

Prediction of MPB outbreaks using Markov process logistic regression

Past and future project milestones

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Abstract

This vignette provides an abbreviated log of milestones that have been reached and that still need to be reached.

About this document

This document was created using Sweave, a literate programming tool for R. To generate this documentation (i.e. weaving) may require a UNIX platform to allow for system calls. Weaving may take a long time. To speed up repeated weaving intermediate data and figures may be cached. For system requirements see end of document. This document (incl. the source) is available at <https://github.com/mariopineda>.

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Achieved milestones

- Obtained raw red top data from Fangliang He with an email confirmation its Open Data status.
-

Todo milestones

Todo Check on CSI data integrity. BioSim flaked out over parts of BC in the initial runs, need to check that the corrupted data has been removed and replaced by the correct version.

Todo Follow up on CSI data conversion with GIS Analyst

Todo Perform model selection. We would like to use BIC. Mark had an argument for why BIC would be preferred over AIC in this case. Request a copy of AP's write-up on the virtues of BIC.

Todo It appears the nn1 and nn2 variables include the focal location in the summation. Figure out how to deal with this.

Session information

- R version 2.15.1 (2012-06-22), i386-apple-darwin9.8.0
- Locale: C/en_US.UTF-8/C/C/C/C
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Loaded via a namespace (and not attached): tools 2.15.1

The R code in this chapter took 0 seconds to execute, the last time the source file was modified was on 2012-10-15 19:23:58 and the last time the PDF file was modified was on 2012-10-15 18:45:15.



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