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Small-Scale Surveillance of Rodent-borne Pathogens – a Simulation Model

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Introduction

The bank vole *Myodes glareolus* is a vole species that occurs almost everywhere in Europe. The population size varies seasonally and outbreaks occur frequently with up to several hundred animals per hectare (1, 2, 5). These outbreaks play a major role in forest habitats through damage in plantations but can also affect public health as bank voles are carriers for zoonotic pathogens. Such pathogens are for example the Puumala virus, a hantavirus causing the majority of human cases of haemorrhagic fever with renal syndrome in northern, western and central Europe (6), and the cowpox virus (4). Human disease caused by hantaviruses and other rodent-borne pathogens are notifiable in many European countries. However, information about the occurrence of these pathogens in reservoirs is often only available as presence/absence data or as prevalence estimates on a limited geographical scale. Importantly, it is often not known whether trapping may have biased the outcome of these reservoir investigations since trapping is non-random sampling, while random sampling is usually an important assumption for standard sample size calculations.

The novel simulation framework described here aims to validate the correctness, especially of negative results for pathogen occurrence. On the basis of abundance data of bank voles a simulation model was developed to show the relation of varying pathogen prevalences and pathogen distributions within the study area with the derived estimates of population density.

Material and method

Study area: trapping of bank voles in a woodland area close to Heimerdingen within the district Böblingen (federal state Baden-Wuerttemberg, Germany)

- **Time period:** spring, summer and autumn 2010 – 2013 and three to five trap inspections per session at about twelve hour intervals
- **Sample size:** 598 rodents captured (or re-captured)
- **Snap-trapping protocol:** 49 Ugglan live traps within a 60x60m study area in a 7x7 trapping grid (3)
- **Population density estimates:** 0 – 174.3 bank voles per ha
- **Probability of trapping:** 22 % - 52 %
- **Mean maximum distance moved for re-captured individuals:** 10.1 and 23.0 m

Figure 1: Field work (Source: C. Imholt)

Simulation study:

- Abundance data of bank voles within the study plot were used to develop a simulation concept for small-scale surveillance of rodent-borne pathogens

Assumptions:

- Number of individuals as fixed parameter depending on estimated **population density** and **constant** during simulation
- **Distribution of population**: random or clustered
- Additional cells around the trap grid to manage boundary effects
- **Distribution of infection**: random or clustered
- Pathogen prevalence as parameter constant during simulation

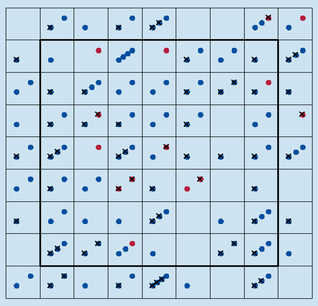

Figure 2: Example for a simulated infection with 10 % prevalence within a population with estimated density of 174.3 individuals per ha. The trapping probability was assumed to 44 %.

Results

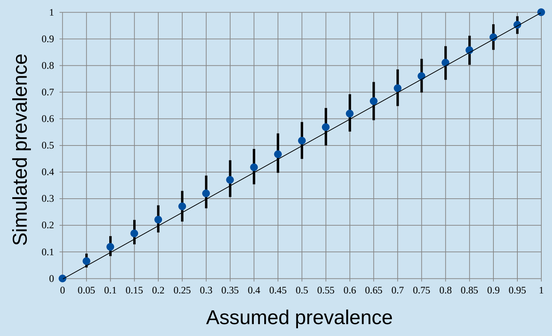

Figure 3: Example for simulation output for a randomly distributed infection with 10 % prevalence within a population with estimated density of 174.3 individuals per ha. The trapping probability was assumed to 44 %.

Table 1: Abundance data as base for a simulated randomly distributed infection with 5 % prevalence within different scenarios regarding population densitiy estimations and trapping probabilities and life trapping.

	No. of trap inspections	Estimated population density (per ha)	Trapping probability	Simulated prevalence	Width of 95 % confidence interval	Simulated prevalence	Width of 95 % confidence interval
				Assumed prevalence 5 %		Assumed prevalence 50 %	
Summer 2010	4	174.30	0.44	0.06512471	0.05212054	0.5178071	0.13895993
Autumn 2010	5	109.30	0.29	0.07251926	0.08875	0.53024053	0.2358176
Spring 2011	3	-	-	-	-	-	-
Summer 2011	5	56.90	0.35	0.07403868	0.07598039	0.5403984	0.26082536
Autumn 2011	5	153.34	0.22	0.07758882	0.09778226	0.53573831	0.25
Spring 2012	5	133.58	0.38	0.06825817	0.06416667	0.52988582	0.17324263
Summer 2012	5	80.10	0.29	0.07831709	0.1006494	0.53954321	0.2680758
Autumn 2012	5	36.40	0.52	0.0543722	0.02508013	0.5213286	0.23796791
Spring 2013	5	-	-	-	-	-	-
Summer 2013	5	19.20	0.25	0.1265294	0.25	0.5801772	0.5

Discussion

- Simulated prevalences for randomly infected individuals reflect the assumed values (see for example Figure 3) with a high degree of accuracy, if
  - the value for the population density estimates are large
  - the trapping probability is moderate to high

  } Depending on the considered population **non-influenceable**
  - at least three to five trap inspections were performed
  - live traps for multiple trapping per grid

  } **influenceable**
- High population density variability and trapping probability, which often occurs in the field, pose problems not only for low pathogen prevalences (see Table 1)
- Repeated trap inspections enable to detect even low prevalences
- Low prevalences in clustered pathogen distribution scenarios were difficult to detect as compared to randomly spread positive individuals with the same assumed model prevalence
- In the future, the model will be adapted to special pathogens with their detection characteristics in diagnostic tests due to the fact that sensitivity and specificity are expected to influence the results
- Furthermore, different trapping techniques, cluster scenarios resulting from different transmission and contact structures will be evaluated

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Please contact Marie-Pierre.Ryser@vetsuisse.unibe.ch if you would like to download the Snap trapping standard protocol (3) (please indicate “APHAEA” in the email title) and register as external partner.