Case-study: Rongelap Island

This case-study illustrates a model-based geostatistical analysis combining:

- a Poisson log-linear model for the sampling distribution of the observations, conditional on a latent
  Gaussian process which represents spatial variation
  in the level of contamination

- Bayesian prediction of non-linear functionals of the latent process

- MCMC implementation

Details are in Diggle, Moyeed and Tawn (1998).

Radiological survey of Rongelap Island

- **Rongelap Island**
  - approximately 2500 miles south-west of Hawaii
  - contaminated by nuclear weapons testing during 1950's
  - evacuated in 1985
  - now safe for re-settlement?
- **The statistical problem**
  - field-survey of ^{137}Cs measurements
  - estimate spatial variation in ^{137}Cs radioactivity
  - compare with agreed safe limits

Poisson Model for Rongelap Data

- Basic measurements are nett counts Y_i over time-intervals t_i at locations x_i $(i = 1, ..., n)$

- Suggests following model:

  · $S(x) : x \in R^2$ stationary Gaussian process (local radioactivity)

  · $Y_i | \{S(\cdot)\} \sim$ Poisson(μ_i)

  · $\mu_i = t_i \lambda(x_i) = t_i \exp\{S(x_i)\}$.

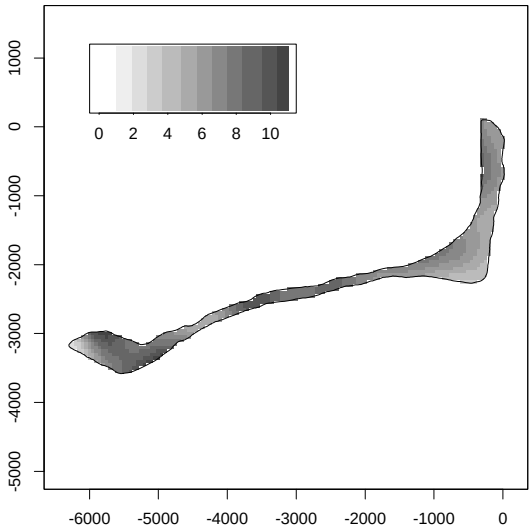
- Aims:

  · predict $\lambda(x)$ over whole island

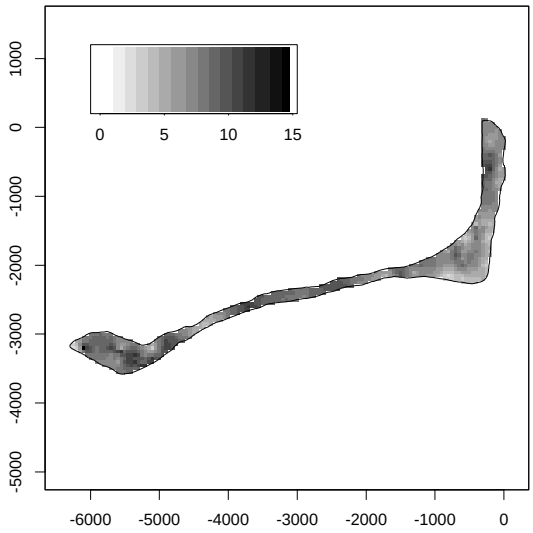
  · max $\lambda(x)$

  · arg(max $\lambda(x)$)

Predicted radioactivity surface using log-Gaussian kriging



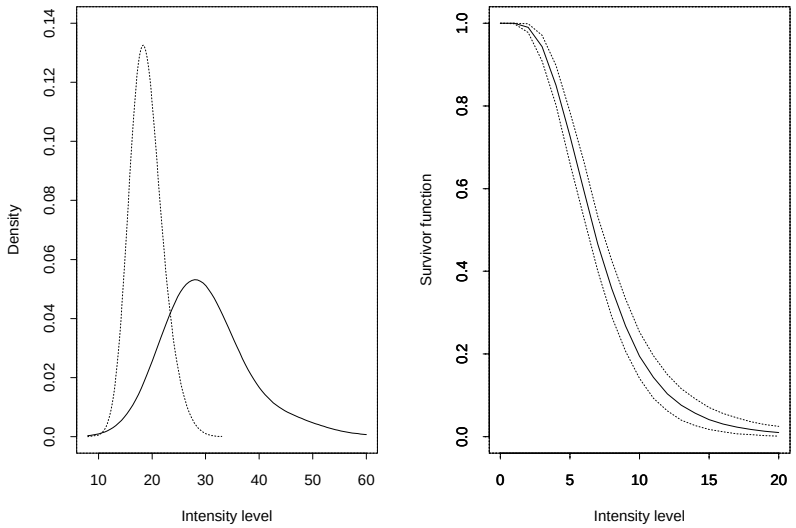
Predicted radioactivity surface using Poisson log-linear model with latent Gaussian process



- The two maps above show the difference between:
  - log-Gaussian kriging of observed counts per unit time
  - log-linear analysis of observed counts
- the principal visual difference is in the extent of spatial smoothing of the data, which in turn stems from the different treatments of the nugget variance

Bayesian prediction of non-linear functionals of the radioactivity surface

The left-hand panel shows the predictive distribution of maximum radioactivity, contrasting the effects of allowing for (solid line) or ignoring (dotted line) parameter uncertainty; the right-hand panel shows 95% pointwise credible intervals for the proportion of the island over which radioactivity exceeds a given threshold.



- The two panels of the above diagram illustrate Bayesian prediction of non-linear functionals of the latent
  Gaussian process in the Poisson log-linear model

- the left-hand panel contrasts posterior distributions of the maximum radioactivity based on:
  (i) the fully Bayesian analysis incorporating the effects of parameter uncertainty in addition to uncertainty in the latent process (solid line)
  (ii) fixing the model parameters at their estimated values, ie allowing for uncertainty only in the latent process

- the right-hand panel gives posterior estimates with 95% point-wise credible intervals for the proportion of the island over which radioactivity exceeds a given threshold (dotted line).

Case-study: Gambia malaria

- In this example, the spatial variation is of secondary scientific importance.
- The primary scientific interest is to describe how the prevalence of malarial parasites depends on explanatory variables measured:
  - on villages
  - on individual children
- There is a particular scientific interest in whether a vegetation index derived from satellite data is a useful predictor of malaria prevalence, as this would help health workers to decide how to make best use of scarce resources.

Data-structure

- 2039 children in 65 villages
- test each child for presence/absence of malaria parasites

Covariate information at child level:

- age (days)
- sex (F/M)
- use of mosquito net (none, untreated, treated)

Covariate information at village level:

- location
- vegetation index, from satellite data
- presence/absence of public health centre

Logistic regression model

Logistic model for presence/absence in each child:

- $Y_{ij} = 0/1$ for absence/presence of malaria parasites in jth child in ith village
- $f_{ij} =$ child-specific covariates
- $w_i =$ village-specific covariate
- $\text{logit}P(Y_{ij} = 1|S(\cdot)) = f_{ij}'\beta_1 + w_i'\beta_2 + S(x_i)$

Is it reasonable to assume conditionally independent infections within same village?

If not, we might wish to extend the model to allow for non-spatial extra-binomial variation:

- $U_i \sim \text{N}(0, \nu^2)$
- $\text{logit}P(Y_{ij} = 1|S(\cdot), U) = f_{ij}'\beta_1 + w_i'\beta_2 + U_i + S(x_i)$

Exploratory analysis

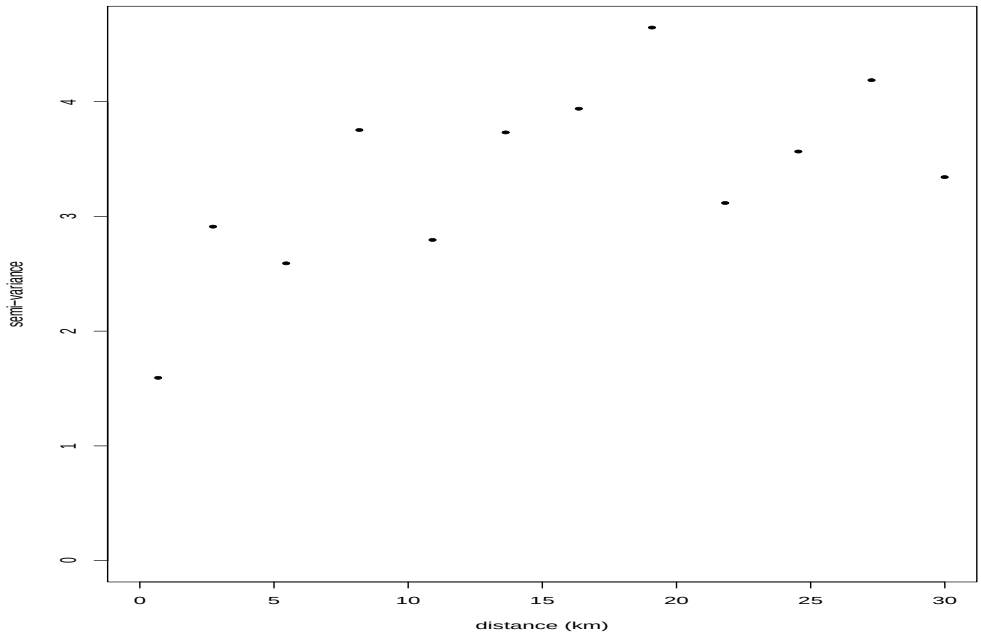
- fit standard logistic linear model, ignoring $S(x)$ and/or U
- compute for each village:

  $N_i = \sum_{j=1}^{n_i} Y_{ij}$

  $\mu_i = \sum_{j=1}^{n_i} \hat{P}_{ij}$

  $\sigma_i^2 = \sum_{j=1}^{n_i} \hat{P}_{ij}(1 - \hat{P}_{ij})$
- compute village-residuals, $r_i = (N_i - \mu_i)/\sigma_i$
- apply conventional geostatistics to derived data r_i
- variogram indicates residual spatial structure

Variogram of residuals



Model-based geostatistical analysis

α = intercept term in linear predictor

β_1 = regression coefficient for age

β_2 = regression coefficient for bed-net use

β_3 = regression coefficient for treated bed-net

β_4 = regression coefficient for green-ness index

β_5 = regression coefficient for presence of public health centre in village

ν^2 = variance of non-spatial random effects U_i

σ^2 = variance of spatial process $S(x)$

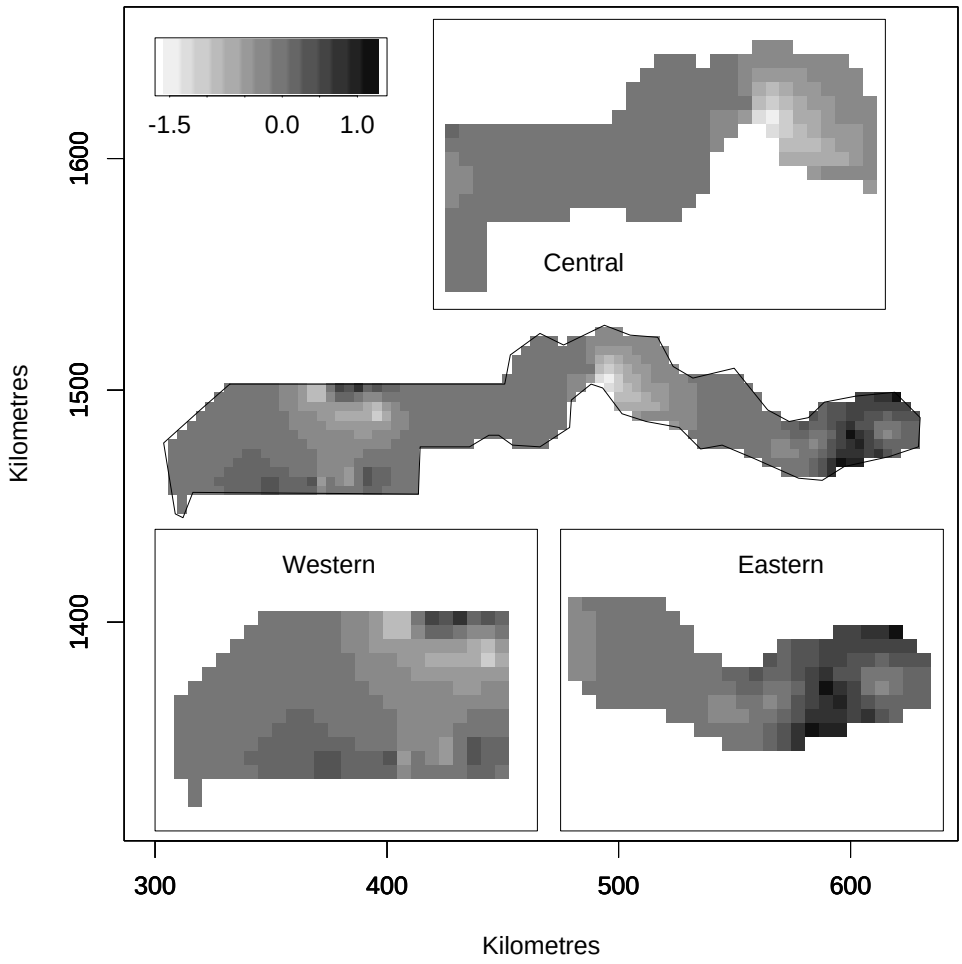
ϕ = rate of decay of spatial correlation with distance

κ = shape parameter for Matérn correlation function

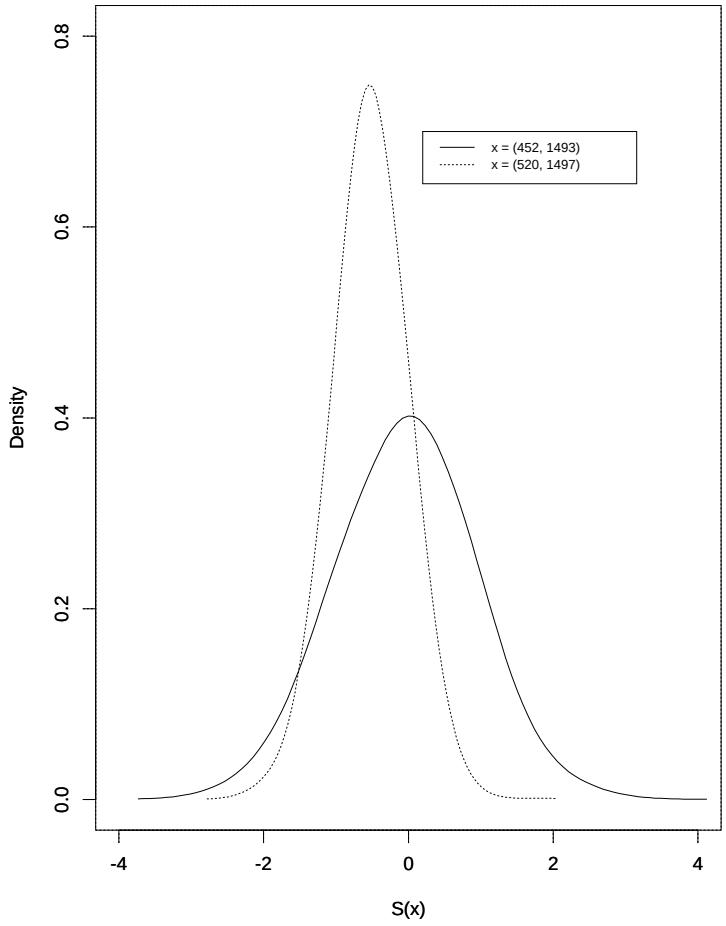
Param.	2.5% Qt.	97.5% Qt.	Mean	Median
α	-4.232073	1.114734	-1.664353	-1.696228
β_1	0.000442	0.000918	0.000677	0.000676
β_2	-0.684407	-0.083811	-0.383750	-0.385772
β_3	-0.778149	0.054543	-0.355655	-0.355632
β_4	-0.039706	0.071505	0.018833	0.020079
β_5	-0.791741	0.180737	-0.324738	-0.322760
ν^2	0.000002	0.515847	0.117876	0.018630
σ^2	0.240826	1.662284	0.793031	0.740790
ϕ	1.242164	53.351207	11.653717	7.032258
κ	0.150735	1.955524	0.935064	0.830548

- note concentration of posterior for ν^2 close to zero

Map of the predicted surface $\hat{S}(x)$ (posterior mean)

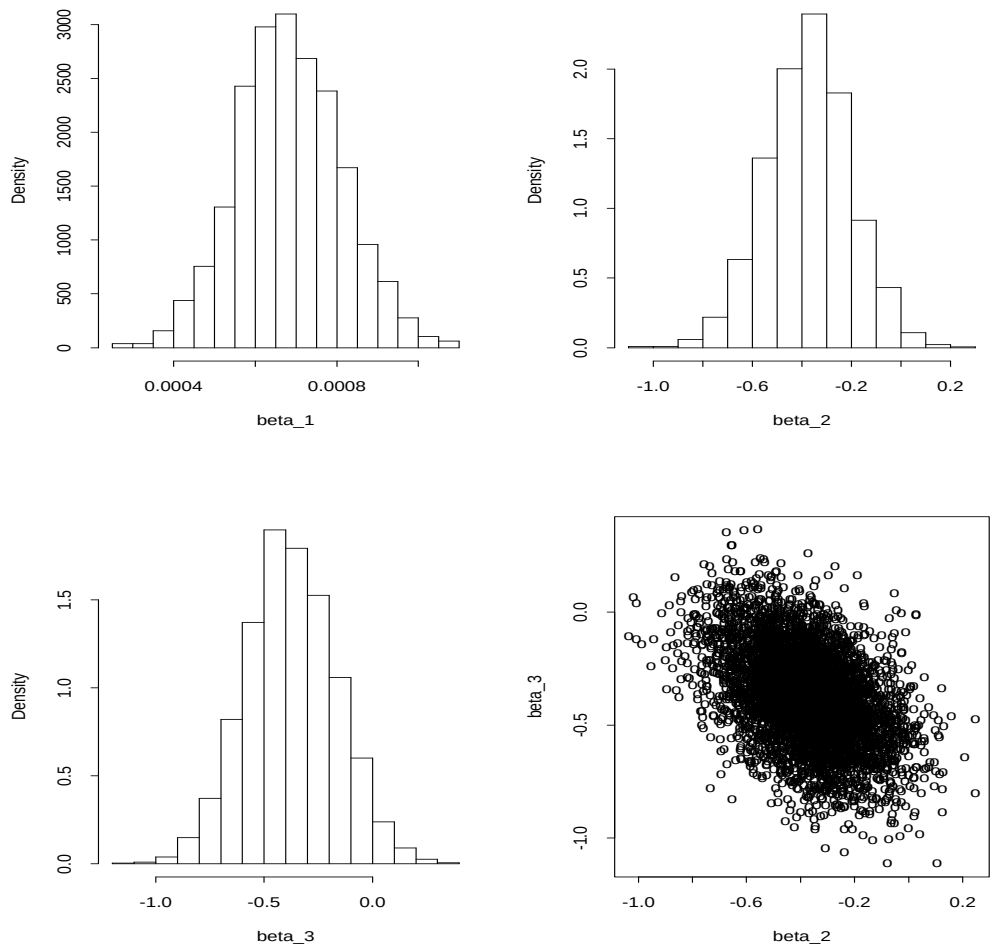


Posterior density estimates for $S(x)$ at two selected locations.



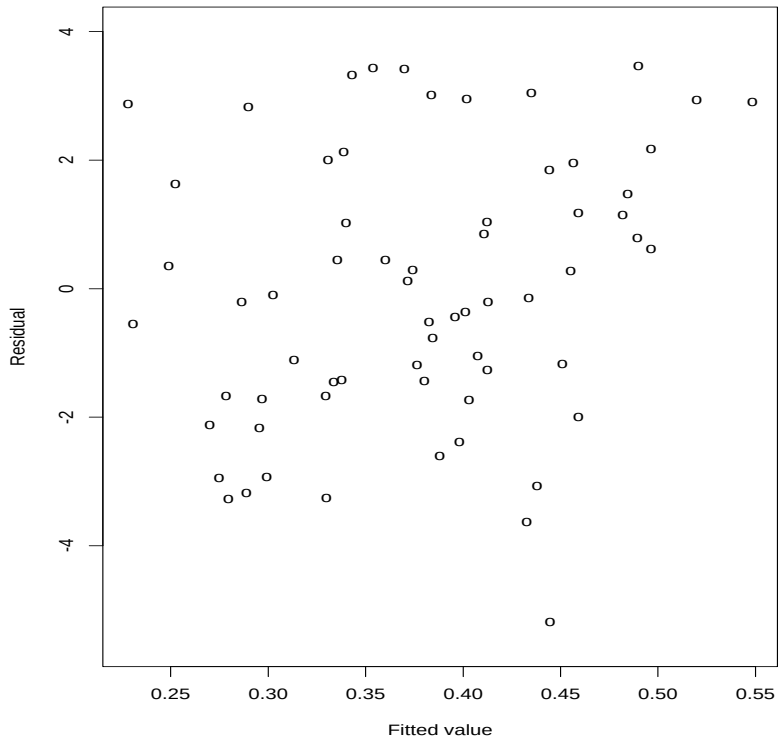
- solid curve – remote location (452, 1493),
- dashed curve – location (520, 1497), close to observed sites in central region.

Empirical posterior distributions for regression parameters



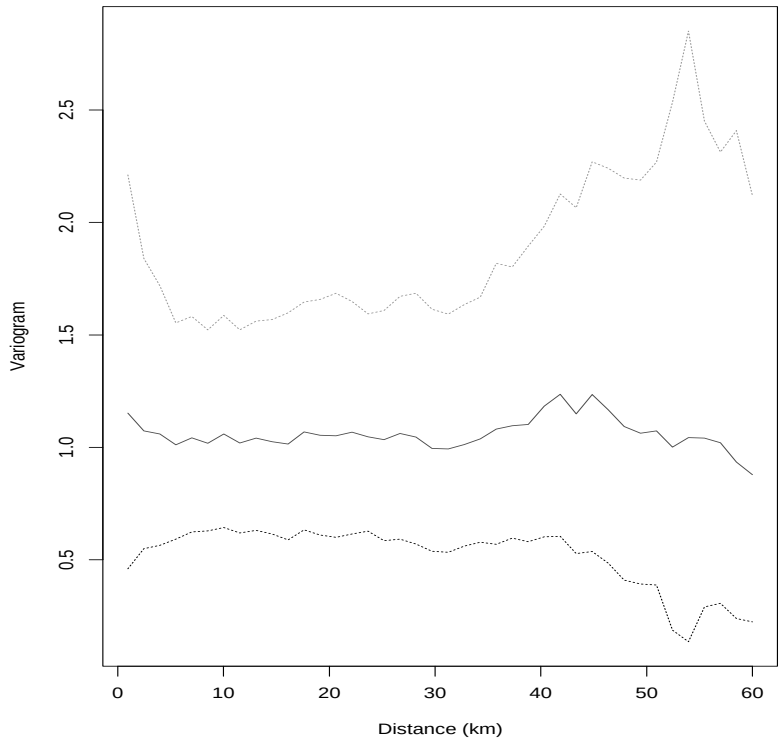
- $\beta_1 =$ effect of age
- $\beta_2 =$ effect of untreated bed-nets
- $\beta_3 =$ additional effect of treated bed-nets

Goodness-of-fit for Gambia malaria model



Village-level residuals against fitted values.

- $r_{ij} = (Y_{ij} - \hat{p}_{ij})/\sqrt{\{\hat{p}_{ij}(1 - \hat{p}_{ij})\}}$
- $r_i = \sum r_{ij}/\sqrt{n_i}$
- intended to check adequacy of model for p_{ij}



Standardised residual empirical variogram plot (village-level data and pointwise 95% posterior intervals constructed from simulated realisations of fitted model).

- $r_{ij} = (Y_{ij} - \hat{p}^*_{ij})/\sqrt{\{\hat{p}^*_{ij}(1 - \hat{p}^*_{ij})\}}$
- $r_i = \sum r_{ij}/\sqrt{n_i}$
- $\text{logit}p^*_{ij} = \hat{\alpha} + f'_{ij}\hat{\beta} + \hat{S}(x_i)$
- intended to check adequacy of model for $S(x)$