

APHIS-simulation

The ALB spread simulation takes a set of trees with an initial ALB infestation, and models insect spread for a desired length of time.

Required setup

The APHIS simulation is performed in R, and takes advantage of R's spatial analysis capabilities. (More on R and spatial data at <https://cran.r-project.org/view=Spatial>.)

To get set up: 1. Install the latest version of R. (<https://cran.r-project.org/>) 2. If you are working on a computer running Windows, install RTools, which can be found under the R Binaries section of the website above. Follow the directions to make sure R and RTools can find each other. 3. Install the additional packages “sp” and “sf”. Be sure to use dependencies=TRUE when you do! 4. Additionally, the packages “dplyr”, “raster” and “magick” may be required for certain types of output.

Input

The input is a dataframe of trees that are potential ALB victims. All are assumed to be Acers. The dataframe should have the following fields, with these exact case-sensitive names (there can be other fields, they'll be ignored):

- “x”, “y”: location coordinates. Point of origin doesn't matter, this will only be used to calculate distances between points. SPECIFY THE LINEAR UNITS BELOW (feet or meters are the only choices; data in a projection where the linear units are degrees must be projected).
- “mean_noforestdist”: the mean distance to the forest edges in each of the 8 cardinal and intercardinal directions, in m. If the tree isn't in a forest landcover, this is 0.
- “dbh”: tree's DBH in cm

OPTIONAL: - “infested”: integer, 0 being uninfested, 1 being infested. If this field is included and there is at least 1 tree with a 1 status, the trees marked as 1 will be the seed of the outbreak. If either this field is not included or all the values are 0, a select number of trees will be randomly assigned to be the seed of the outbreak (number settable below).

The “mean_noforestdist” field can be calculated with the script “Get non forest landcover in 8 directions.R.”

Output

A `SpatialPointsDataFrame` that is a copy of the input dataframe, with additional fields for dates of infestation and removal (“year_infested” and “year_removed”).

A `SpatialPointsDataFrame` is a dataframe with spatial information for each line, equivalent to a points shapefile in ArcGIS. In most cases, dataframe syntax can be used on it directly; for instance, the `$` operator will work as expected. It can be coerced into a regular dataframe using `as.data.frame`.

The `SpatialPointsDataFrame` can be easily be plotted as a set of points on a map using `plot()`, or used in other spatial analyses. It can also be written out as a shapefile compatible with a variety of GIS software using the “`rgdal`” package in R.

Risk model: determining which trees are infested

Uninfested trees have a certain probability of being infested each timestep, as a function of number of and distance to post-emergence infested source trees and various tree characteristics (see below).

Source trees are trees which are infested, post-emergence, and have not been removed. A tree which is infested is pre-emergence until the lag period has passed (see biology settings of the model). Pre-emergence trees do not infest other trees. The lag period could be set to 0 to remove the pre- and post-emergence distinction.

A tree’s risk is calculated according to the assigned risk model (currently only Long Island’s model (“LI”) is supported).

LI risk model

The Long Island model assesses tree risk as a function of source pressure, DBH of tree, number of nearby Acer neighbors, and landcover.

The probability that a tree will be infested is: