Annals of Applied Biology **Supporting Information (With TabS2 corrected in August 2015)**

Article title: Transmission of *Leptosphaeria maculans* from a cropping season to the following one.
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The following Supporting Information is available for this article:

Fig. S1 Mean and cumulative temperature, rainfall and wind distance per month in cropping seasons from 2009-2010 to 2012-2013. Wind distance is calculated as the product of duration by intensity. Data were obtained from the INRA CLIMATIK database, for Le Rheu weather station, on a hourly basis.

Fig. S2 Mean hourly wind distance (km) per autumn (from September 1st to November 30th) for autumns 2009 to 2012. Wind distance is calculated as the product of duration by intensity. Data were obtained from the INRA CLIMATIK database, for Le Rheu weather station, on a hourly basis.

Fig. S3 Cumulative potential distance travelled by spores (km) per month in September, October and November for autumns 2009 to 2012 in the landscape represented in Fig. 2, 3. Potential travelled distance is calculated as the product of wind duration by intensity, for each of 8 directions. Data were obtained from the INRA CLIMATIK database, for Le Rheu weather station, on a hourly basis. For the ease of reading, a different color is used for each season.

Fig. S4 Posterior distribution of parameters of the model fitted to 2009-2010 data.

Fig. S5 Posterior distribution of parameters of the model fitted to 2011-2012 data.

Fig. S6 Observed disease measurements versus model predictions for source plots (top left panel) and target plots (bottom left panel) for the 2009-2010 data set. The model predictions correspond to the posterior medians (circles) of the disease measurements and their 95%-posterior intervals (endpoints of grey vertical segments correspond to the 2.5% and 97.5% posterior quantiles). Circles drawn in blue (resp. green) correspond to observed disease measurements whose prediction is too small (resp. too large) (i.e. observed disease measurement is not in the corresponding 95% posterior intervals). The blue and green circles are represented in space in the right panels.

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Fig. S8 Observed disease measurements versus model predictions for target plots (left), for the 2009-2010 data set. The model predictions correspond to the posterior medians (circles) of the disease measurements and their 95%-posterior intervals (endpoints of grey vertical segments correspond to the 2.5% and 97.5% posterior quantiles). Circles drawn in blue correspond to large observed disease measurements (greater than 50) whose predictions are generally smaller in expectation. The blue circles are represented in space in the right panel.

Table S1 Prior distributions and proposal distributions of model parameters (or their logarithms).

Table S2 Assessment of prediction performance in source and target plots for the 2009-2010 and 2011-2012 data sets, with sample sizes and coverage rates of disease measurements by their 95%-posterior intervals. For each disease measurement, we computed a 95%-posterior interval based on parameter posterior distributions and the randomness of the observation process (Poisson randomness for measurements in source plots; negative Binomial randomness for measurements in target plots). The coverage of a disease measurement by its 95%-posterior interval is a binary variable that is equal to 1 if the measurement is included in the interval, 0 otherwise. The coverage rate is the proportion of disease measurements for which the binary variable is equal to 1.

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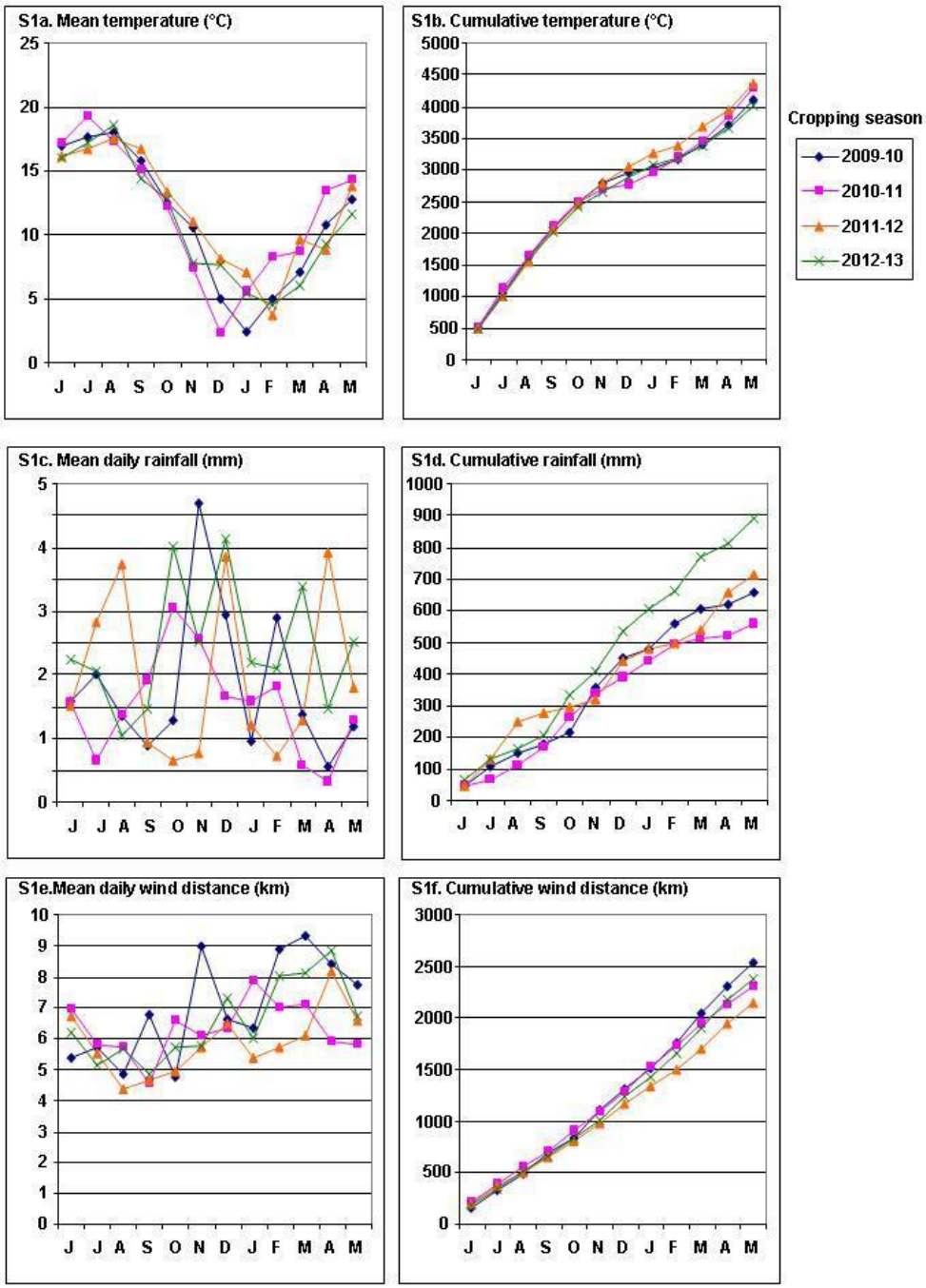

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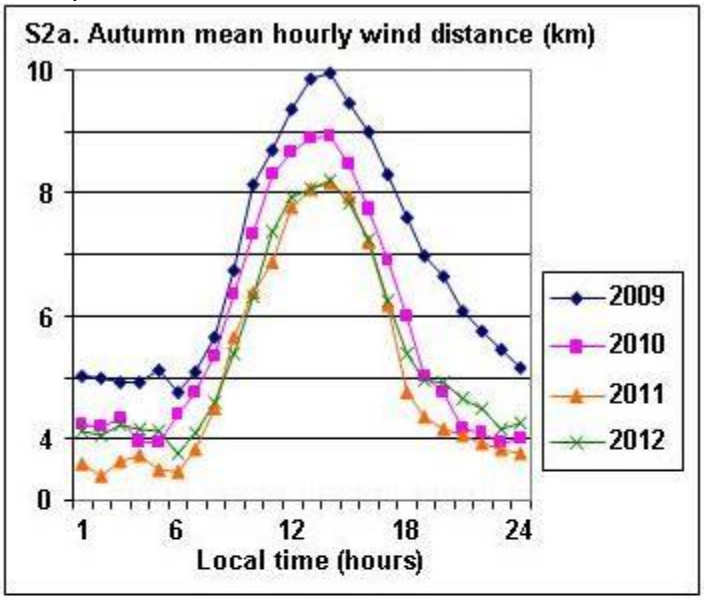

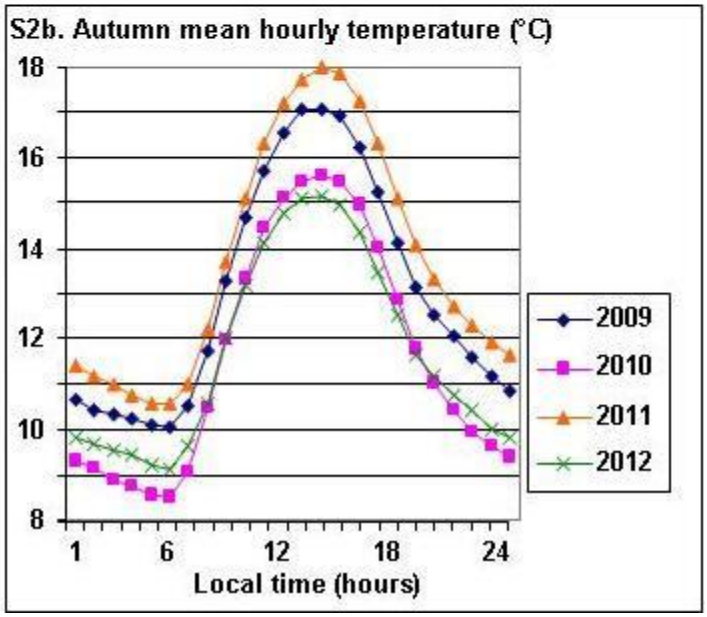

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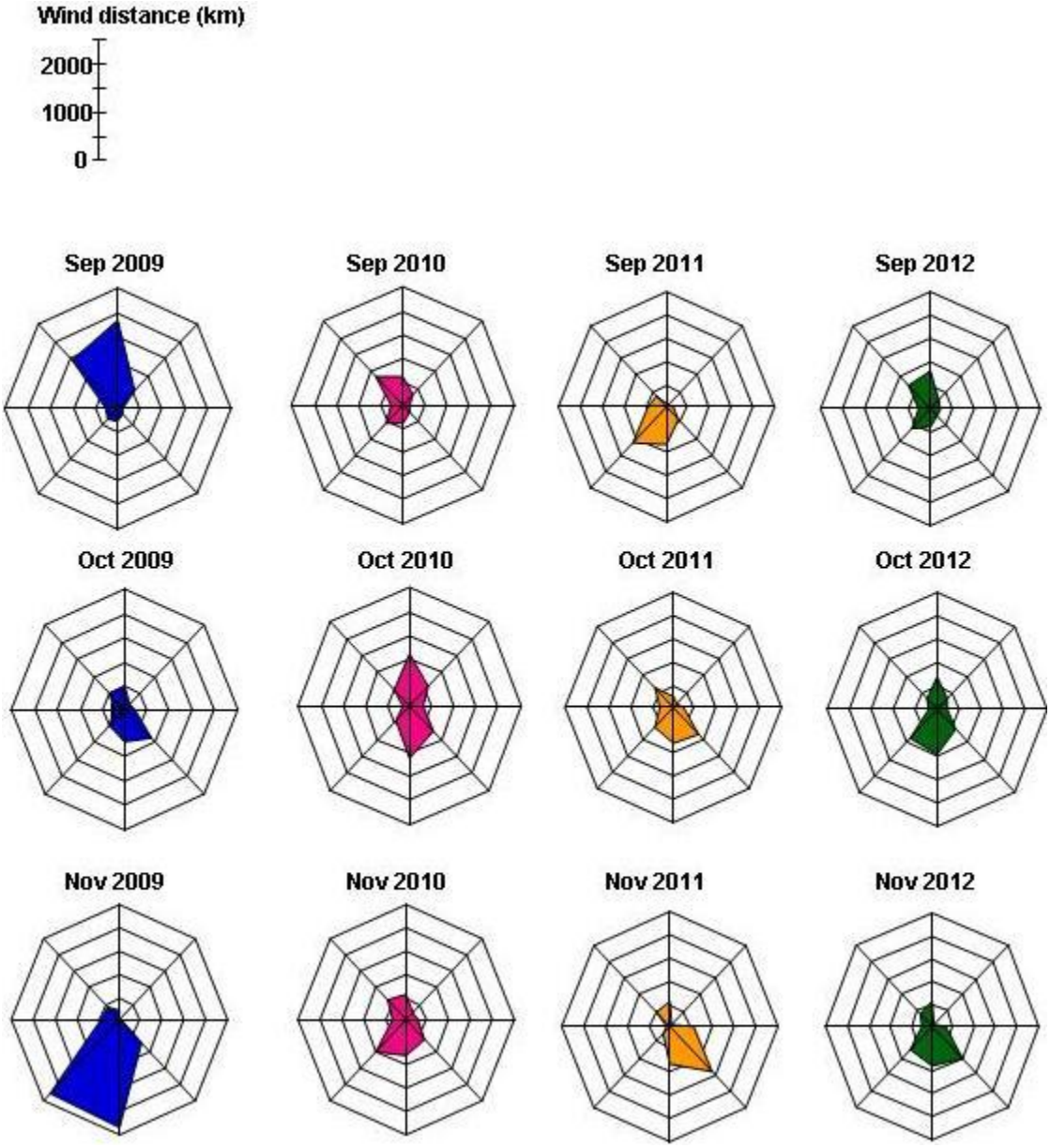

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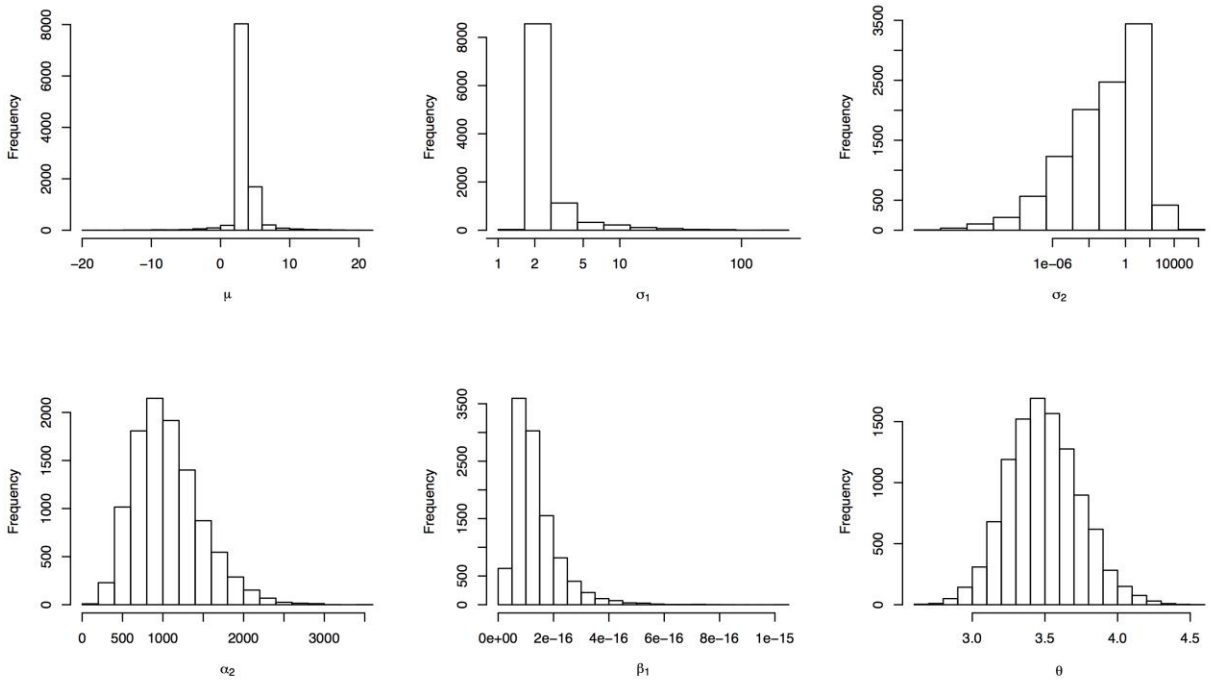
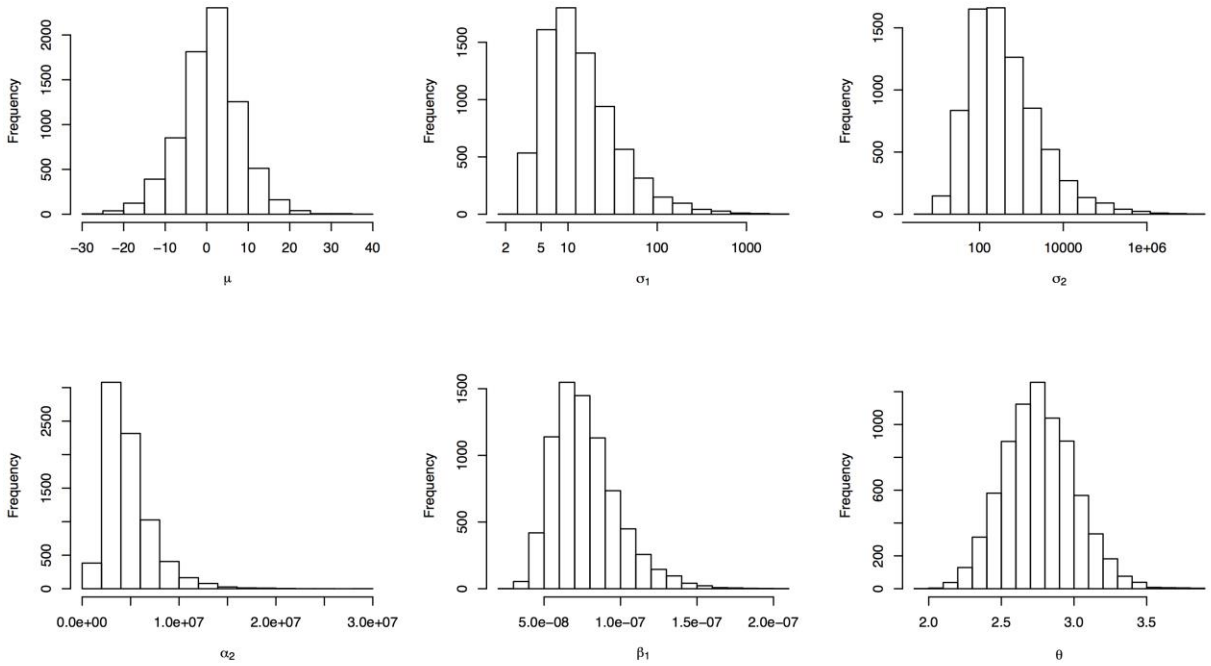


Fig. S5 Posterior distribution of parameters of the model fitted to 2011-2012 data.



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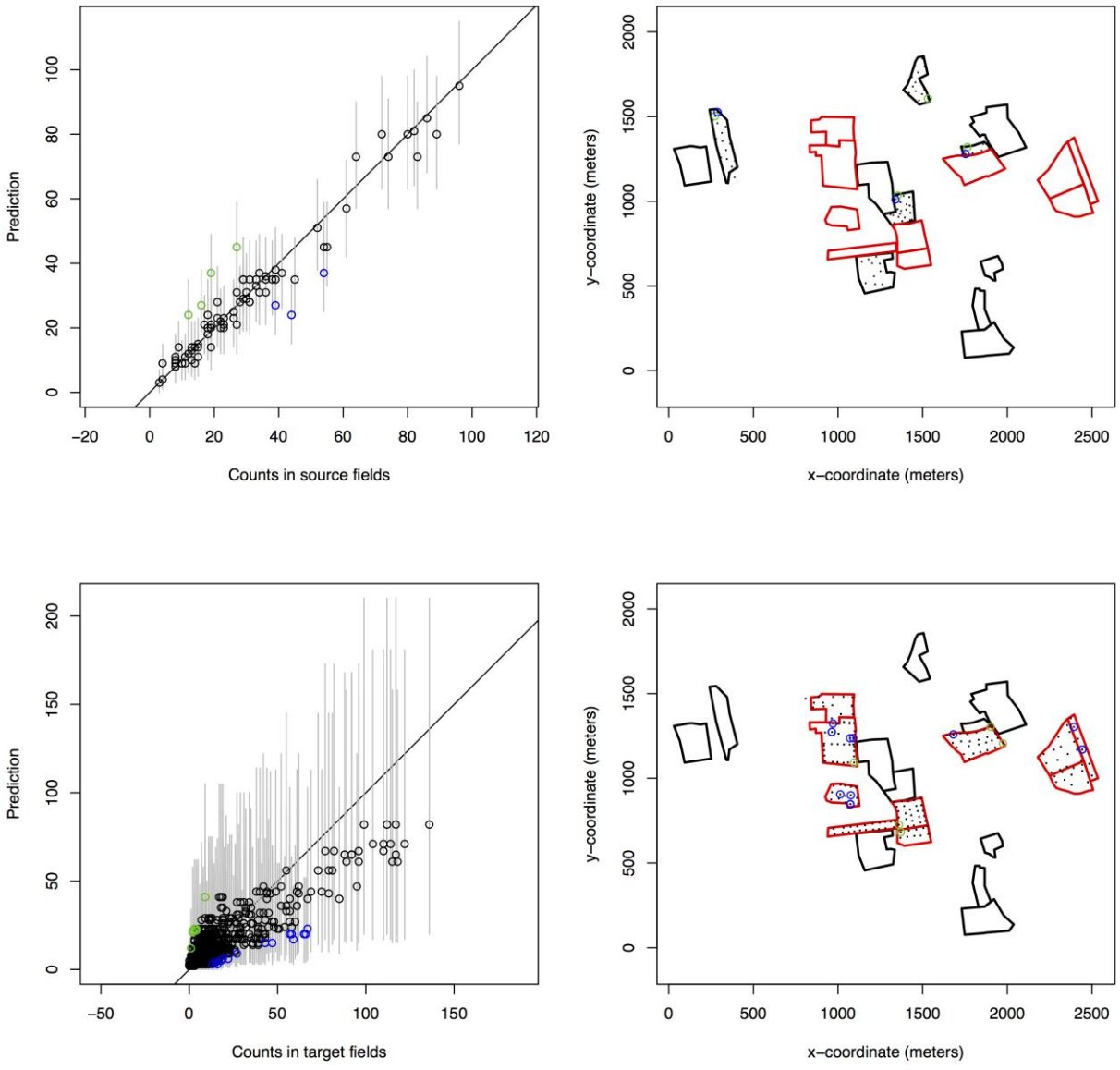

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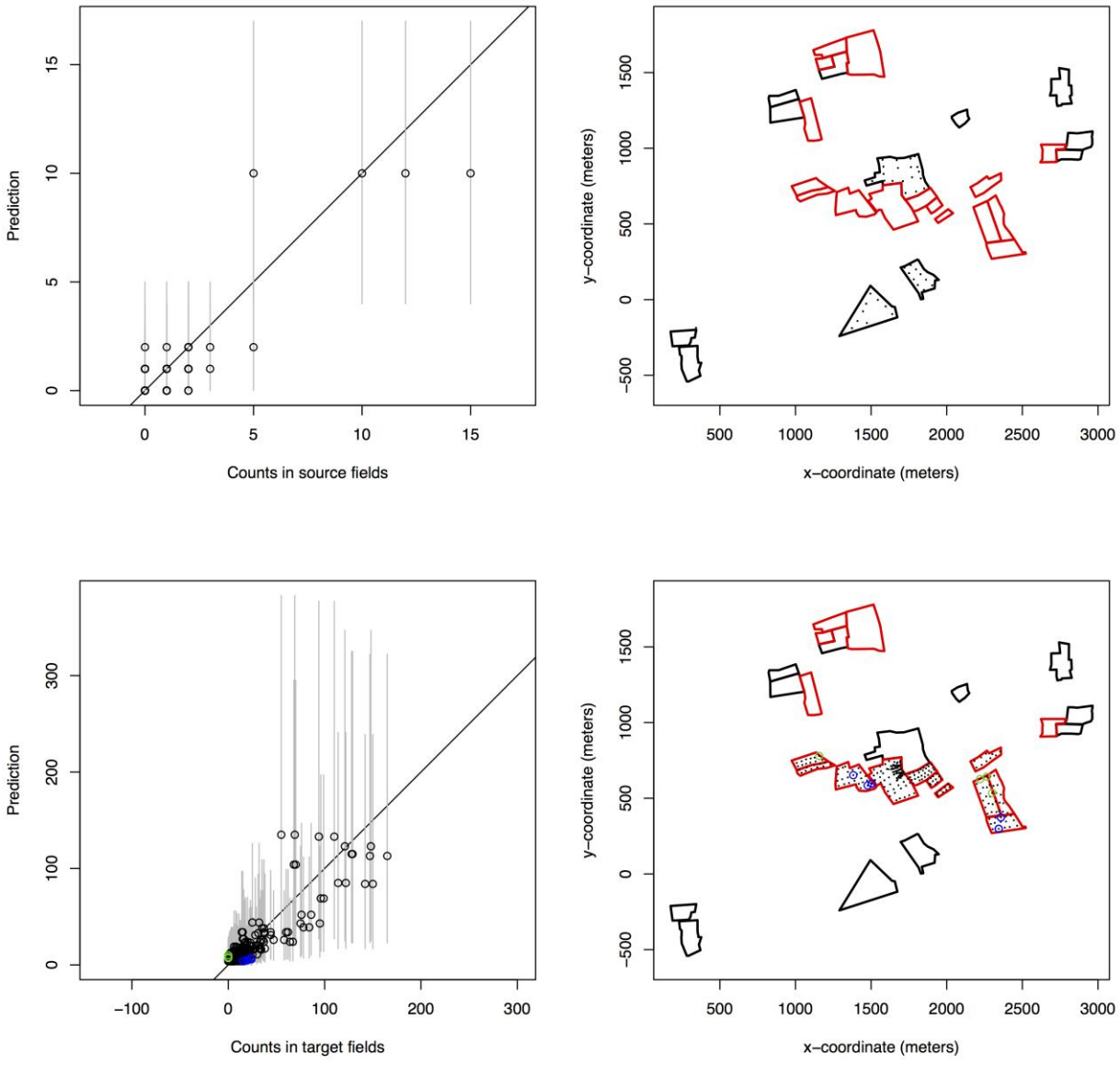

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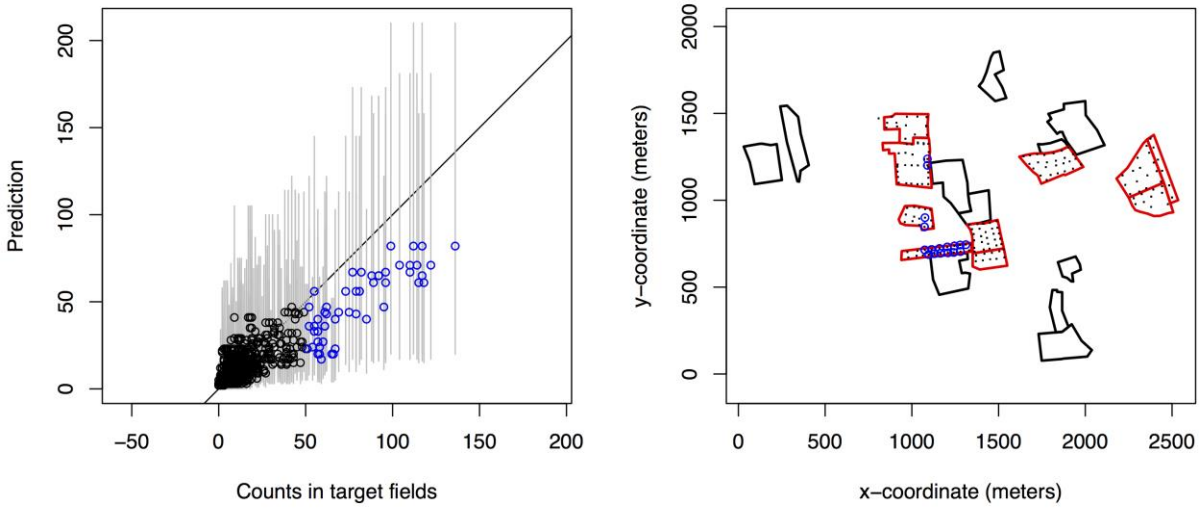

Table S1 Prior distributions and proposal distributions of model parameters (or their logarithms).

Parameter	Prior distribution[a]	Proposal distribution
μ	Normal(mean=0, sd=10)	Normal(mean=0, sd=0.5)
$\log \sigma_1$	Normal(mean=0, sd=10)	Normal(mean=0, sd=0.5)
$\log \sigma_2$	Normal(mean=0, sd=10)	Normal(mean=0, sd=0.5)
σ_3	Dirac(a) with a=0.5 (auto-covariance function yielding rough spatial processes), a=1.0 (exponential auto-covariance function) or a=1.5 (auto-covariance function yielding smooth spatial processes); see Stein (1999).	Dirac(a)
$\log \beta_1$	Normal(mean=0, sd=10)	Normal(mean=0, sd=0.2)
β_2	Dirac(b) with b=0.02, 0.05, 0.08, 0.1, 0.2, 0.5, 1.0 or 2.0 (the dispersal kernel K is Exponential when b=1 and Normal when b=2; lower b, fatter the tail of the kernel; see Austerlitz *et al*., 2004).	Dirac(b)
α_1	Dirac(1)	Dirac(1)
$\log \alpha_2$	Normal(mean=0, sd=10)	Normal(mean=0, sd=0.5)
$\log \theta$	Normal(mean=0, sd=10)	Normal(mean=0, sd=0.2)
$\log \Lambda_S(x_i)$	See main text.	Normal(mean=0, sd=0.5)

[a] Parameterization of the normal distribution is the default one in the R statistical software (mean and standard deviation). The Dirac distribution allows the parameter to be equal to only one value (i.e. all the mass of the distribution is at this point value). Parameters have independent prior distributions (then, the joint prior distribution of the parameters is the product of their marginal distributions given below). Similarly, the parameter values in the MCMC algorithm are proposed independently from their marginal proposal distributions. In addition, in the MCMC, μ, σ_1 and σ_2 were simultaneously updated (block updating), β_1, α_2 and θ were also simultaneously updated, each value of $\Lambda_S(x_i)$, $i = 1,\ldots,n_G$, was updated separately in a uniformly random order.

Table S2 (Corrected in August 2015) Assessment of prediction performance in source and target plots for the 2009-2010 and 2011-2012 data sets, with sample sizes and coverage rates of disease measurements by their 95%-posterior intervals. For each disease measurement, we computed a 95%-posterior interval based on parameter posterior distributions and the randomness of the observation process (Poisson randomness for measurements in source plots; negative Binomial randomness for measurements in target plots). The coverage of a disease measurement by its 95%-posterior interval is a binary variable that is equal to 1 if the measurement is included in the interval, 0 otherwise. The coverage rate is the proportion of disease measurements for which the binary variable is equal to 1.

	2009-2010 data	2011-2012 data
Sample size in source plots	83	156
Coverage rate of disease measurements in source plots	0.916	1.000
Sample size in target plots	688	494
Coverage rate of disease measurements in target plots	0.968	0.976