\gamma_1 x_1 + \gamma_2 x_2}$$

- $\gamma_1 = \beta_1 \Rightarrow x_1$ has AFT interpretation; $\beta_1 = 0 \Rightarrow x_1$ has PH interpretation; $\gamma_1 = 0 \Rightarrow x_1$ has AH interpretation.
- Likelihood for observing $\{(t_i, \mathbf{x}_i, \delta_i)\}_{i=1}^n$

$$L(\beta,\gamma,\lambda_{0}(\cdot))=\prod_{i=1}^{n}\left\{e^{\gamma'\mathbf{x}_{i}}\lambda_{0}(e^{\beta'\mathbf{x}_{i}}t_{i})\right\}^{\delta_{i}}\exp\left\{-e^{\gamma'\mathbf{x}_{i}}\int_{0}^{t_{i}}\lambda_{0}(te^{\beta'\mathbf{x}_{i}})dt\right\}$$

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Baseline hazard $\lambda_0(t)$

Want to shrink λ₀(t) toward parametric target λ_θ(t):

$$\lambda_0(t) = \sum_{j=1}^J b_j B_{kj}(t)$$

where $B_{k1}(\cdot), \ldots, B_{k,J}(\cdot)$ are *k*th order B-spline basis function over knots (s_1, \ldots, s_{J+k}) .

- Let $\tilde{s}_j = \sum_{j=k+1}^{j+k} s_k/(k-1)$ and $b_j = \lambda_{\theta}(\tilde{s}_j)$.
- Schoenberg's approximation theorem (Marsden 1972) says max_{0≤t≤s_{J+1}} ||λ₀(t) − λ_θ(t)|| ≤ ε(λ_θ, k, J).

Posterior updating of model

- Step 1: Update the blocks {β, γ}, θ, c separately using adaptive Metropolis-Hastings algorithms (Haario, Saksman, and Tamminen 2005).
- Step 2: Sample g-prior parameters g_1^{-1} from Gamma $(a_g + 1, b_g + \beta' \mathbf{x}' \mathbf{x} \beta/2n + b_g)$ and g_2^{-1} from Gamma $(a_g + 1, b_g + \gamma' \mathbf{x}' \mathbf{x} \beta/2n + b_g)$.
- Step 3: Sample the latent random vectors u_i from

$$\mathbf{u}_i|\boldsymbol{\beta},\boldsymbol{\gamma},\mathbf{b},\boldsymbol{\theta},\mathbf{u}_{-i} \sim \mathsf{Mult}\left(\frac{b_1 B_1(\boldsymbol{e}^{\boldsymbol{\beta}'\mathbf{x}_i}t_i)}{\sum_{j=1}^n b_j B_j(\boldsymbol{e}^{\boldsymbol{\beta}'\mathbf{x}_i}t_i)},\ldots,\frac{b_J B_J(\boldsymbol{e}^{\boldsymbol{\beta}'\mathbf{x}_i}t_i)}{\sum_{j=1}^n b_j B_j^*(\boldsymbol{e}^{\boldsymbol{\beta}'\mathbf{x}_i}t_i)}\right)$$

• Step 4: B-spline coefficients are updated by

$$b_{j}|\boldsymbol{\beta},\boldsymbol{\gamma},\mathbf{b}_{-j},\boldsymbol{\theta},\{\mathbf{u}_{i}\}\sim\operatorname{Gamma}\left(\sum_{i\in\mathcal{S}}u_{ij}+c\lambda_{\boldsymbol{\theta}}(\tilde{s}_{j}),c+\sum_{i=1}^{n}e^{\boldsymbol{\gamma}'\mathbf{x}_{i}}\int_{0}^{t_{i}}B_{j}(te^{\boldsymbol{\beta}'\mathbf{x}_{i}})dt\right)$$

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Works great on simulated data



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Spatial dependence via frailties impractical

PH with frailties:

$$\lambda(t_i|\mathbf{x}) = \lambda_0(t_i) e^{\boldsymbol{\gamma}' \mathbf{x}_i + g_{c_i}},$$

where g_{ci} are county-level frailties, c_i is county subject *i* in.
EH with frailties:

$$\lambda(t_i|\mathbf{x}) = \lambda_0\{t_i e^{\beta' \mathbf{x}_i + b_{c_i}}\} e^{\gamma' \mathbf{x}_i + g_{c_i}},$$

where, for our data, b_1, \ldots, b_{46} and g_1, \ldots, g_{46} are county-level frailties.

• Possible but impractical, and hard to interpret.

Spatial dependence via copula works great

- Define $Y_i = \Phi^{-1} \{ 1 e^{\Lambda_i(T_i)} \}$ where $\Phi(\cdot)$ is the standard normal cumulative distribution function.
- Under Li and Lin (2006)

$$\mathbf{Y} \sim N(\mathbf{0}, \mathbf{\Gamma}).$$

• Likelihood ffrom data $\{(t_i, \mathbf{x}_i, \delta_i)\}_{i=1}^n$ is

$$\mathcal{L}_{s}(\beta, \gamma, \mathbf{b}, \boldsymbol{\theta}, \boldsymbol{\Gamma}) = \int \left[\prod_{i \in S} \frac{f_{i}(t_{i})}{\phi(y_{i})}\right] \left[\prod_{i \in S^{c}} \frac{f_{i}(z_{i})}{\phi(y_{i})} I(z_{i} > t_{i})\right] \phi(\mathbf{y}; \mathbf{0}, \boldsymbol{\Gamma}) \prod_{i \in S^{c}} dz_{i}$$

- How to define Γ?
- We consider county-level lattice data; popular correlation model is intrinsic conditional autoregressive (ICAR) prior.

ICAR definition

- $\alpha = (\alpha_1, \cdots, \alpha_m)$ is vector of correlated effects on a lattice.
- ICAR prior on α is $p(\alpha) \propto \exp\{-\varphi \alpha' (\mathbf{D} \mathbf{W}) \alpha/2\}$
- Implication of ICAR prior:

$$\alpha_j | \boldsymbol{\alpha}_{-j}, \varphi \sim N\left(\sum_{j=1}^n \omega_{ij} \alpha_j / \omega_{j+}, 1 / (\varphi \omega_{j+})\right).$$

- Random effects approach
 - $\tilde{\mathbf{Y}} = (\tilde{\mathbf{Y}}_1, \dots, \tilde{\mathbf{Y}}_m) = (\tilde{Y}_{11}, \dots, \tilde{Y}_{1n_1}, \dots, \tilde{Y}_{m1}, \dots, \tilde{Y}_{mn_m}).$
 - $\tilde{Y}_{ij} = \alpha_i + \epsilon_{ij}, \ \boldsymbol{\alpha} \sim N_m(\mathbf{0}, \boldsymbol{\Omega}), \ \boldsymbol{\epsilon} \sim N_n(\mathbf{0}, \mathbf{I}\sigma^2).$
 - Resulting correlation matrix **Γ** = corr(**Υ**) involves one unknown parameter φ^{*}.

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Posterior updating-latent survival approach

- MCMC sampling steps 1 to 3 are the same as before.
- Step 4: Propose b_i^{new} from

$$\operatorname{Gamma}\left(\sum_{i\in S^c} u_{ij} + c\lambda_{\theta}(\tilde{s}_j), c + \sum_{i=1}^n e^{\gamma' \mathbf{x}_i} \int_0^{t_i} B_j(te^{\beta' \mathbf{x}_i}) dt\right)$$

and accept it with probability

$$\min\left\{1, \frac{\prod_{i=1}^{n} \phi(\mathbf{y}_i) e^{-\mathbf{y}^{new}' \Gamma^{-1} \mathbf{y}^{new}/2}}{\prod_{i=1}^{n} \phi(\mathbf{y}_i^{new}) e^{-\mathbf{y}' \Gamma^{-1} \mathbf{y}/2}}\right\}$$

where \mathbf{y}^{new} is new transformed failure time vector corresponding to b_i^{new} .

- Step 5: Sample $Y_i \sim N(y_i | \mathbf{y}_{-i}, \mathbf{\Gamma}) I(y_i > \Phi^{-1} \{ F_i(t_i) \}$ then set $z_i = F_i^{-1} \{ \Phi(y_i) \}$.
- Step 6: Update φ^* using adaptive Metropolis-Hastings.

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Efficient evaluation of $\mathbf{y}' \mathbf{\Gamma}^{-1} \mathbf{y}$

- Γ is a $n \times n$ matrix
- Elements of Γ^{-1} can be easily computed using SVD, $\Gamma^{-1} = \mathbf{A}^{-1}\mathbf{U}_1 \left((\mathbf{K}^* + \sigma^2 \mathbf{I}_m)^{-1} - \sigma^{-2} \mathbf{I}_m \right) \mathbf{U}'_1 \mathbf{A}^{-1} + \sigma^{-2} \mathbf{A}^{-2}$ where **A** is a diagonal matrix, $\mathbf{U}_1 = (\mathbf{u}_1, \dots, \mathbf{u}_m)$, \mathbf{u}_i is a vector of length *n* with ones corresponding to county *i* and zero elsewhere.

•
$$\mathbf{y}' \mathbf{\Gamma}^{-1} \mathbf{y} = \mathbf{x}' \left((\mathbf{K}^* + \sigma^2 \mathbf{I}_m)^{-1} - \sigma^{-2} \mathbf{I}_m \right) \mathbf{x} + \sigma^{-2} \mathbf{y}' \mathbf{A}^{-2} \mathbf{y}$$

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Savage-Dickey ratio for global and per-variable tests

• Example of global test of PH vs. EH

$$BF_{12} = rac{\pi(eta = \mathbf{0} | \mathcal{D}, EH)}{\pi(eta = \mathbf{0} | EH)}$$

• Example of per-variable of PH for x_j vs. EH

$$BF_{12} = \frac{\pi(\beta_j = 0 | \mathcal{D}, EH)}{\pi(\beta_j = 0 | EH)}.$$

SCCCR data

- SCCCR prostate cancer data for the period 1996–2004.
- Baseline covariates are county of residence, age, race, marital status, grade of tumor differentiation, and SEER summary stage.
- *n* = 20599 patients in the dataset after excluding subjects with missing information.
- 72.3% of the survival times are right-censored.

Goal: assess racial disparity in prostate cancer survival, adjusting for the remaining risk factors and accounting for the county the subject lives in.

SCCCR data

Table: Summary characteristics of prostate cancer patients in SC from 1996-2004.

Covariate		п	Sample percentage
Race	Black	6483	0.32
	White	14116	0.68
Marital status	Non-married	4525	0.22
	Married	16074	0.78
Grade well or moderately differentiated		15309	0.74
	poorly differentiated or undifferentiated	5290	0.26
SEER summary stage	Localized or regional	19792	0.96
, -	Distant	807	0.04

Model Analysis of SCCCR prostate cancer survival

Non-spatial EH and reduced models

Table: Summary of fitting the extended hazard model EH, the reduced model, AFT, and PH; * indicates *LPML* – 21000 and *DIC* – 42000.

Covar		EH	Reduced	AFT	PH	PH+additive age
				$oldsymbol{eta}=oldsymbol{\gamma}$	$oldsymbol{eta}=0$	$oldsymbol{eta}={\sf 0}$
Age	β_1	0.50(0.48,0.52)	0.48(0.46,0.50)	0.48(0.45,0.51)	-	
	γ_1	0.45(0.42,0.49)	$\gamma_1 = \beta_1$	-	0.65(0.62,0.68)	-
Race	β_2	0.18(0.15,0.21)	0.20(0.16,0.21)	0.18(0.15,0.22)	-	-
	γ_2	0.18(0.12,0.24)	$\gamma_2 = \beta_2$	-	0.26(0.21,0.32)	0.26(0.20,0.31)
Marital	β_3	-0.06(-0.11,-0.02)	-0.05(-0.09,-0.00)	0.26(0.21,0.30)	-	-
status	γ_3	0.35(0.29,0.40)	0.33(0.28,0.40)	-	0.33(0.27,0.39)	0.31(0.26,0.37)
Grade	β_4	0.03(-0.02,0.08)	$\beta_4 = 0$	0.27(0.22,0.32)	-	-
	γ_4	0.36(0.29,0.41)	0.37(0.31,0.43)	-	0.38(0.32,0.44)	0.37(0.33,0.43)
SEER	β_5	3.19(2.80,3.53)	3.27(2.79,3.57)	1.50(1.41,1.59)	-	-
stage	γ_5	1.02(0.83,1.20)	1.00(0.82,1.19)	-	1.56(1.47,1.64)	1.57(1.19,1.65)
LPML*		-161.0	-162.0	-206.5	-242.5	-231.9
DIC*		267.7	270.7	366.0	443.0	412.8

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Non-spatial EH and reduced models

Table: Bayes factors for comparing EH to PH, AFT, and AH with and without spatial correlation.

-		EH			Spatial+EH	
Covariate	PH	AFT	AH	PH	AFT	AH
Age	> 1000	0.08	> 1000	> 1000	0.01	> 1000
Race	> 1000	0.01	> 1000	> 1000	< 0.01	> 1000
Marital status	1.79	> 1000	> 1000	1.18	> 1000	> 1000
Grade	0.14	> 1000	> 1000	0.08	> 1000	> 1000
SEER stage	> 1000	> 1000	> 1000	> 1000	> 1000	> 1000

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Spatial EH and reduced models

Table: Summary of spatial models; * indicates LPML - 21000 and DIC - 42000.

Covariates		Marginal EH	Marginal reduced	PH+ICAR+additive age
		-	-	$\beta = 0$
				p = 0
Age	β_1	0.50(0.47,0.52)	0.47(0.46,0.49)	-
	γ_1	0.46(0.43,0.49)	$\gamma_1 = \beta_1$	-
Race	β_2	0.18(0.15,0.21)	0.20(0.17,0.22)	-
	γ_2	0.17(0.11,0.23)	$\gamma_2 = \beta_2$	0.24(0.18,0.30)
Marital status	β_3	-0.06(-0.10,-0.02)	-0.02(-0.05,-0.00)	-
	γ_3	0.34(0.28,0.41)	0.33(0.27,0.39)	0.32(0.25,0.38)
Grade	β_4	0.03(-0.01,0.07)	$\beta_4 = 0$	-
	γ_4	0.36(0.30,0.42)	0.38(0.32,0.43)	0.37(0.32,0.44)
SEER stage	β_5	3.16(2.86,3.34)	2.77(2.72,2.82)	-
	γ_5	1.10(0.94,1.26)	1.21(1.01,1.33)	1.55(1.46,1.64)
$arphi^*$		50.1(19.9,113.7)	54.6(22.7,120.8)	33.08(9.2,100.1)
LPML*		-142.7	-143.2	-215.7
DIC*		192.4	164.0	332.5

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Spatial EH and reduced models



Figure: Map of (a) Mortality rate, (b) ICAR frailties in the PH model and (c) random effects in the marginal reduced model for SC counties.

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Spatial EH and reduced models



Figure: Baseline hazard (left) and survival probabilities (right) estimates.

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Spatial EH and reduced models



Figure: Hazard and survival for black patients (solid line) and white patients; baseline covariates.

Model Analysis of SCCCR prostate cancer survival

Interpretation for race effect

- Based on the fitted results of the reduced models with and without spatial dependence, white South Carolina subjects diagnosed with prostrate cancer in live 22% longer ($e^{0.20} \approx 1.22$) than black patients (95% CI is 18% to 25%), fixing age, stage, and SEER stage.
- Cox said "...the physical or substantive basis for...proportional hazards models...is one of its weaknesses..." and goes on to suggest that "...accelerated failure time models are in many ways more appealing because of their quite direct physical interpretation."
- The SCCCR analysis showed that the main covariate of interest, race, is best modeled as an AFT effect.
- Survival probabilities for black patients are significantly lower than those for white patients when other factors are fixed at the same levels.

More interpretation

- Decreasing age by one year increases survival time by 5.4%.
- Hazard of dying increases 46% for poorly or undifferentiated grades vs. well or moderately differentiated, holding age, race, and SEER stage constant.
- SEER stage has general EH effects, $e^{2.77} \approx 16$ (AH) and $e^{1.21} \approx 3.4$ (PH). Those with distant stage are at least three times worse in one-sixteenth of the time as those with localized or regional.
- Marital status essentially has PH interpretation; single (including widowed or separated) subjects are $e^{0.33} \approx 1.39$ times more likely to die at any instant than married.

About this work

- Joint work with Haiming Zhou and Roland Knapp (Sierra Nevada Aquatic Research Laboratory).
- Frogs and other amphibians have been dying off in large numbers since the 1980s because of a deadly fungus called Batrachochytrium dendrobatidis, also known as Bd.
- Dr. Knapp has been studying the amphibian declines for the past decade at Sierra Nevada Aquatic Research Laboratory; he has hiked thousands of miles and surveyed hundreds of frog populations in Sequoia-Kings Canyon National Park collecting the data by hand.
- Again, proportional hazards is grossly violated for these data.

Model Analysis of frog population extinction

The Frog Data (2000-2011)

- Contains 309 frog populations. Each was followed up until infection or being censored (10% censoring).
- The response is the Bd infection time (i.e. Bd arrival year – baseline year).
- Main covariates:

bdwater: whether or not Bd has been found in the watershed. bddistance: straight-line distance to the nearest Bd location.

• Populations near each other tend to become infected at about the same time.



Objectives

- $T_i = T(\mathbf{s}_i)$ is time to local extinction for pop'n located at \mathbf{s}_i .
- $\mathbf{x}_i = \mathbf{x}(\mathbf{s}_i)$: a $p \times 1$ vector of covariates.
- Goal 1: describe the association between **x**(*s*) and *T*(*s*) while allowing for spatial dependence.
- Goal 2: predict $T(s_0)$ given $\mathbf{x}(s_0)$ at any new location s_0 .

Model Analysis of frog population extinction

LDDPM model and Spatial Extension

LDDPM (De lorio et al., 2009; Jara et al., 2010): Y_i = log T_i given x_i independently follow mixture model

$$F_{\mathbf{x}_i}(y|G) = \int \Phi\left(rac{y - \mathbf{x}_i'eta}{\sigma}
ight) dG\{eta, \sigma^2\},$$

where *G* follows a Dirichlet Process (DP) prior, i.e. $G \sim DP(\alpha, G_0)$.

• Model the joint distribution of $\mathbf{Y} = (Y_1, \dots, Y_n)'$ by

$$F(t_1,\ldots,t_n|G)=C(F_{\mathbf{x}_1}(t_1|G),\ldots,F_{\mathbf{x}_n}(t_n|G);\theta),$$

where $C(u_1, \ldots, u_n; \theta)$ is a spatial copula with parameter θ , which is used for capturing spatial dependence.

• We use point-referenced Gaussian copula of Li and Lin (2006).

Model Analysis of frog population extinction

Specification of $F_{\mathbf{x}_i}(y|G)$

• Assume $Y_i = \log T_i$ given \mathbf{x}_i follows a mixture model

$$F_{\mathbf{x}_{i}}(\mathbf{y}|\mathbf{G}) = \int \Phi\left(\frac{\mathbf{y} - \mathbf{x}_{i}^{\prime}\boldsymbol{\beta}}{\sigma}\right) d\mathbf{G}\{\boldsymbol{\beta}, \sigma^{2}\},$$

where $G \sim DP(\alpha, G_0)$ with concentration parameter α .

• G in truncated stick-breaking form (Sethuraman, 1994) as

$$G = \sum_{k=1}^{N} w_k \delta_{(\beta_k, \sigma_k^2)}, \quad w_k = V_k \prod_{j < k} (1 - V_j),$$

where $V_k | \alpha \stackrel{iid}{\sim} \text{Beta}(1, \alpha)$, $(\beta_k, \sigma_k^2) \stackrel{iid}{\sim} G_0$.

The Likelihood

- Observed data $\{(y_i^o, \delta_i, \mathbf{x}_i, \mathbf{s}_i) : i = 1, \dots, n\}.$
- Denote by y_i the latent true log event-time corresponding to y_i^o.
- Then $\delta_i = I(y_i = y_i^o)$, where $\delta_i = 0$ implies $y_i > y_i^o$.
- The augmented likelihood for parameters {y₁,..., y_n, G, θ} is

$$\begin{split} \mathcal{L} &= \prod_{i=1}^{n} f_{\mathbf{x}_{i}}(y_{i}|G) \Big\{ \delta_{i} I(y_{i} = y_{i}^{o}) + (1 - \delta_{i}) I(y_{i} > y_{i}^{o}) \Big\} \\ &\times |\boldsymbol{C}|^{-1/2} \exp \left\{ -\frac{1}{2} \mathbf{z}' (\boldsymbol{C}^{-1} - \mathbf{I}_{n}) \mathbf{z} \right\} \end{split}$$

where $f_{\mathbf{x}_i}(y_i|G)$ is the density w.r.t. $F_{\mathbf{x}_i}(y_i|G)$,

and
$$\mathbf{z} = (z_1, ..., z_n)'$$
 with $z_i = \Phi^{-1} \{ F_{\mathbf{x}_i}(y_i | G) \}$.

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MCMC Overview

- All parameters involved in *G* are updated based on a modification of the blocked Gibbs sampler (Ishwaran and James, 2001): M-H samplers with independent proposals.
- The latent y_i s are updated via independent M-H sampler.
- Delayed rejection (Tierney and Mira, 1999) used for several parameters; helps sampler not get "stuck."
- The correlation parameters θ are updated using adaptive M-H (Haario et al., 2001).
- For large n, the inversion of the n × n matrix C substantially sped up using a full scale approximation (FSA) (Sang and Huang, 2012).

Simulated Data

- Assume the log *T* given *x* follows a mixture of normals $f(y|x) = 0.4N(3.5 + 0.5x, 1^2) + 0.6N(2.5 x, 0.5^2).$
- Specify covariance matrix **C** with $\theta_1 = 0.98$ and $\theta_2 = 0.1$.
- Around 10% of survival times are right-censored.



Model Analysis of frog population extinction

Simulated Data: Inference on Spatial Correlation

Table: Posterior summary statistics for the spatial correlation parameters

Par.	True	Mean	Median	Std. dev.	95% HPD Interval
θ_1	0.98	0.968	0.971	0.019	(0.933, 1.000)
θ_2	0.10	0.095	0.093	0.021	(0.056, 0.138)

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Simulated Data: Estimated Density



Figure: Estimated density of log(*T*) when x = 1 (left) and x = -1 (right). Recall: $f(y|x) = 0.4N(3.5 + 0.5x, 1^2) + 0.6N(2.5 - x, 0.5^2)$.

Model Analysis of frog population extinction

Simulated Data: Prediction

Table: The mean squared prediction error (MSPE) for the held-out 30 locations under two different methods

Method	MSPE
De lorio	1.325
Ours	0.269

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Frog Data: Inference on Spatial Correlation

- FYI: the spatial Gaussian copula involves the $n \times n$ correlation matrix $C(\mathbf{s}_i, \mathbf{s}_j; \theta) = \theta_1 \rho(\mathbf{s}_i, \mathbf{s}_j) + (1 \theta_1) I(\mathbf{s}_i = \mathbf{s}_j)$, where $\theta_1 \in [0, 1]$ and $\rho(\mathbf{s}_i, \mathbf{s}_j) = \exp \{-\theta_2 ||\mathbf{s}_i \mathbf{s}_j||\}$.
- Posterior mean $\hat{\theta}_1 = 0.9937$.
- Posterior mean θ̂₂ = 0.0866, indicating the correlation decays by 1 exp(-0.0866 × 1) = 8% for every 1-km increase in distance and 1 exp(-0.0866 × 10) = 58% for every 10-km increase in distance.

Par.	Mean	Median	Std. dev.	95% HPD Interval
θ_1	0.9937	0.9941	0.0029	(0.9879, 0.9988)
θ_2	0.0866	0.0841	0.0211	(0.0493, 0.1297)

Table: Posterior summary statistics for the spatial correlation parameters

Model Analysis of frog population extinction

Frog Data: Estimated Hazard



Figure: Estimated hazard function with 90% point-wise CI for *bdwater* = 1 vs *bdwater* = 0 when the bddistance is fixed at its population mean.

Model Analysis of frog population extinction

Frog Data: Spatial Prediction

Spatial map for the transformed process $z(\mathbf{s}) = \Phi^{-1} \{ F_{\mathbf{x}(\mathbf{s})}(\log T(\mathbf{s}) | G) \}.$



Figure: Predictive spatial map based on new 2000 random locations in \mathcal{D} .

Remarks

- Proposed Bayesian spatial copula approaches to estimate survival curves semiparametrically (EH model) and nonparametrically (LDDPM) while allowing for spatial dependence, leading to high predictive accuracy.
- Adopted the FSA approach to compute the inversion of *n*-dimensional spatial covariance matrices for georeferenced data.
- Future research involves use of low-rank approaches to modeling data with lots of spatial locations, e.g. random projections (Banerjee et al., 2012) or predictive processes (Banerjee et al., 2008). Two different Banerjees!
- Extension to simpler semiparametric models such as proportional odds.
- Thanks to my colleagues Li Li, Haiming Zhou, Roland Knapp, and Jiajia Zhang. Thanks for the invitation!