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**Modelling Killer Whale Feeding Behaviour Using a Spatially Adaptive Complex Region Spatial Smoother (CReSS) and Generalised Estimating Equations (GEEs)**

P. 305-322

Lindesay A. S. Scott-Hayward...

**Abstract**

To develop appropriate spatial conservation planning for individual species, it is important to understand their habitat requirements and in particular to identify areas where critical life-history process such as breeding, weaning or feeding take place. The process of defining critical habitat often ignores behavioural aspects of animal distribution, which for highly migratory species like baleen whales whose feeding and breeding grounds are clearly demarcated and widely separated is not a problem. However, for other species like the endangered 'Eastern North Pacific southern resident' killer whale stock, critical life-history processes occur in the same waters. This killer whale stock lives in a topographically complex region (many islands) off the west coast of Canada/USA, which makes accurate mapping of densities or behaviours difficult using traditional generalised additive models. We present results on the spatial distribution of southern resident killer whale feeding grounds in 2006, using a binomial, complex region spatial smoothing model within a generalised estimating equation framework, which allows for both complex topography and correlated residuals. The model performs well and suggests a region to the south of San Juan Island as an area with a high probability of feeding, which could not have been as accurately established from a more traditional presence-absence model. We also calculate estimates of precision, which other studies did not include, enabling more informed management decisions for spatial conservation planning. A vignette containing the code along with an R workspace and function file is provided to allow the user to fit the models presented in this paper.

Supplementary materials accompanying this paper appear on-line.

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**Stochastic Modeling for Velocity of Climate Change**

P. 323-342

Erin M. Schliep, Alan E. Gelfand...

**Abstract**

The velocity of climate change is defined as an instantaneous rate of change needed to maintain a constant climate. It is developed as the ratio of the temporal gradient of climate change over the spatial gradient of climate change. Ecologically, understanding these rates of climate change is critical since the range limits of plants and animals are changing in response to climate change. Additionally, species respond differently to changes in climate due to varying tolerances and adaptability. A fully stochastic hierarchical model is proposed that incorporates the inherent relationship between climate, time, and space. Space-time processes are employed to capture the spatial correlation in both the climate variable and the rate of change in climate over time. Directional derivative processes yield spatial and temporal gradients and, thus, the resulting velocities for a climate variable. The gradients and velocities can be obtained at any location in any direction and any time. In fact, maximum gradients and their directions can be obtained, hence minimum velocities. Explicit parametric forms for the directional derivative processes provide full inference on the gradients and velocities including estimates of uncertainty. The model is applied to annual average temperature across the eastern United States for the years 1963– 2012. Maps of the spatial and temporal gradients are produced as well as velocities of temperature change.

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**Individual Heterogeneity in Growth and Age at Sexual Maturity: A Gamma Process Analysis of Capture–Mark–Recapture Data**

P. 343-352

William A. Link, Kyle Miller Hesed

**Abstract**

Knowledge of organisms' growth rates and ages at sexual maturity is important for conservation efforts and a wide variety of studies in ecology and evolutionary biology. However, these life history parameters may be difficult to obtain from natural populations: individuals encountered may be of unknown age, information on age at sexual maturity may be uncertain and interval-censored, and growth data may include both individual heterogeneity and measurement errors. We analyzed mark–recapture data for Red-backed Salamanders (*Plethodon cinereus*) to compare sex-specific growth rates and ages at sexual maturity. Aging of individuals was made possible by the use of a von Bertalanffy model of growth, complemented with models for interval-censored and imperfect observations at sexual maturation. Individual heterogeneity in growth was modeled through the use of Gamma processes. Our analysis indicates that female *P. cinereus* mature earlier and grow more quickly than males, growing to nearly identical asymptotic size distributions as males.

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**Marginal Functional Regression Models for Analyzing the Feeding Behavior of Pigs**

P. 353-370

Jan Gertheiss, Verena Maier, Engel F. Hessel...

**Abstract**

We observe a group of pigs over a period of about 100 days. Using high frequency radio frequency identification, it is recorded when each pig is feeding, leading to very dense binary functional data for each pig and day. One aim of the data analysis is to find pig-specific feeding profiles showing us the typical feeding pattern of each pig. For modeling the data, we use a marginal functional logistic regression approach, allowing us to model the densely observed binary measurements by assuming an underlying smooth subject-specific profile. The method also allows to incorporate additional covariates such as temperature and humidity that may influence the pigs' behavior. To account for correlation of measurements, we use robust standard errors and corresponding pointwise confidence intervals. Before analyzing the feeding behavior of pigs, the method employed is evaluated in simulation studies. As our approach is rather general, it may also be applied to other types of generalized functional data with similar characteristics as the pig data.

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**Efficient Estimation of Elliptical Hysteresis with Application to the Characterization of Heat Stress**

P. 371-388

F. Yang, A. M. Parkhurst

**Abstract**

When biological systems undergo hysteretic behavior of stress and recovery due to global warming or other changes in environment and resources, modeling hysteresis becomes increasingly important. A system displays hysteresis if the output depends on past history of changes in the input. Moreover, the trajectory of rate-dependent hysteresis may be viewed as a loop when the period is known. Consider the thermoregulatory response of an animal, hysteresis appears as the delay in body temperature when an animal experiences heat stress produced by elevated air temperature. If air temperature is controlled as a sinusoidal, the hysteresis loop shows an elliptical pattern. The parameters of such loops are useful for describing rhythmic biological processes. Three analytic methods, linear, nonlinear, and two-step harmonic, are developed to fit an elliptical hysteretic process. Formulas for parameters that characterize the dynamics are obtained. Statistical efficiency of parameter estimation is evaluated by simulations using both the delta method and bootstrap. Overall, two-step simple harmonic regression with bootstrap produces the most efficient estimates for parameters of the elliptical hysteresis loop. Application of this procedure to control-chamber data reveals differences between animals in response to heat stress.

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Sandra Jane Clarke, Stuart Andrew Jones

**Abstract**

Diagnostic testing is used by biosecurity officers for the detection and identification of plant and animal pathogens, often informing high-consequence decisions such as restricting the entry of trade goods. It is rare that such tests can be considered gold standards; however, uncertainty can be reduced by using the results of other tests, measuring performance on samples of known status and incorporating prior knowledge from expert judgement. This article presents an extension to the methods of Joseph et al. (Am J Epidemiol 141:263–272, 1995), and Dendukuri and Joseph (Biometrics 57:158–167, 2001) for Bayesian estimation in the absence of a gold standard test, which allows for the use of incomplete test data. This extension is demonstrated with a novel application: the case study of myrtle rust from Holliday et al. (Plant Dis 97:828–834, 2013), which involves samples from potential biosecurity risk material on importation pathways to Australia. The samples were tested at two laboratories, and prior estimates for pathway prevalence were obtained by expert elicitation. The Bayesian estimation was based on a model with and without covariances for the test results to assess the assumption of conditional independence. The results show that pathogen prevalence, diagnostic sensitivity and diagnostic specificity can be estimated using all available data even where some samples have been subject to only one of two available tests. The results also indicate the importance of consideration of the assumption of conditional independence. The findings enable diagnostic testing laboratories and decision makers to make use of all test results and to explicitly incorporate prior knowledge to estimate pathogen prevalence and test accuracy.

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Fumiaki Kobayashi, Manabu Kuroki

**Abstract**

In randomized clinical trials, true clinical endpoints that are rare or difficult to measure can be costly and time consuming. Therefore, there is an increasing need to substitute true clinical endpoints with surrogate endpoints. However, candidate surrogate endpoints require appropriate validation. To evaluate the extent of a treatment effect (TE) captured by candidate surrogate endpoints, various surrogacy measures have been proposed by biostatisticians and medical professionals. Although many researchers stated that it is desirable that surrogacy measures should take values between zero to one, those often fall outside a range  $[0, 1]$  without suitable assumptions. To overcome this problem, we propose two types of surrogacy measures based on the causal association (CA) paradigm and the causal effect (CE) paradigm. These operate by decomposing the TE into those parts that are and are not captured by candidate surrogate endpoints. The surrogacy measures based on the CA paradigm mainly consider how much of the TE of the treatment on the true clinical endpoint can be predicted through the TE on the candidate surrogate endpoints, while the surrogacy measures based on the CE paradigm are concerned with how much of the TE on the true clinical endpoint is a result of the candidate surrogate endpoints. In addition, we demonstrate some properties of the proposed surrogacy measures, and show that they always fall inside the range  $[0, 1]$ . Furthermore, they can be considered as improved and extended versions of existing surrogacy measures. Based on simulation experiments and applications of the proposed surrogacy measures to a case study of the Olmesartan Reducing Incidence of End-stage Renal Disease in Diabetic Nephropathy Trial, we show that the proposed surrogacy measures solve the problems encountered by the existing surrogacy measures. This paper presents new quantitative surrogacy measures that reliably evaluate the proportion of the TE captured by candidate surrogate endpoints. Supplementary materials accompanying this paper appear online.

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