

DATA PAPER

Four Rodent and Vole Biodiversity Models for Europe

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The mechanisms underlying associations between rodent diversity and the spread of rodent borne diseases are still unclear. The number of potential host species may influence a disease by either spreading the pathogen (or vectors) more rapidly or conversely by reducing contact with other hosts through the effects of dilution. In either case the number of potential hosts may impact on the distribution of a disease or its vectors. Four spatially modelled indices of rodent species richness have been generated to support distribution modelling of rodent borne diseases specifically initially focusing on Hantaviruses and tick borne diseases.

Keywords: rodent, vole, biodiversity, tick-borne, hantavirus, linear regression, random forest, generalised linear modelling

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(1) Overview**Context****Spatial coverage**

Description: This dataset is clipped to the EDENext¹ extent that covers the continent of Europe and parts of North Africa down to 34 degrees latitude. The projection is WGS84 (ESPG:4326).

Northern boundary: 72.3

Southern boundary: 34.0

Eastern boundary: -12.0

Western boundary: 47.6

Temporal coverage

01/01/2012 (Current)

Species

Striped Field Mouse, *Apodemus agrarius*; Yellow-necked Mouse, *Apodemus flavicollis*; Broad-toothed Field Mouse, *Apodemus mystacinus*; Wood Mouse, *Apodemus sylvatica*; Bank vole, *Clethrionomys glareolus*; Common vole, *Microtus arvalis*; European pine vole, *Microtus subterraneus*; Norway rat, *Rattus norvegicus*; Black Rat, *Rattus rattus*; Common Shrew, *Sorex araneus*; Eurasian Pygmy Shrew, *Sorex minutus*

(2) Methods**Steps****Input Datasets**

- The rodent distribution layers that were modelled models were compiled from several sources as follows:
- The EMMA Database²: Mapping Europe's mammals using data from the Atlas of European Mammals.
- IUCN Red List Dataset³
- The National Biodiversity Network⁴ UK 10k Data- Making all biological records freely and easily available to everyone
- Globcover 2009 Land cover map⁵

Four biodiversity indices - the number of species recorded at a single location - were defined according to different species lists suggested by various experts identified in the Acknowledgements section. The species for each index are identified in Table 1.

Species\Index	sp04no	sp05n0	Hanta10	ters4
<i>Apodemus agrarius</i>	X	X	X	
<i>Apodemus flavicollis</i>	X	X	X	X
<i>Apodemus mystacinus</i>			X	
<i>Apodemus sylvatica</i>		X	X	X
<i>Clethrionomys glareolus</i>	X	X	X	

Species\Index	sp04no	sp05n0	Hanta10	ters4
<i>Microtus arvalis</i>	X	X	X	X
<i>Microtus subterraneus</i>			X	
<i>Rattus norvegicus</i>			X	
<i>Rattus rattus</i>			X	
<i>Sorex araneus</i>			X	X
<i>Sorex minutus</i>			X	

Table 1: Species included in each index are marked with an "X". For more details please see the supporting document (edenextvolelayers.docx) within the data download.

The spatial modelling also requires a comprehensive predictor variable suite which included a wide range of remotely sensed variables as follows:

1. Remotely sensed climatic indicators derived by Temporal Fourier Analysis (TFA) of MODIS satellite imagery of several temperature parameters, and vegetation indices for the period 2001-2008⁶
2. Digital Elevation from the Shuttle Radar Topography Mission, together with derived aspect and ruggedness⁷
3. Fourier Processed Precipitation, and allied Bioclimatic Indicator (Bioclim) precipitation variables from the WORLDCLIM datasets⁸
4. Length of Growing Period from United Nations Food and Agriculture Organisation⁹
5. Travel Time to major towns from the Joint Research Centre at Ispra¹⁰
6. Human population density derived from the Global Rural Urban Mapping project at CEISIN¹¹
7. A weighted human population proximity layer¹²

The four different rodent biodiversity index layers were modelled using a range of techniques:

1. zoned random forest¹⁴ method calculated via the VECMAP¹⁵ modelling system using a point input dataset
2. zoned bootstrapped General Linear Model (GLM)¹⁶ method calculated via VECMAP¹⁵ modelling system using a point input dataset
3. zoned regression calculated using the FARMS¹⁷ modelling suite using an polygon input dataset

An ensemble mean was taken of the three model outputs for each Biodiversity variable.

Output Datasets

Each of the four Biodiversity indices has been provided as a quick look map in JPEG format to view from any image viewer. The data itself is distributed as GIS Raster data in two formats. GeoTIFFs which is a standard proprietary GIS raster format. GeoJP2 (JPEG 2000 format) which is a non-proprietary format. Please note that as the GeoJP2 format is an integer-only format, the values found in this format have been multiplied by 100 to minimise the loss of data.

To access and analyse the Raster data directly GeoTIFFs and GeoJPGs can be read by most GIS software and some other software packages These formats are compatible with proprietary (ESRI ArcGIS) and open source (Quantum GIS (QGIS) or R-project raster package)

Folder Structure

- quicklooks - JPEG maps for viewing only
- tiff - GeoTIFF data 0.008333 degree (~1km) 32bit floating point
- geoJPG2k - GeoJPG 2000, 0.008333 degree (~1km) 16bit unsigned Integer data. ***This data has been multiplied by 100 to save as an integer value with minimum loss of data.***

Sampling Strategy

Sample points were extracted for input into the three different models from a 20km matrix defining the number of key rodent species for each index (as defined in table 1). Depending on the model 1000-2000 sample points were used in each of 25 bootstraps.

Quality Control

These models are a first attempt at quantifying the rodent biodiversity at this scale and there has been no ground truth validation of these maps so far. The model outputs all, however, satisfy standard accuracy metrics (AIC, R squared and Kappa statistic) assuring statistical reliability. They have also been informally reviewed by project Rodent-Borne disease experts.

Constraints

There were no constraints involved in data production.

Privacy

N/A

(3) Dataset Description

Object Name

volebiodiv2.zip

Data Type

Primary data, Processed data, Interpretation of data.

Format Names and Versions

JPG, TIF, TFW, XML

Creation Dates

15/08/2012 - 15/08/2012

Dataset Creators

William Wint, David Morley, Neil S. Alexander.

Repository Location

<http://dx.doi.org/10.5061/dryad.771gr>

Publication Date

08/07/2013

Language

English

License

CC0

(4) Reuse potential

The subject of the effect of rodent biodiversity upon the spread of vector-borne disease is a fairly new topic. These layers are a first attempt to provide a description of rodent biodiversity at a continental scale. They have been developed in the hope they will aid epidemiologists test hypotheses relating to the role of rodent biodiversity' in the spread of infectious disease.

Areas of future development on the dataset itself might be to: assess the accuracy of the maps through ground-truthing; a comparison of the three different models used in this analysis and an assessment of which model provides the most accurate outputs; the application of this approach to different groups of species thought to be related to the spread of different diseases.

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