Quantifying Spatio-Temporal Variation of Invasion Spread:

the **invasionSpeed** Package

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1 Introduction

The invasionSpeed package provides user-friendly tools in **R** to quantify spatiotemporal variation of spread patterns of invasive species and infectious diseases. The data sets are assumed to contain observations of the time of first appearance and their spatial locations. This package build on Gaussian process gradient models (Goldstein et al., 2018; Banerjee et al., 2003), which are useful for estimating both the speed and direction of continuous expansion, as well as detecting the long-range jumps of such processes. The invasionSpeed package implements Bayesian inference for gradient models and provides tools for visualizing inference results. Bayesian inference is carried out via Markov chain Monte Carlo (MCMC) by using functions from the spBayes package. This vignette provides a data analysis example using the Hemlock Wolly Adelgid data¹.

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¹Records are from the US Forest Service Forest Health Protection.

Load the invasionSpeed package as follows.

> library(invasionSpeed)

2 Detecting continuous expansion

localgrad function in the invasionSpeed package estimates the speed and direction of spread of processes under a Gaussian process framework. The localgrad function fits spatial regression models, where a response variable is time to first appearance and the predictors are spatially varying environmental and geographical covariates (e.g. coordinates). If the response surface is the waiting time to first appearance, then the reciprocal of the gradient length is a measure of the invasion speed; fast spread leads to shallow waiting time surfaces, while slow spread results in steep surfaces. For given fitted spatial regression model parameters, the speed and dominant directions of processes are estimated by evaluating gradients of the model.

2.1 Fitting Gaussian process gradient models

Load the hemlock data as follows.

```
> data(hemlock)
```

Then, specify longitude and latitude coordinates and years of the first appearance from the hemlock data.

```
> coord = cbind(hemlock$long,hemlock$lat)  # longitude latitude coordinates
> dates = hemlock$first.year  # quaratine data by county
```

To estimate model parameters users can specify the number of batches, batch length, and the acceptance rate, which are tuning parameters for an MCMC sampler. These MCMC tuning parameters come with default values.

```
> amcmc=list(n.batch=10,batch.length=100,accept.rate=0.3)
```

In the localgrad function, users can specify time of first appearance (for our wolly adelgid example, this is the year of first appearance), and coordinates associated with each appearance. When the process of interest is on the longitude and latitude domain, users have to specify the 2-dimensional Albers equal area projection parameter. If there are additional covariates except for the coordinates of the process, users can also specify covar. Then a Bayesian spatial regression model is fitted as follows.

The localgrad function returns an object of class "localgrad".

2.2 Summary and visualization

summary function displays the number of locations where there is a statistically significant continuous spread of the process. Mean and median speed of spread are printed on the km scale for the process, which is on the longitude and latitude domain.

```
> summary(out.grad)
Call:
  localgrad(dates = dates, coord.longlat = coord, Albers = c(29.5, 45.5), n.samp = 1000, amon
Speed of spread estimated at 340 locations.
Of these, 180 are significantly nonzero.

Mean speed of spread is estimated as 21.45447 km.
  Median speed of spread is estimated as 13.75958 km.
```

plotgrad function draws the vector field plot for the significant gradients.

```
> plotgrad(out.grad,cex=1,pch=".",database="state")
```

In Figure 1, arrows indicate direction and speed of spread. As the speed of spread increases, the length of the arrows becomes longer. The color of the each arrow represents the time of first appearance of the process. Red implies the earliest appearance, and blue indicates the latest one.

3 Detecting long-range jumps

The **invasionSpeed** package identifies candidate locations for long-range jumps in two ways. The first is the Rayleigh test (Jammalamadaka and Sengupta, 2001), and the second is a direct test using Gaussian process gradient models (Goldstein et al., 2018; Banerjee and Gelfand, 2006).

3.1 Rayleigh test

The Rayleigh test is a statistical test of whether a circular distribution is random or non-random. When applied to the gradients of spread near a point, a non-random distribution implies a potential long range spread through that point. longrange.localgrad function conducts Rayleigh test to the gradients from the class "localgrad" and points out candidate locations on the map.

```
> plotgrad(out.grad,cex=1,pch=".",database="state")
> out.longrange = longrange.localgrad(out.grad,add=TRUE)
```

In Figure 2, the black square dots represent candidate locations for long-range jumps. longrange.localgrad function tests long range jumps for a given radius

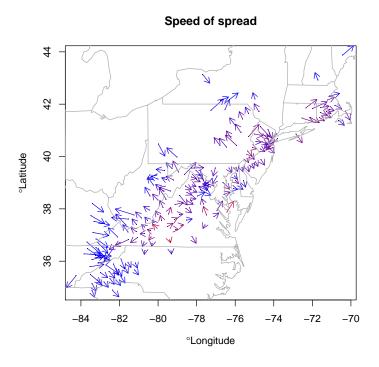


Figure 1: gradient plot for localgrad object

Long range jumps tested for 61.84688 km.

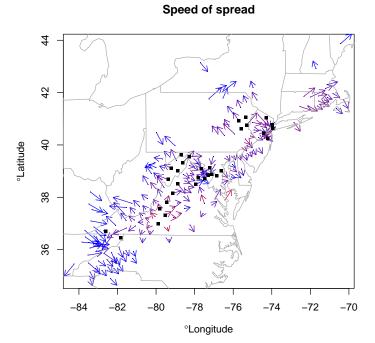


Figure 2: Detecting long-range jump using the Rayleigh test

(61.84688km in this example). User can specify the radius of jumps to perform the Rayleigh test using r option in the longrange.localgrad function. Otherwise, a default value is used for testing.

3.2 Radial expansion of gradient models

jump.scan function directly tests if there is significant radial expansion around a point. For each spatial location, the jump.scan function tests the gradient normal on four sides of a square with sides of length r. As a heuristic we can flag the location as a potential site of a long-range jump if the spread is significantly out of at least two sides of the box. We can plug in parameter estimates for the Gaussian process gradient model using the posterior samples from class "localgrad".

Long range jumps tested for 61.84688 km.

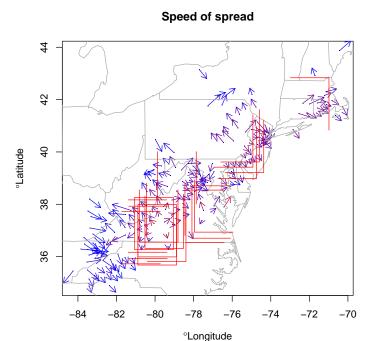


Figure 3: Detecting long-range jump using a Gaussian process gradient model

> class(out.jump)

[1] "jump.scan"

The jump.scan function returns an object of class "jump.scan". The plot-boxes function draws boxes, which represent the detected long-range jumps from class "jump.scan". The num.sides option decides the number of significant sides to be drawn.

> plotgrad(out.grad,cex=1,pch=".",database="state")
> plotboxes(object = out.jump, num.sides = 2,method="box")

We can check candidate locations for long-range jumps (center of the boxes) from Figure 3. In addition, plotboxes function prints the tested radius of the jumps (61.84688km in this example). User can specify the radius of jumps using the r option in the jump.scan function; otherwise a default value is used for testing.

Long range jumps tested for 61.84688 km.

Speed of spread 4 42 4 °Latitude 38 36 -84 -82 -80 -78 -76 -74 -72 -70 °Longitude

Figure 4: Detecting long-range jump using a Gaussian process gradient model

```
> plotgrad(out.grad,cex=1,pch=".",database="state")
> plotboxes(object = out.jump, num.sides = 2,method="arrow",point=TRUE)
```

We can draw arrow plots by specifying method as arrow. In Figure 4, we plot candidate locations and arrows according to the detected direction of long-range jumps.

References

Banerjee, S., Gelfand, A., and Sirmans, C., 2003, Directional rates of change under spatial process models, Journal of the American Statistical Association, 98(464):946-954.

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