Paul.Johnson@glasgow.ac.uk @paulcdjo

University of Glasgow

Zoonoses & Emerging Livestock Systems

A model of inter-market livestock movement in northern Tanzania: exploiting routinely collected data to investigate infectious disease transmission

Introduction

Background

- Inter-market livestock movements can spread disease rapidly and over long distances.
- Surveillance and control measures depend on knowledge of the market movement network, which is seldom available in developing countries.

Aims (as part of the SEEDZ project: tinyurl.com/SEEDZproject)

- Collect, clean and model livestock movement data from routinely collected permits in northern Tanzania (Fig. 1).
- Identify characteristics of origins and destinations associated with livestock movement.
- Infer inter-market movement networks for cattle and small ruminants (only results for cattle shown here).
- Develop a simulation model of livestock movement that will provide the basis for a model of infectious disease spread.

Authors: Johnson PCD[1]*, Chaters GL[1]*, de Glanville WA[1], Davis A[1], Yoder J[2], Halliday JEB[1], Lankester F[2], Buza J[3], Nyasebwa OM[4], Swai E[4], Cleaveland S[1], Matthews L[1], Kao R[5]
[1]University of Glasgow, UK; [2]Washington State University, USA; [3]NM-AIST, Tanzania; [4]Ministry of Agriculture, Tanzania; [5]University of Edinburgh
*PJ & GC contributed equally to this work

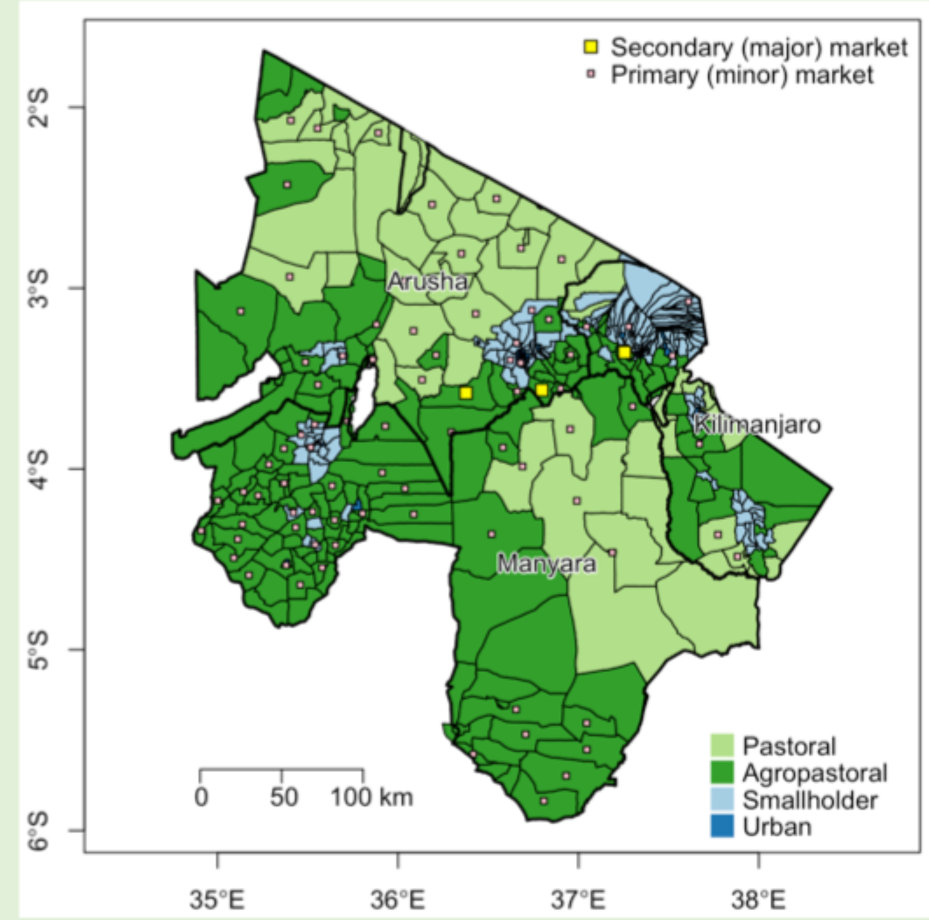


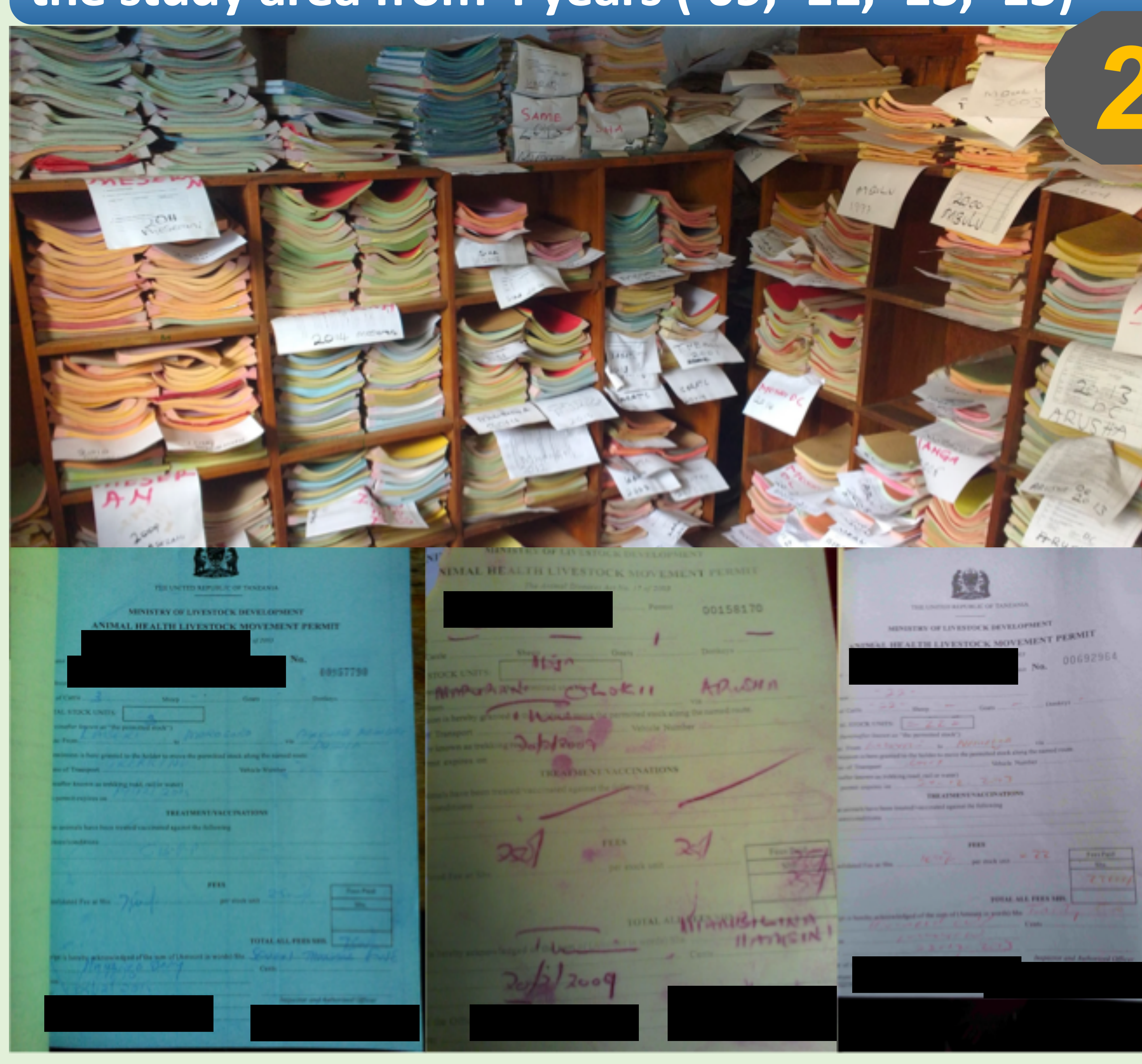
Fig. 1. The study area: Arusha, Manyara & Kilimanjaro regions in northern Tanzania. Wards (administrative areas with population ~12,000) are shaded by agro-ecological system (a preliminary classification; see WDG's talk, Salon C-D, Mon 25 June, 10:30-12:15). Wards containing primary and secondary markets are indicated.

Methods

Follow the data processing and modelling pipeline, starting at 1

1 **Livestock leaving a market generate movement permits**, recording origin market, destination, date, species and number of animals.

2 **We collected all ~60,000 movement permits in the study area from 4 years ('09, '11, '13, '15)**



3 **Raw data:** 56,849 photographed permits + 5,045 entered manually, from which we cleaned a 45% stratified sub-sample.

We're grateful to Rigobert Tarimo, Robert Chuwa and Sambeke Kiruswa for data entry.

4 **Cleaned data:** 17,841 movements of 160,590 animals

5 **Merge movements by ward & by month**, giving inter-ward movement networks for all 48 months (78,956 cattle and 35,106 small ruminants), restricted to within-study-area movements. Below is an example network for 1 month for 3 origin wards & 3 destination wards:

N cattle moved Jan 2009		Destination ward		
		Elerai	Kikatiti	Kiusa
Origin ward	Bwawani	32	0	0
	Meserani	1	0	0
	Naberera	0	14	0

6 **Are the zeroes in the network above real, or due to missing permits?** Use a zero-inflated GLM† to decide.

7 **Model inter-ward livestock movement** as a two-step process:

1. Model the *probability* of any movement between two wards in a given month as a binomial GLMM†.
2. Model the *number* of animals moved (≥1) given any movement as a zero-truncated negative binomial GLMM†.

This two-step (hurdle) model allows movement to depend on the *distance* between origin and destination wards and their *masses* (population sizes), in addition to other characteristics (Table 1), so can be viewed as a gravity model of the livestock movement network.

8 **Finally, simulate monthly inter-ward livestock movements from the model**, imputing missing data identified in step 6 (Fig. 2).

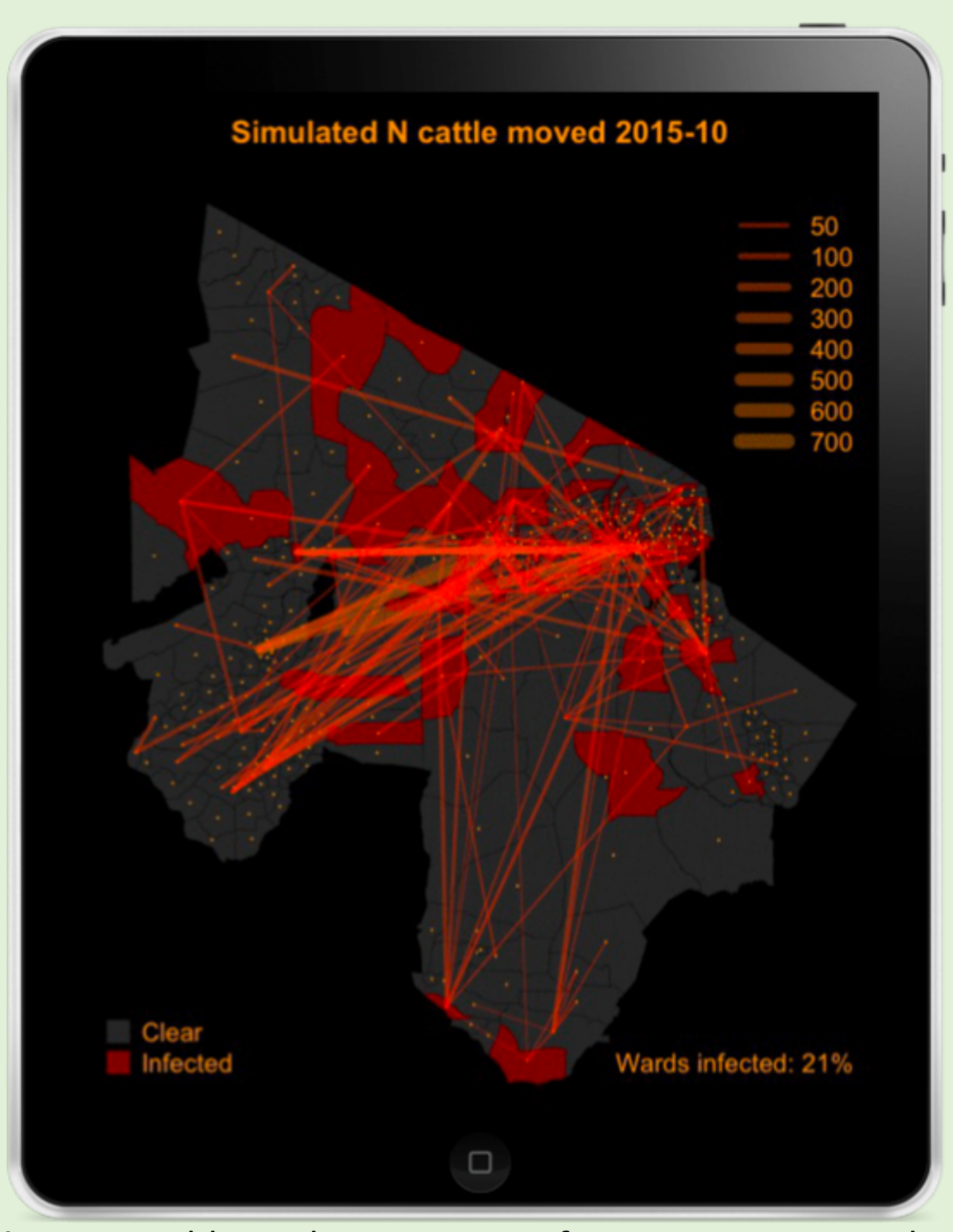
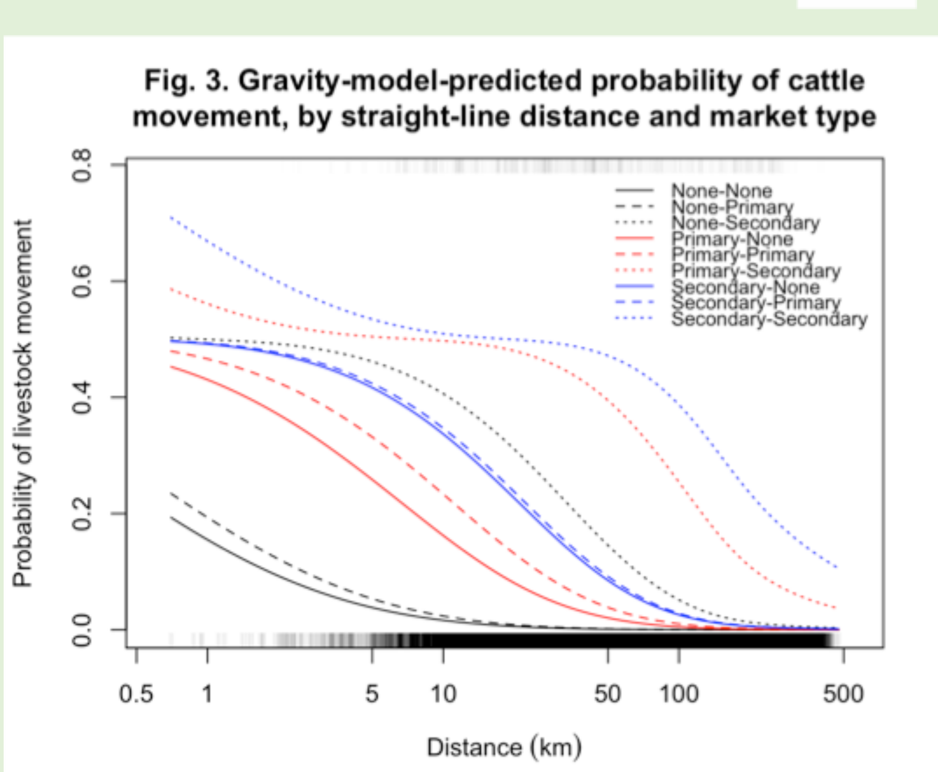


Fig. 2. Monthly cattle movements for one year among the 398 wards in the study area, simulated from the model described in 7. For illustration, a simple infectious disease model is superimposed on the movement network: a destination ward is infected by an origin ward if $(1 - p)^N < 0.5$ (p: probability of an animal transmitting infection from an infected origin ward to an infection-free destination ward, p = 5%; N: number of cattle moved).

If the dynamic network animation is not running you can watch it at ***tinyurl.com/cattle-net*** *or scan the QR code →*



Results

The model explained a substantial proportion of spatial and temporal variation in cattle movement, with movement being more likely over short distances and into wards containing a secondary market (Table 1; Fig. 3).

Conclusions

- It is feasible to use routinely collected data to infer livestock movement networks in a developing country setting.
- We will use these network models to underpin models of disease dynamics to address questions around livestock movement and zoonotic disease risk, such as how pathogen dynamics might respond to interventions or social, economic and environmental change. **To find out more, see poster 437 (Chaters *et al.*).**

Table 1. Predictors of monthly inter-ward cattle movement. Strong (effect > 10%) and significant (P < 0.05) associations are underlined.
Continuous predictors were fitted as natural cubic splines with 3 d.f. Random effects were fitted for origin and destination ward and time period (48 months). Effect: reduction in MSS† when predictor is removed. R^2_{LATENT}: proportion of spatial and temporal variation explained by the predictors.

	Model stage predicting probability of movement (R^2_{LATENT} = 41%)		Model stage predicting number of animals moved (R^2_{LATENT} = 23%)	
Predictor	Effect	P-value	Effect	P-value
$\log_{10}$(**distance**/km) [spline]	57%	0.000	-1%	0.000
$\log_{10}$(**origin human pop. size**) [spline]	5%	0.024	23%	0.057
$\log_{10}$(**destination human pop. size**) [spline]	14%	0.000	0%	0.248
$\log_{10}$(**origin cattle pop. size** [GWA†]) [spline]	0%	0.974	0%	0.343
$\log_{10}$(**destination cattle pop. size** [GWA†]) [spline]	0%	0.963	4%	0.388
$\log_{10}$(**origin area**/km^2) [spline]	1%	0.289	9%	0.826
$\log_{10}$(**destination area**/km^2) [spline]	2%	0.023	-1%	0.398
Calendar month [spline]	0%	0.086	4%	0.000
Year [categorical]	3%	0.000	3%	0.000
1ary/2ary market in origin/destn? [categorical]	26%	0.000	27%	0.000
Origin agro-ecological system [categorical]	6%	0.035	30%	0.049
Destination agro-ecological system [categorical]	6%	0.000	2%	0.658

†GLM: generalised linear model; GLMM: generalised linear mixed-effects model; MSS: model sum of squares; GLW: Gridded livestock of the world 2007

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