

# The WeedMap Package

February 16, 2008

**Title** Map of weed intensity

**Version** 0.1

**Author** Gilles Guillot

**Description** Compute spatial predictions from exact count and a covariate

**Depends** RandomFields, fields

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**URL** [www.inapg.inra.fr/ens\\_rech/mathinfo/personnel/guillot/welcome.html](http://www.inapg.inra.fr/ens_rech/mathinfo/personnel/guillot/welcome.html)

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## R topics documented:

WeedMap-package . . . . .	1
check.model.weed . . . . .	4
pred.weed . . . . .	5
show.pred.weed . . . . .	7
show.sim.weed . . . . .	8
sim.weed . . . . .	9

<b>Index</b>	<b>11</b>
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WeedMap-package      *Spatial prediction of weed intensities*

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## Description

Simulation, inference and prediction for a Bayesian spatial statistical model for weed intensities and a covariate

## Details

Package: WeedMap  
 Type: Package  
 Version: 0.1  
 Date: 2006-09-28  
 License: GPL

The function `sim.weed` makes simulation from the model. The simulated dataset can be graphically displayed with `show.sim.weed`. The function `pred.weed` makes inference and prediction whose results can be graphically displayed with `show.pred.weed` (monitoring of Markov chain simulation) and with `check.model.weed` (goodness of fit assessment).

### Author(s)

Gilles Guillot [www.inapg.inra.fr/ens\\_rech/mathinfo/personnel/guillot/welcome.html](http://www.inapg.inra.fr/ens_rech/mathinfo/personnel/guillot/welcome.html)

### References

G. Guillot, N. Loren, M. Rudemo, Bayesian spatial prediction of weed intensities from exact count data and picture based indexes, 2006, submitted

### Examples

```

## Simulate a data set
sim <- sim.weed(nx=30, ny=20, nxy=20, nz=49,
               param.cov=c(mean=0, variance=1, nugget=0, scale=.1),
               mu=80, sigma=70, lambda=1, tau=0.2, nbin=10,
               true.field = TRUE, npix = c(100,100), z.on.grid = TRUE)

## show the graphics
show.sim.weed(sim)

## Not run:

## make joint inference and prediction
res <- pred.weed(nit=10000,
                 thin=10,
                 ## data
                 x=sim$x,
                 xy=sim$xy,
                 y=sim$y,
                 z=sim$z,
                 wx=sim$wx,
                 wxy=sim$wxy,
                 i=sim$i,
                 ## init
                 #alpha=alpha,
                 #beta=beta,
                 lambda=1,

```

```
#tau=tau,
#kappa=kappa,
## proposals
sd.prop.h=0.1,
sd.prop.alpha=0.1,
sd.prop.beta=0.01,
sd.prop.lambda=0.,
sd.prop.tau=0.5,
delta.prop.kappa=2,
## priors
mprior.alpha=0.625,
vprior.alpha=1,
mprior.beta=0.0125,
vprior.beta=1,
mprior.kappa=.5,
vprior.kappa=999,
mprior.lambda=1,
vprior.lambda=1,
mprior.tau=0.1,
vprior.tau=10,
n.kappa=30,
kappa.max=5*sim$param.cov[4])

show.pred.weed(sim=sim,
               res=res,
               param=TRUE,
               pairs=TRUE,
               wy=FALSE,
               wz=FALSE,
               nit=res$nit,
               thin=res$thin,
               burnin=500)

check.model.weed(x=sim$x,
                 xy=sim$xy,
                 y=sim$y,
                 wx=sim$wx,
                 wxy=sim$wxy,
                 i=sim$i,
                 ## output of MCMC run
                 res=res,
                 ## options
                 nit=res$nit,
                 thin=res$thin,
                 burnin=500,
                 bin=seq(.1, .5, .05),
                 nqqplot=500,
                 nresamp=200)

## End(Not run)
```

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check.model.weed    *Check goodness of fit of the model*

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### Description

Plot various graphics to assess goddness of fit of the transformed Gaussian model

### Usage

```
check.model.weed(x, xy, y, wx, wxy, i, res, nit, thin, burnin, bin, nqqplot, nresamp)
```

### Arguments

x	Coordinates of sites where weed counts only are given
xy	Coordinates of sites where weeds and images are given
y	Coordinates of sites where image indexes only are given
wx	Weed values at sites x
wxy	Weed values at sites xy
i	Image values at sites xy and y. Values are concatenated in the same vector in this order
res	Output of pred.weed
nit	Number of iterations
thin	Thinning of the Markov chain
burnin	Number of values to discard before computing statistics about the empirical posterior
bin	Binning for the empirical variograms
nqqplot	Number of observation in the qqplot
nresamp	Number of realisation resampled to get envelope estimates

### Details

#### Value

None

#### Author(s)

Gilles Guillot

#### References

G. Guillot, N. Loren, M. Rudemo, Bayesian spatial prediction of weed intensities from exact count data and picture based indexes, 2006, submitted

**Examples**


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```
pred.weed          Spatial prediction of weed counts
```

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**Description**

Makes joint Bayesian inference and spatial prediction within a model for weed count data and a covariate

**Usage**

```
pred.weed(nit, thin = 1, x = NULL, xy = NULL, y = NULL, z, wx = NULL,
wxy = NULL,
i = NULL, alpha = NULL, beta = NULL, lambda = NULL, tau = NULL, kappa =
NULL,
sd.prop.h = 0.1, sd.prop.alpha = 0.5, sd.prop.beta = 0.5, sd.prop.lambda
= 0.1, sd.prop.tau = 0.1,
delta.prop.kappa = 2, mprior.alpha, vprior.alpha, mprior.beta, vprior.beta, mprior.
```

**Arguments**

nit	Number of iterations
thin	Thinning of the Markov chain
x	Coordinates of sites where weed counts only are given
xy	Coordinates of sites where weeds and images are given
y	Coordinates of sites where image indexes only are given
z	Coordinates of sites where predicted values are sought
wx	Weed values at sites x
wxy	Weed values at sites xy
i	Image values at sites xy and y. Values have to be concatenated in the same vector in this order
alpha	Init value for the shape parameter of w
beta	Init value for the scale parameter of w
lambda	Init value for the scaling parameter relating w and i as $i = \lambda w \epsilon$
tau	Init value for the variance of noise <i>epsilon</i>
kappa	Init value for the spatial scale parameter of the Gaussian random field
sd.prop.h	Standard deviation of the Gaussian increment in the proposal of Gaussian components <i>h</i>
sd.prop.alpha	Standard deviation of the Gaussian increment in the proposal for alpha

<code>sd.prop.beta</code>	Standard deviation of the Gaussian increment in the proposal for beta
<code>sd.prop.lambda</code>	Standard deviation of the Gaussian increment in the proposal for lambda
<code>sd.prop.tau</code>	Standard deviation of the Gaussian increment in the proposal for tau
<code>delta.prop.kappa</code>	Maximum number of increments allowed (the amplitude of an increment being $\text{kappa.max}/n.\text{kappa}$ ) for a move in the proposal of kappa
<code>mprior.alpha</code>	A priori mean of alpha
<code>vprior.alpha</code>	A priori variance of alpha
<code>mprior.beta</code>	A priori mean of beta
<code>vprior.beta</code>	A priori variance of beta
<code>mprior.kappa</code>	A priori mean of kappa
<code>vprior.kappa</code>	A priori variance of kappa
<code>mprior.tau</code>	A priori mean of tau
<code>vprior.tau</code>	A priori variance of tau
<code>mprior.lambda</code>	A priori mean of lambda
<code>vprior.lambda</code>	A priori variance of lambda
<code>n.kappa</code>	Number of steps in the discretisation of the support of kappa
<code>kappa.max</code>	Maximum value in the truncation of the support of kappa

### Details

If standard deviation of the Gaussian increment in the update of alpha, beta, lambda or tau, or if the step in the increment of kappa is equal to 0, then this variable is not processed in the MCMC run and stays at its initial value. This is the way to specify that inference should not be made on a one or several variable. See examples in [WeedMap](#) where lambda is initialised at 1 and not updated (`sd.prop.lambda=0`).

If init values are not given, the corresponding parameters are initialised from the prior.

### Value

A list whose elements are:

<code>x</code>	Coordinates of sites where weed counts only are given
<code>y</code>	Coordinates of sites where image indexes only are given
<code>z</code>	Coordinates of sites where predicted values are sought
<code>wx</code>	Weed values at sites <code>x</code>
<code>i</code>	Image values at sites <code>xy</code> and <code>y</code> . Values are concatenated in the same vector in this order
<code>nit</code>	Number of iterations
<code>thin</code>	Thinning of the Markov chain

<code>wy.MC</code>	A matrix with <code>ny</code> rows and <code>nit/thin</code> columns containing sampled values of <code>wy</code>
<code>wz.MC</code>	A matrix with <code>nz</code> rows and <code>nit/thin</code> columns containing sampled values of <code>wz</code>
<code>alpha.MC</code>	A vector of length <code>nit/thin</code> of simulated <code>alpha</code> values
<code>beta.MC</code>	A vector of length <code>nit/thin</code> of simulated <code>beta</code> values
<code>lambda.MC</code>	A vector of length <code>nit/thin</code> of simulated <code>lambda</code> values
<code>tau.MC</code>	A vector of length <code>nit/thin</code> of simulated <code>tau</code> values
<code>kappa.MC</code>	A vector of length <code>nit/thin</code> of simulated <code>kappa</code> values
<code>n.kappa</code>	Number of steps in the discretisation of the support of <code>kappa</code>
<code>kappa.max</code>	Maximum value in the truncation of the support of <code>kappa</code>

**Author(s)**

Gilles Guillot

**References**

G. Guillot, N. Loren, M. Rudemo, Bayesian spatial prediction of weed intensities from exact count data and picture based indexes, 2006, submitted

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<code>show.pred.weed</code>	<i>Plot results of pred.weed</i>
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**Description**

Plot traces of Markov chains simulated by `pred.weed`, compute statistics on the posterior distribution, compare to known true values. (if any)

**Usage**

```
show.pred.weed(sim = NULL, res, param = TRUE, pairs = TRUE, wy = TRUE, wz = TRUE, r
```

**Arguments**

<code>sim</code>	A list, typically the output of function <code>sim.weed</code>
<code>res</code>	A list, typically the output of function <code>pred.weed</code>
<code>param</code>	Logical: if <code>TRUE</code> graphs of simulated parameters contained in <code>res</code> are displayed
<code>pairs</code>	Logical: if <code>TRUE</code> pair plots of predicted weed values are plotted against known true values provided as output of function <code>sim</code> are displayed (for debugging and convergence checking)
<code>wy</code>	Logical: if <code>TRUE</code> chains corresponding to the nine first sites in <code>y</code> are displayed
<code>wz</code>	Logical: if <code>TRUE</code> chains corresponding to the nine first sites in <code>z</code> are displayed

<code>nit</code>	Number of Markov iterations
<code>thin</code>	Thinning of the chain
<code>burnin</code>	Number of values to discard before computing statistics about the empirical posterior. The number of iterations discarded is the number of stored iterations, e.g. if <code>nit=10000</code> and <code>thin=10</code> , then only 1000 iterations are stored and <code>burnin=100</code> will remove the 100 first which correspond to actually <code>thin*burnin=1000</code> Markov iterations.

**Value**

No value returned

**Author(s)**

Gilles Guillot

**References**

G. Guillot, N. Loren, M. Rudemo, Bayesian spatial prediction of weed intensities from exact count data and picture based indexes, 2006, submitted

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`show.sim.weed`      *Plot simulated weed dataset*

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**Description**

Takes the output of `sim.weed` and plot the different variables according to the options of simulations

**Usage**

```
show.sim.weed(sim)
```

**Arguments**

<code>sim</code>	A list as produced by <code>sim.weed</code>
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**Value**

No value is returned

**Author(s)**

Gilles Guillot

**References**

G. Guillot, N. Loren, M. Rudemo, Bayesian spatial prediction of weed intensities from exact count data and picture based indexes, 2006, submitted

sim.weed

*Simulate weed exact count data and a covariate***Description**

The data simulated are of two kinds: exact weed counts and image derived indexes. The counts  $w$  arise from a transformed Gaussian model with Gamma marginal. The image indexes  $i$  relate to  $w$  as  $i(s) = \lambda w(s) * \epsilon(s)$ , where  $\epsilon$  is a spatially uncorrelated noise. The simulation is carried out on the unit square.

**Usage**

```
sim.weed(nx, ny, nxy, nz, param.cov, mu, sigma, lambda, tau, nbin, true.field = FALSE)
```

**Arguments**

<code>nx</code>	number of sites where only $w$ is observed
<code>ny</code>	number of sites where only $i$ is observed
<code>nxy</code>	number of sites where $w$ and $i$ are observed
<code>nz</code>	number of sites where $w$ will be predicted. If <code>z.on.grid=TRUE</code> , <code>nz</code> should be a square.
<code>param.cov</code>	Vector of parameters of the underlying Gaussian randomFields. The simulation of the Gaussian random fields performed assuming an exponential covariance function. The vector of parameters should have four components, namely: mean, variance, nugget, scale and should be given as e.g.: <code>c(mean=0, variance=1, nugget=0, scale=.1)</code> . See the documentation of <a href="#">GaussRF</a> in package <a href="#">RandomFields</a> for details.
<code>mu</code>	Mean of $w$
<code>sigma</code>	Variance of $w$
<code>lambda</code>	Scaling factor relating $w$ and $i$
<code>tau</code>	Variance of $\epsilon$
<code>nbin</code>	Number of bins for the binned data
<code>true.field</code>	Logical: should values on a dense grid be given
<code>npix</code>	A vector giving the number of pixels horizontally and vertically of the grid if <code>true.field=TRUE</code>
<code>z.on.grid</code>	Logical: set TRUE if sites of prediction $z$ are required on a grid; then <code>nz</code> should be a square.

**Details**

**Value**

x	Coordinates of sites where weed counts only are given
xy	Coordinates of sites where weeds and images are given
y	Coordinates of sites where image indexes only are given
z	Coordinates of sites where predicted values are sought
coord.grid	Logical telling whether all the realisation of the weed random field is also given on a grid
wx	Weed values at sites x
wy	Weed values at sites y
wxy	Weed values at sites xy
wz	Weed values at sites z
vx	Binned weed values at sites x
vxy	Binned weed values at sites xy
i	Image values at sites xy and y. Values are concatenated in the same vector in this order
wgrid	Weed counts values at the node of a grid
igrd	Image index values at the node of a grid
bin	Binning of the weed counts
param.cov	Parameters of the covariance function of the underlying Gaussian random field
mu	Mean of w
sigma	Variance of w
alpha	Shape parameter of w
beta	Scale parameter of w
lambda	Scaling parameter relating w and i as $i = \lambda w \epsilon$
tau	Variance of noise <i>epsilon</i>
npix	number of pixel in the horizontal direction (same value is assumed for the vertical direction)

**Author(s)**

Gilles Guillot

**References**

G. Guillot, N. Loren, M. Rudemo, Bayesian spatial prediction of weed intensities from exact count data and picture based indexes, 2006, submitted

# Index

## \*Topic **package**

WeedMap-package, [1](#)

`check.model.weed`, [2, 3](#)

GaussRF, [9](#)

`pred.weed`, [2, 5](#)

RandomFields, [9](#)

`show.pred.weed`, [2, 7](#)

`show.sim.weed`, [2, 8](#)

`sim.weed`, [2, 9](#)

WeedMap, [6](#)

WeedMap (*WeedMap-package*), [1](#)

WeedMap-package, [1](#)