# Herd management and response to livestock disease losses in livestock-dependent households of northern Tanzania

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## Acknowledgements

This work was supported by funding from the Biotechnology and Biological Sciences Research Council, the Department for International Development, the Economic & Social Research Council, the Medical Research Council, the Natural Environment Research Council and the Defence Science & Technology Laboratory, under the Zoonoses and Emerging Livestock Systems programme (grant no: BB/L018926/1)

We would like to thank Phillip Wandschneider, Benjamin Cowan, Thomas Marsh, Nicholas Hanley and participants of 168th EAAE Seminar for extremely helpful comments.

## Abstract

Livestock-dependent households in East Africa face substantial livestock disease risk and use various livestock management strategies in response. This article examines the relationships between disease-related livestock death and abortion, and vaccination and herd restocking decisions. We develop a theoretical model and derive testable hypotheses about the relationships between these outcomes and practices, and test them using a system of econometric regressions. We find that herd owners restock in response to disease-related death and abortions, but replacement is less than one-for-one, suggesting the presence of credit constraints and households' limited ability to insure against catastrophic events. We also find modest evidence of cattle restocking as a contributor to higher cattle disease death, presumably through inter-herd disease transmission. Lastly, our results suggest moderate effects of vaccinations for reducing disease deaths in small stock. Policy implications are discussed in light of the connection between animal health and poverty alleviation in livestock-dependent households.

## Introduction

Livestock keepers in East Africa often live with precarious environmental and economic conditions and use a variety of risk management practices in the face of weather variability and disease risk (Little et al. 2001; Smith, Barrett and Box 2000; Bailey et al. 1999). Livestock disease and health outcomes depend on a host of environmental factors and household herd management decisions. Management strategies like livestock quarantine and vaccination can limit individual animal exposure and susceptibility and are valuable measures to prevent diseases that negatively affect households (Marsh et al. 2016).

When livestock losses do occur, replacing livestock (restocking by introduction of new animals into the herd) after a death or an abortion through purchase, lending, or by gift receipts within informal social networks is common and important household strategy for herd maintenance (McPeak and Barrett 2001; McPeak 2006; Toth 2015). However, livestock introductions from outside the herd can also be a source of infectious disease (Fèvre et. al 2001; Gardener, Willeberg and Mousing 2007; Marshall, Carpender and Thunes 2009). This risk of pathogen transmission and consequent losses due to restocking may be more acute in pastoral areas where herds are grazed communally and access to veterinary services is limited (Inagolet et al. 2008; Selby et al. 2013).

This paper examines the relationships between livestock management practices and disease-related livestock losses based on primary survey-based cross-sectional data collected in northern Tanzania. We focus specifically on livestock death due to disease and abortion, and management in the form of vaccination for illness prevention and animal introduction decisions for herd maintenance. To examine these relationships, we develop a theoretical model of livestock management decisions in the context of herd disease challenge, and derive a set of testable hypotheses relating to the objectives above. Because livestock health management practices are theoretically responsive to disease and illness risk through herd owner disease management incentives, management activities and disease outcomes are jointly determined. Therefore, a system of econometric regression equations is developed and used to test the hypotheses about livestock introductions and vaccination, and their relationship with livestock abortions and disease-related deaths.

Using our econometric regression strategy, we test whether: (i) animal introductions are related to increased abortion incidence and disease-related deaths in a herd; (ii) whether disease prevention in the form of vaccinations curtails livestock death due to disease; (iii) whether the demand for animal introductions responds to abortion incidence and livestock deaths due to disease in herds.

We find that herd owners restock in response to disease-related deaths and abortions, but replacement is less than one-for-one. The magnitude of introductions is smaller than the size of negative asset shocks in our data, which may indicate households' limited ability to insure against negative shocks to the herd. Further, restocking may not just be costly in terms of replacement costs, but is potentially also a contributor to livestock disease deaths, presumably as an inter-herd disease transmission mechanism. Finally, we find evidence that vaccinations are moderately effective in reducing disease death rates in small stock, suggesting that vaccination availability and use may improve herd and household welfare; however, no sampled household vaccinated against more than three livestock diseases, possibly due to credit constraints and lack of vaccine availability or access to veterinary services. These results have important policy implications in terms reaching the goal of healthier livestock, which is critical in multidimensional poverty alleviation through various channels like wealth, income, health and nutrition in livestock-dependent households.

While livestock acquisition and herd dynamics are extensively studied in relation to poverty, poverty traps and consumption smoothing (Fafchamps et al. 1998; Kazianga and Udry 2006; Lybbert et al. 2004; Barrett 2005; Carter and Barrett 2006; Santos and Barrett 2016), the literature on demand for vaccinations, herd introductions and its relationship with animal health outcomes is scant. We present a novel integrated model of herd restocking, vaccination decisions and disease-related death and abortion outcomes, and econometrically address the feedback mechanisms between these management decisions and economic outcomes by using a set of simultaneous regression equations. To our knowledge, this simultaneous interaction between disease risk, restocking and vaccination decisions and outcomes has not been explored in this way in the literature.

## A Model of Vaccination Use and Livestock Introductions

A theoretical model of the relationship between livestock introductions, disease outcomes, and vaccination is developed next as a foundation for deriving hypotheses and to guide estimation. We assume that households act as if to maximize net herd value by utilizing quasi-fixed inputs such as available labor and accessible land, livestock vaccination investments and herd introductions, where herd introductions can be both a response to disease losses and a source of disease introduction into the herd. Although not a focus of this paper, we also account for drought losses because they can be substantial in these environments and we capture them in our data.

For simplicity we assume one livestock type, and combine disease-related deaths and/or abortions into a general concept of livestock loss, but we later distinguish these for estimation.[1] To support our analysis based on cross sectional data in a parsimonious framework, we develop a static model that focuses attention on how the potential for livestock disease or drought loss provide an incentive to both vaccinate to reduce loss, and to introduce animals for portfolio management and/or loss replacement. The household's decision problem is characterized as

$$\max_{l,v,n} \ \pi = p(y(l;k) + n)\big(1 - \delta(v,n;g,\rho,\gamma)\big) - mn - cv - wl - r, \qquad (1)$$

where $p$ is the marginal value of an animal to the household in terms of its productivity in the herd, $y$ is the "initial" herd size prior to introductions and losses, which might be thought of as a target or preferred herd size in the absence of livestock losses. Labor available for husbandry, $l$, and carrying capacity, $k$, are quasi-fixed with respect to herd size decisions, therefore $y$ is quasi-fixed in the model. The loss rate, $\delta(\cdot) \in [0,1]$, is the fraction of animal units lost by drought and disease through abortions and/or death. Vaccinations, $v$, reduce losses at decreasing rate ($\delta_v < 0, \delta_{vv} > 0$), marginal losses from introductions, $n$, are assumed to increase at an increasing rate ($\delta_n > 0, \delta_{nn} > 0$), and the marginal value of vaccinations increases with increase in introductions (assuming symmetry, $\delta_{vn} = \delta_{nv} > 0$), where subscripts indicate partial derivatives.[2] The loss rate is also assumed to be positively associated with a background disease burden $\rho$, ($\delta_\rho > 0$); general grazing/feeding practices, $g$, ($\delta_g > 0$) that we take as quasi-

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[1] While assuming one livestock type reduces the dimensionality of the problem, it is worth noting that animal introductions will have differentiated demands based on species, sex, and breed. Furthermore, livestock markets may sell predominantly male cattle and finding a healthy female cattle replacement through market mechanisms might be difficult. In other words, market for female cattle may be plagued by the 'lemons problem' (Akerlof 1970). In the following sections, we disaggregate livestock type by species but our data does not allow disaggregation by sex.

[2] We do not model the uncertainty or variance associated with the loss function, $\delta$. The model therefore does not capture the producer's management behavior resulting from uncertainty associated with death loss.

fixed and related to land tenure and cultural norms such as communal or zero grazing; and rainfall, $\gamma$, which we assume reduces losses $\left(\delta_\gamma < 0\right)$. General livestock grazing practices, $g$ and introductions, $n$, capture inter-herd contact, which is related to disease prevalence in the region (Bronsvoort et al., 2004; Rufael et al., 2008; Schoonman and Swai, 2010). The marginal cost of an introduction is $m$ (e.g. the market price of an animal), $c$ is the marginal cost of vaccination, $w$ is the cost of labor and $r$ represent any purely fixed costs such as land or capital rent applicable to the livestock enterprise.

The first-order necessary conditions for maximizing with respect to $v, n$ and $l$ are

$$\frac{\partial \pi}{\partial v} = -p\delta_v(y+n) - c = 0 \tag{2}$$

$$\frac{\partial \pi}{\partial n} = p(1-\delta) - p\delta_n(y+n) - m = 0 \tag{3}$$

$$\frac{\partial \pi}{\partial l} = py_l(1-\delta) - w = 0. \tag{4}$$

Equation 2 implies that households choose to vaccinate to the point that the marginal benefit of vaccinations in terms of loss mitigation,$-p\delta_v(y+n),$ is equal to the marginal cost of vaccinations, $c$. Equation 3 implies that households will supplement after-loss herd size with introductions as long as the purchase cost is no greater than the in-herd value net of disease losses to introductions $(p(1-\delta))$ plus the marginal cost of disease transmission due to herd introduction, $-p\delta_n(y+n)$. Equation 4 implies that households choose to allocate labor for livestock management to the point that marginal revenue product, $py_l(1-\delta)$, is equal to the marginal cost of labor, $w$.[3]

Given exogenous factors $\boldsymbol{\theta} = (p, m, c, w, g, \rho, k, \gamma)$, the first-order conditions (Equations 2 and 3) implicitly define the optimal demand functions for vaccinations, $v^* = v(\boldsymbol{\theta})$, and

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[3] Second-order sufficient conditions for a maximum are available from the corresponding author.

introductions, $n^* = n(\boldsymbol{\theta})$, which in-turn implies endogenous damage rate $\delta^* = \delta(v^*, n^*; g, \rho, \gamma) \equiv \delta(\boldsymbol{\theta})$. Background disease risk $\rho$, weather $\gamma$, and general grazing practices $g$ have both direct effects on loss rates and indirect effects through vaccination and reintroduction demands. One might expect, for example, that a higher background disease risk $\rho$ would instigate more vaccination through its effect on the value of the marginal product of vaccination (for example), which would partially offset the disease losses that would otherwise accrue through the direct effect of background disease risk. To the extent that communal grazing heightens herd interactions and disease transmission, herd loss and subsequent animal acquisition for replacement may lead to an additional (indirect) herd infection risk.

Livestock loss from illness is $L^* = \delta^*(y^* + n^*)$, and depends on endogenous introductions and vaccination use. The value of disease losses would be $pL^* = p\delta^*(y^* + n^*)$. Equation 4 implicitly defines the optimal demand function for labor, $l^* = l(\boldsymbol{\theta})$.

Several hypotheses and implications for empirical strategies follow. Vaccinations reduce disease losses by $\frac{\partial L^*}{\partial v^*} = p\delta_v(y^* + n^*) < 0$, and this value is larger when the value of the herd is large, suggesting the following hypotheses:

*Hypothesis 1: Disease losses are negatively related to vaccinations.*

*Hypothesis 2: Vaccination use is positively related to the value of the herd.*

The marginal effect of herd introductions $n^*$ on losses $L^*$ evaluated at $v^*, l^*$ and $n^*$ is represented by $\frac{\partial L^*}{\partial n^*} = \delta_n(y^* + n^*) + \delta^* > 0$, suggesting:

*Hypothesis 3: Increase in herd introductions are positively associated with increase in disease losses.*

Further, after a catastrophic event, households may introduce animals in the herd to maintain or grow the pre-loss herd size. Assuming no substantive liquidity constraints and approximately efficient markets, equilibrium introductions in the herd will equal the disease losses if pre-loss herd size is to be maintained, i.e., $n^* = \delta^*(y^* + n^*), \ \Rightarrow n^* = \frac{\delta^*}{1-\delta^*}y$. This equation can help us derive the relationship between introductions and fraction of losses, evaluated at $v^*, L^*$ and $n^*$, as $\frac{\partial n^*}{\partial \delta^*} = \frac{1}{(1-\delta^*)^2} > 0$, which implies our fourth hypothesis:

*Hypothesis 4: Increase in disease losses are related to an increase in the demand for animal introductions.*

While the hypotheses derived from the model are intuitive, this model highlights two issues that are important for guiding empirical methodology. First, $v^* = v(\boldsymbol{\theta})$ and introductions $n^* = n(\boldsymbol{\theta})$ are endogenous choices, driven by exogenous biophysical and economic factors. Disease losses $L^* = L(v^*, n^*, l^*; g, \rho, k, \gamma)$ are directly affected by management decisions and a set of exogenous household characteristics and disease conditions, and indirectly affected through management decisions by a broader set of exogenous variables. The endogeneity of vaccinations and introductions as components of the set of factors affecting disease losses has important implications for econometric estimation strategy, but because the specifics of the available data also inform estimation strategy, a description of the data is provided next. Second, the hypotheses each reflect model-based correlations between two endogenous variables conditional on exogenous factors. Thus, while we utilize regression methods to control for exogenous factors in assessing relationship, our regression results relating directly to hypotheses 1 through 4 should not be interpreted as implying direct causality in any given direction.

## Data

Data were collected as part of the "Social, Economic and Environmental Drivers of Zoonotic Disease in Tanzania" (SEEDZ) project. This was a cross-sectional survey conducted across six districts in Arusha Region (Arusha, Karatu, Longido, Meru, Monduli, and Ngorongoro Districts) and four districts in Manyara Region (Babati Rural, Babati Urban, Mbulu, and Simanjiro Districts) between January and December, 2016. A multistage sampling design was used. Villages were selected from a spatially referenced list of all villages in the study area (from the Tanzanian National Bureau of Statistics (NBS)) using a generalised random tessalation stratified sampling (GRTS) approach (Stevens and Olsen 2004). Within each village, two to three sub-villages were randomly selected, and data collection was performed at a central point within each village (up to 10 households were included in each sub-village based on willingness to participate.) In total, data were collected from 404 households in 49 sub-villages, and the dataset is made up of one record (observation) per household collected from a questionnaire survey conducted with the household head.[4]

Table 1 describes the variables used in the analysis, and Table 2 provides summary statistics. *Vaccinations* ($v$ in our theoretical model) is the count of vaccine types used for different diseases within a household (variable names are presented in italics throughout). The diseases covered by these vaccinations include anthrax, foot and mouth disease, lumpy skin disease, black quarter, East Coast fever, contagious bovine pleuro-pneumonia, peste de petis ruminants, and Rift Valley fever.[5] *Vaccinations* range from zero to three, which implies that

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[4] All participants conducting questionnaires provided written informed consent. The protocols, questionnaire and consent procedures were approved by the ethical review committees of the Kilimanjaro Christian Medical Centre (KCMC/832) and National Institute of Medical Research (NIMR/2028) in Tanzania, and in the UK by the ethical review committee of the College of Medical, Veterinary and Life Sciences, University of Glasgow.

[5] No Rift Valley fever vaccine was licensed in Tanzania at the time of the study. However, the vaccine may have been acquired across the border from Kenya. There can be potential recall bias in vaccination reporting as households may not know which diseases have animals been vaccinated against or may forget.

although vaccinations are being used, they do not cover the wide range of livestock diseases faced by households. Of the households in our sample, 81.5 percent reported having not vaccinated their livestock in the last 12 months, 16 percent reported using one type of vaccine, 2.5 percent reported using 2, and 1 percent reported using three. The most frequently used vaccines were for contagious bovine pleuro-pneumonia and anthrax, followed by vaccines for lumpy skin disease and foot-and-mouth disease.

Our analytical model focuses on general disease losses $L^{*} = L(v^{*}, n^{*}, l^{*}; g, \rho, k, \gamma)$. Our data distinguish between livestock abortions and other livestock deaths. Average $Total$ *Disease Deaths* in the past 12 months in the sample is 11.15 animals (including cattle, sheep, and goats). Mean deaths due to drought are about 9 animals in the preceding year. The average number of *Livestock Abortions* reported in the past 12 months by the household is 3.04 (Table 2).

Only one livestock type is distinguished in the analytical model, but our data distinguish between *Cattle* and *Shoats* (sheep and goats). *[Cattle, Shoats] Introductions* (represented by $n$) are count variables for the number of livestock of each type introduced into the herd from any source in the past 12 months. Sources of animal introductions include purchases from the livestock market, borrowing, and gifts from informal networks of kin in our sample. *Cattle* and *Shoats Introductions* means are 1.61 and 2.17, respectively (Table 2).

The mean gross herd size (net of introductions, $y$ in our model) are 53 and 95 for cattle and sheep and goats, respectively, and are represented by the variables *Cattle* and *Shoats*. The initial or target herd size $y(l; k)$ is a function of labor available for herd management, $l$, and land and capital resources available to the household, $k$. In northern Tanzania where our sample is taken, herds are generally managed by the family, and land tenure for local support of the herd, regardless of the land tenure characteristics available (e.g. private holdings or communal holdings) is relatively inflexible relative to short-term herd losses. We therefore focus on land ownership, household size and fixed assets as quasi-fixed determinants of initial herd size.

*Land Owned* is the amount of cropland and grazing land owned by the household, and averages about 9 acres per household in our sample. We use this variable as a proxy for resources available for supporting a herd, and hypothesize that it might contribute to herd size decisions. We utilize a set of variables relating to grazing and watering practices, which we hypothesize may affect disease transmission through inter-herd contact. On average in our sample, households cover about 10 kilometers of *Transhumance Distance* seasonally to find suitable grazing areas, and they travel, on average, for about an hour daily for grazing and watering purposes (*Grazing Time* and *Watering Time*, respectively). To capture the village-level disease environment within which each household resides, we create *Sub-Village Vaccination*, *Sub-Village Disease Deaths* and *Sub-Village Abortion* rates. Table 1 provides information on how these sub-village averages for vaccinations, disease deaths and abortions are created. These variables help as exogenous instruments in the identification of our endogenous variables.[6]

## Estimation

To test our hypotheses and estimate the relationships between management and disease outcomes, we estimate (i) the effect of disease prevention (vaccinations) on abortions and disease deaths, (ii) the demand for animal introductions in response to abortions and disease-related deaths in a herd and (iii) the effect of herd accumulation on abortions and disease-related deaths.

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[6] Note that the intent of these sub-village means is to capture by proxy the regional disease burden based on household outcomes beyond the control of the household represented by a given record. It is not an attempt to infer how the behavior of other households in the village affects the behavior of the household in question, and as such does not directly implicate the reflection effect identified by Manski (1993).

The theoretical model suggests a system of equations and a strategy for identifying the drivers of management decisions. Our data distinguish between abortion and death, so let $L = (d, a)$, where $d$ is *[Stock] Disease Deaths* and $a$ is *[Stock] Abortions*, where *Stock* refers to *Cattle* or *Shoats*. Introductions in our data are specific to livestock type, so redefine $n$ as the vector $\boldsymbol{n}$ includes *Cattle Introductions* and *Shoat Introductions*. Together, the analytical model and data suggest five sets of equations that provide a basis for testing our hypotheses and estimating relationships (bold variables indicate a vector of variables):

$$v = f_v(\boldsymbol{n}^*, d^*, \mathbf{y}^*, Z_1, \boldsymbol{Z_2}; \varepsilon_v) \tag{5$a$}$$
$$\boldsymbol{n} = f_n(d^*, a^*, \boldsymbol{y}^*, \boldsymbol{Z_3}; \varepsilon_n) \tag{5b}$$
$$\boldsymbol{d} = f_d(v^*, \boldsymbol{n}^*, \boldsymbol{y}^*, \boldsymbol{Z_2}, Z_4; \varepsilon_d) \tag{5c}$$
$$\boldsymbol{a} = f_a(\boldsymbol{n}^*, \boldsymbol{y}^*, \boldsymbol{Z_2}, Z_5; \varepsilon_a). \tag{5d}$$
$$\mathbf{y} = f_y\big(\mathbf{Z_6}; \varepsilon_y\big). \tag{5e}$$

*Vaccinations* $(v)$ and *Cattle* and *Shoats Introductions* $(\boldsymbol{n})$ are management decisions, whereas *[Stock] Disease Deaths* $(\boldsymbol{d})$ and *[Stock] Abortions* $(\boldsymbol{a})$ are outcomes. Furthermore, management decisions and outcomes depend on gross herd size, $\boldsymbol{y}$, which is endogenized in the system and depends on a host of exogenous and quasi-fixed factors. As in the analytical model, the asterisks associated with each of them on the right-hand-side of the equations are intended to highlight that these variables are endogenously determined within the system as a function of several sets of exogenous variables $\boldsymbol{Z}_i$, representing factors affecting management choices, where:

$Z_1$ = leave-out Sub-Village Vaccination averages
$\boldsymbol{Z}_2$ = Grazing Time, Watering Time, and Transhumance Distance
$\boldsymbol{Z}_3$ = Cattle, Sheep & Goat Drought Deaths; Land Owned & Household Size
$Z_4$ = Sub-Village Disease Death
$Z_5$ = Sub-Village Abortion
$\boldsymbol{Z_6}$ = Household Size, Compound Size, Land Owned, Maasai Ethnicity, Electricity

$Z_1 - Z_6$ are assumed to be exogenous covariates that satisfy rank conditions and exclusion restrictions. Discussion of each exclusion restriction follows with description of each of the above equation. Unobserved, random elements $\varepsilon_i$ in Equations 5a-5e are included to recognize random elements of the associated regression estimated below. Figure 1 illustrates the relationships embodied in these equations.

Vaccination demand $v$ (Equation 5a) depends on introductions ($\boldsymbol{n}$) of sheep/goats and cattle, respectively, *Disease Deaths* ($\boldsymbol{d}$), pre-existing herd size ($\boldsymbol{y}$), and a set of exogenous variables that directly impact incentives to vaccinate, including grazing practices ($\boldsymbol{Z}_2$), which we hypothesize to be correlated with disease transmission risk. The leave-out *Sub-Village Vaccination* average ($Z_1$) is exogenous to the household's vaccination decisions and included in the equation to account for sub-village level exogenous factors affecting local supply of vaccinations and factors affecting general vaccination demand in the sub-village (e.g. general information and acceptance of vaccinations in the area).[7] Introductions may drive vaccination use if introduced livestock are regularly vaccinated; and introductions may introduce disease in the herd, indirectly increasing demand for vaccination. Because of the cross-sectional nature of our data, we hypothesize that *Total Disease Deaths* and *Vaccinations* simultaneously affect each other in that deaths provide information feedback on disease risk and therefore affect vaccination demand, and vaccinations may directly affect disease losses through the inoculation effect within the survey recall time frame.

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[7] In addition to vaccinations, quarantine practices like separating the newly introduced animal from herd to identify disease symptoms or treatment with acaricide or anthelmintics prior to introduction can also be important disease prevention strategies, but our data do not allow us to capture these practices with any accuracy. Vaccination rates also depend on vaccination supply factors such as ease of access and cost. However, our data are limited in this regard.

*Introductions* $\boldsymbol{n}$ (Equation 5b) depend on endogenous variables *Total Disease Death* $(d)$ and *Livestock Abortions* $(a)$, herd sizes $(\boldsymbol{y})$, and livestock drought deaths, owned land and the number of household members $(\boldsymbol{Z}_3)$. Livestock losses $(d$ and $a)$ are included as direct determinants of *Introductions* because owners may replace lost animals by acquiring replacements from outside the herd in the event of a livestock death or the abortion, which represents the loss of an expected introduction from within the herd. $\boldsymbol{Z_3}$ captures the exogenous drought shocks and carrying capacity of households through land and number of household members, which is expected to directly affect *Introductions*.

*[Stock] Disease Death* $(\boldsymbol{d})$ in Equation 5c depends on *Vaccinations* $(v)$, *Introductions* $(\boldsymbol{n})$, herd sizes $(\boldsymbol{y})$, grazing and watering practices $(\boldsymbol{Z}_2)$, and *Sub-Village Disease Death* $(Z_4)$. $Z_4$ and $\boldsymbol{Z_2}$ are the exclusion restrictions for this equation. *[Stock] Disease Death* $(\boldsymbol{d})$ is directly affected by the exogenous environmental disease burden faced by household captured through *Sub-village Disease Death* $(Z_4)$ and grazing and watering practices $(\boldsymbol{Z}_2)$ which captures disease transmission risk through herd contact.

In Equation 4d, *[Stock] Abortions* $(\boldsymbol{a})$ depend on livestock introductions $(\boldsymbol{n})$, herd sizes $(\boldsymbol{y})$, grazing and watering distances $(\boldsymbol{Z}_2)$**,** and the leave-out sub-village abortion average, *Sub-Village Abortion* $(Z_5)$. Like Equation 5c, exclusion restriction is the exogenous environmental disease burden, captured through leave-out sub-village abortion averages. *Introductions* are included in Equations 5c and 5d because the introduction of livestock from outside the herd may also lead to disease introduction into the herd, and therefore higher disease-related livestock death and abortion rates. Livestock introductions are unique in our modeling framework because they have a clear bi-directional relationship with disease outcomes: introductions may be a response to loss, and may also increase loss rates.

Lastly, herd sizes ($\boldsymbol{y}$) in each equation depend on quasi-fixed labor available for animal husbandry, available land and capital represented by vector $\boldsymbol{Z_6}$.

Endogeneity of regressors may lead to biased and statistically inconsistent parameter estimates, and false inference. For example, while vaccinations are expected to reduce livestock disease losses, they are likely to be used more where the prevalence of the related disease is highest, potentially leading to a positive correlation between vaccination and livestock losses in the data even if vaccinations are largely effective at reducing losses.

A standard two-stage instrumental variable approach is therefore used. The two-stage process is as follows (Green 2011). In stage 1, reduced form equations for $v, \boldsymbol{n}, \boldsymbol{d}, \boldsymbol{a}$ and $\boldsymbol{y}$ are estimated first based only on exogenous variables in the system, omitting the left-hand-side endogenous variables, and including additional exogenous variables in the system. In stage 2, the predicted values from these first-stage regressions, (basically the empirical counterparts to $v^*, \boldsymbol{n}^*, \boldsymbol{d}^*, \boldsymbol{a}^*$ and $\boldsymbol{y}^*$ but purged of the regression residuals) are included in the outcome regressions as instruments in place of the original endogenous variables. This process in principle purges correlation between endogenous regressors and the regression disturbance that is the source of bias. Because predicted values from first-stage regressions are included in the second-stage regressions, the covariance matrix for each second-stage equation is adjusted to obtain unbiased standard errors.[8]

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[8] The covariance adjustment is as follows. The Maximum Likelihood covariance matrix is $\hat{\sigma}^2(\boldsymbol{Z}'\boldsymbol{X}(\boldsymbol{X}'\boldsymbol{X})^{-1}\boldsymbol{X}'\boldsymbol{Z})^{-1}$, where $\boldsymbol{Z}$ are potentially endogenous variables and $X$ are exogenous (Greene, 2011). This estimate is biased because the standard second stage estimated variance $\hat{\sigma}^2 = \mathrm{n}^{-1}\left(\boldsymbol{y} - \widehat{\boldsymbol{Z}}\boldsymbol{\beta}\right)'(\boldsymbol{y} - \widehat{\boldsymbol{Z}}\boldsymbol{\beta})$ are calculated using the predicted values from the first stage regressions. A consistent estimate of the $\sigma^2$ is calculated as, $\hat{\sigma}_{ub}^2 = \mathrm{n}^{-1}(\boldsymbol{y} - \boldsymbol{Z\beta})(\boldsymbol{y} - \boldsymbol{Z\beta})'$, based on the original values of instrumented variables in $\mathbf{Z}$, and the unbiased covariance matrix is calculated using , $\hat{\sigma}_{ub}^2$, the unbiased estimate of $\sigma^2$.

Parameter identification in each second-stage equation is dependent on the availability of excluded exogenous variables in the system available for inclusion in the first-stage reduced form regressions. The variables in the vectors $Z_1$ through $\boldsymbol{Z_6}$ are designed to represent sufficient exclusion restrictions to assure identification. In general, for parameter identification in any equation, there must at least one excluded exogenous variable for each included endogenous variable on the right-hand side of a given equation. For example, the *Vaccination* equation $v$ includes five endogenous variables, $\boldsymbol{n}$, $\boldsymbol{d}$ and $\boldsymbol{y}$. The variables $\boldsymbol{Z}_3$, $Z_4$ and $\boldsymbol{Z_6}$ are not included in $v$ but are included in $\boldsymbol{n}$, $\boldsymbol{d}$ and $\boldsymbol{y}$ respectively, and act to identify their associated parameters in the *Vaccination* equation through their effects on the first stage estimates. Similarly, there are by construction in equations 5a-5d enough excluded exogenous variables to account for the included endogenous variables in each regression, thereby satisfying the necessary conditions for parameter identification in each equation.[9]

### *Functional Forms*

Finally, the functional form of the regressions depend in part on the nature of the data. The dependent variable in each of the equation is a count variable. Over-dispersion was found in all equations except the vaccination equation and this could be due to heterogeneity in household preferences or the nature of the process generating the excess zeros (Mullahey, 1986, Yoder et al. 2014). A Poisson regression was used for the vaccination equation, while Negative Binomial

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[9] Since the data were collected at a central point and households could choose into being interviewed or not, we also insert inverse mills ratio in each of the second stage equation to test whether selection model results differed from other model results (Heckman 1979). The inverse mills ratio was estimated based on a sample that includes non-participants, but contains a smaller variables set. A probit model of choosing to attend central point versus not with distance to central point, socioeconomic status of the household, and herd size as regressors. The coefficient on the inverse Mills ratio is never significant and results of the two models do not differ significantly, so we only provide results for the model without the selection correction.

regression is used for introductions and abortion equations. This strategy was guided by Likelihood Ratio tests. Zero-inflation seemed to matter only for the disease death equation.

## Results

We present second stage results for vaccinations, introductions, livestock disease deaths, and livestock abortions in Tables 3 through 6. The first-stage reduced form results for the endogenous variables in our system, *Vaccinations*, *Introductions*, *Disease Mortality*, *Abortions* and *Herd Size* are shown in the Appendix (Table A1-A4).

The results for the *Vaccination* equation are provided in Table 3. The *Sub-Village Vaccination* averages are positively related to *Vaccination* rates. This may indicate the presence of peer effects, learning, or correlations in vaccination access within villages. Informal qualitative data from interaction with respondents during data collection indicates that some communities in the sample have better access to and relationships with veterinary services and hence vaccination adoption could be community-wide phenomenon. In some cases, livestock vaccination in the study area is centrally coordinated through the Ministry of Agriculture, Livestock and Fisheries, typically with mass vaccination of a large of proportion of animals in the same village or sub-village at the same time.[10] However, some vaccinations like ECF are dependent on household's own initiative and are not actively distributed by government programs. Transhumance distance is also shown to be positively correlated with vaccination, Conditional on village-level vaccination activity, other factors seem to have weak effects based

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[10] To account for the unobservable village-level effects, a specification with village fixed-effects was also tested for all regressions. Our results are robust to the inclusion of village-level fixed effects. A joint F-test was conducted for K-1 village-level intercepts and we failed to reject the null hypothesis, $\alpha_i = 0 \; \forall \; i$ (p-value = 0.19).

on our sample. These two variables show themselves to be significant in the second stage and first stage regressions (table A2).

Table 4 provides Negative Binomial regression results for *Cattle* and *Shoats Introductions* in the household. *Cattle* and *Shoat Introductions* are positively related to abortions, while only *Shoat Introductions* are positively related to disease-related deaths, supporting our hypothesis 3. The relationship between death, abortions and introduction is not one-to-one. For example (Table 4, Column 4), a 10% increase in *Total Disease Death* is associated with 4.5% increase in *Shoat Introductions*. Since replacement is costly and one death is not replaced by one introduction, transfers into the herd may not compensate fully for the negative shocks, suggesting limited effectiveness of restocking as a risk management strategy. Given that the magnitude of introductions and negative asset shocks differ significantly, subsistence farmers with small herd sizes may be at risk of losing all of their herd. In expectation of large mortality losses, some farmers may have larger ex ante herd size so that they can have a reasonable ex post herd size (Lybbert et al. 2004; McPeak 2006). It is difficult however to infer whether restocking is pursued as precautionary saving or as ex post herd rehabilitation.

Table 4 regressions show that *Livestock Abortions* induce households to acquire new animals. There could be two reasons for this. First, reproductive loss may be large enough to require purchases after abortions in order to maintain desired herd sizes or to reduce the risk of catastrophic herd losses. Secondly, milk production may be negatively affected by abortion-related illnesses, and purchasing a replacement for the lost animal may be a response to this loss.

Table 5 provides the results of *[Stock] Disease Death* equation. As discussed in the methods section, livestock *Introductions*, *Vaccinations* and herd sizes are replaced with instruments produced as predictions from the equations presented in Tables A1, A2 and A4.

For the *Shoat Disease Death* regression (Column 1 and 2, Table 5), *Vaccinations* are shown to decrease the number of disease-related deaths conditional on death occurring, supporting hypothesis 1 and 2. The estimated marginal effect is -6.25 (p-value = 0.085), so vaccinating against one additional disease is related to a decrease of about 6 disease-related deaths per year in small stock. To put this in context, only 18.5 percent of households have used any type of vaccine in the last 12 months, and the average herd size of goats and sheep in our sample is 95, so the addition of one vaccine type at sample means can save about 6.5% of the small stock from disease-related deaths in representative household in the sample. Ahmed et al. (forthcoming) show that small stock face higher disease risk in northern Tanzania and therefore marginal benefit of vaccinations may be higher in small stock. In percentage terms, a 10 percent increase in type of vaccine use is associated with 1.1 percent (p-value = 0.17) decrease in disease-related deaths.

The most frequently used vaccine in our sample is for anthrax followed by vaccines for lumpy skin disease and foot-and-mouth disease, respectively.[11] Anthrax is an important cause of mortality in all ruminants (Lembo et.al 2011). The not surprising coincidence of active vaccination of this source of disease deaths seems likely to be the basis of the marginal effect of vaccinations on disease death described above. Other studies corroborate these results as well, having shown human capital and productivity benefits of livestock vaccinations and antimicrobials in terms of higher nutritional intake, control of zoonotic diseases and food-borne illnesses, and higher rates of schooling (Marsh et. al 2016; Mosites et al. 2016).

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[11] Some of the vaccinations used in the sample are species-specific - e.g., East Coast fever vaccine may only directly affect cattle health and may have no direct effect on the health of sheep and goats.

For the *Cattle Disease Death* regression (Column 3 and 4, Table 5), *Vaccinations* do not have a significant effect on disease-related death. Furthermore, positive elasticity estimate suggests that vaccinations are potentially applied either when disease outbreak has already occurred or the threat of disease outbreak is imminent. Railey et al. (2018) also suggest that demand for vaccinations in northern Tanzania is higher in response to immediate disease outbreak rather than other dimensions of information regarding the disease. Under such circumstances, the effectiveness of *Vaccinations* will be limited as suggested by our results. It is also important to note that livestock keepers in this setting are currently only using a limited number of vaccines against a limited number of diseases. Moreover, we have no information on vaccination practices used, such as what proportion of the herd are vaccinated. It could be expected that wider uptake of vaccination, whole herd vaccination, and vaccination against the major causes of mortality in the region would contribute to reductions in disease losses, have indirect effects on household welfare more broadly (Marsh et al. 2016).

The exclusion variable used to identify *Vaccinations* is leave-out *Sub-village Vaccinations*. These sub-village vaccination averages may not be completely random and higher sub-village means may reflect a common cause. Since the Ministry of Livestock and Fisheries conducts some vaccination drives in villages and sub-villages and our *Sub-Village Vaccination*s captures this phenomenon; it is possible that the Ministry employs a vaccination drive given a disease threat in the area or an area where the marginal benefit of vaccinations is the highest. If this is the case, then the magnitude of coefficient on *Vaccinations* may be biased upward. However, our modest estimates for vaccine effectiveness in small stock and no effect on cattle suggests the upward bias may not be a concern.

We find no evidence of the effect of *Shoats Introductions* on *Shoat Disease Death*. However, *Cattle Introductions* are positively related to *Cattle Disease Death*, which is consistent with hypothesis 3 of the theoretical model. In percentage terms, a 10% increase in *Cattle Introductions* is associated with a 2.1% increase in *Cattle Disease Death* (p-value = 0.057). Given that the average herd size is 54 and herds range into the thousands, one infected introduced animal may have wide-ranging consequences. The role of livestock introductions and inter-herd transfers through various pathways for herd maintenance, precautionary saving and ex post risk-sharing has been widely recognized in the literature (McPeak 2006; Lybbert et al. 2004; Carter and Barrett 2006). However, our results suggest that disease exposure risk associated with livestock restocking may be among the costs of doing so. If animal introductions are correlated with disease spread and disease losses, then these restocking strategies are costly beyond the purchase cost of animals, and suggests an important risk associated with inter-household trading, lending, and gifting of animals, which is ubiquitous in our setting.

Bidirectional causality between *Disease Death* and *Introductions* is particularly difficult to statistically differentiate given our data limitations. Herd owners may replace livestock to replenish their herd after a death, but livestock *Introductions* may also introduce disease into the herd and affect the incidence of disease-related death and abortions. The identification strategy and the strength of the instruments used in our analysis become critical. Recall that the predicted values of *Introductions* from first-stage regressions are used as instruments in the second stage *Death* and *Abortions* regressions (Table A1). F-statistics in the first stage regressions can be used to assess instrument strength (Staiger and Stock 1997, Greene 2011). The first-stage F-statistics of the joint test of instruments (*Cattle* and *Shoat Drought Death, Land Owned* and *Household Size*) are 26.71 and 27.90 for *Shoats* and *Cattle Introduction* equations, respectively. Our estimates of the effect of introductions on death are modest, F-statistics are greater than 10, suggesting instrumental variable bias of less than 10%, and hence the estimates of *Introductions* are likely not overly influenced by replacement behavior.

*Shoat* and *Cattle* herd sizes are positively related to *[Stock] Disease Death*. This could follow from the fact that there are more animals available to become ill; but it could also be driven in part by a lower labor per animal ratio and less care per animal, by differences in management that influence pathogen transmission, or because disease control may be costly for larger herds. Herd size has been identified as a risk factor for infection prevalence for several livestock diseases (Makita et al., 2011; Rizzo et al., 2016). Transhumance and daily grazing activities are statistically significant at conventional levels in this regression, corroborating studies that show that these activities lead to higher disease transmission (Ahmed et al. 2018; Bronsvoort et al., 2004; Rufael et al., 2008; Schoonman and Swai, 2010).

Table 6 provides the results of the *Abortions* equation. First, notice that *Vaccinations* is not included as a regressor in this model. Since the pathogens against which animals are vaccinated against in the sample are not major causes of abortion, we do not make abortion a function of vaccinations: vaccinations play a limited role in preventing abortive diseases in our sample. Nonetheless, a regression with predicted values of vaccinations was also performed, and the results with and without *Vaccinations* do not differ substantively.

*Introductions* do not appear to significantly affect abortions in these regression results. *Watering* and *Grazing Time* is positively related to *Shoat Abortion* incidence suggesting that animals may be becoming infected with pathogens that cause reproductive losses at or during travel to communal water points. It could also be that animals walking further to grazing/water are more energetically compromised or in poorer condition, resulting in more abortions due to metabolic causes (i.e. not directly infectious disease-related).

The cross-sectional nature of our data presents two challenges. One, the bidirectional causality between introductions and livestock death is difficult to disentangle. Future research using panel data and temporal sequencing may help in disentangling herd introductions made as ex-ante precautionary savings and ex-post herd replacement. Second, we are unable to provide evidence on the changes in herd composition over time, which can be important for livestock income and household wellbeing in these particular communities. Furthermore, the demand for introductions may be sensitive to sex, breed, age and species of the animal. While we examine demand for introductions disaggregated by species, we are unable to examine transfers disaggregated by sex or breed of the animal which may be important in this context.

## Conclusion

Vaccinations and herd restocking are two important herd management strategies especially in relation to livestock disease outcomes. While herd composition and dynamics in relation to poverty and insurance are widely discussed in the literature, evidence on demand for restocking and vaccination and their relationship with livestock disease losses and household welfare is limited. We contribute to the understanding of restocking and vaccinations and their relationships with disease losses by developing a theoretical model of these livestock management decisions in the context of herd disease challenge, and use this model to derive a set of hypotheses. Livestock management decisions and outcomes may be jointly (endogenously) determined, therefore a system of econometric regression equations is developed to test hypotheses about livestock introduction, vaccination, and their relationship with abortions and disease-related death.

Our results suggest that livestock mortality is an important driver of animal introductions into household herds. The relationship between mortality and introduction may not be one-to-one, suggesting that households take time to rebuild herds after animal losses. The slow rate of herd restocking may be a matter of consumption smoothing over time. It may also be a consequence of limited saving, credit, and insurance opportunities in low-income rural communities. While a great diversity of informal mechanisms for credit and insurance exist among pastoralists and agro-pastoralists (Besley 1995; Dercon 2005), liquidity and credit constraints may still persist and may hamper the ability of the household to restock their herds as they would like, potentially leading to lower herd sizes and poverty traps. Policies aimed at providing safety nets and insurances for productive asset build up may help households overcome constraints and achieve healthier herd sizes leading to poverty alleviation.

Further, we find modest evidence of the effectiveness of vaccinations in reducing disease deaths in small stock but no effect for cattle. These results have important policy implications in terms of vaccine supply chains and farmer’s incentives to vaccinate given disease risk and credit and/or liquidity constraints. Evaluation of the relationship between asymmetric information regarding the disease risk, credit constraints and their impact on vaccine adoption are topics for future work.

Lastly, we find some evidence of a relationship between herd introductions and disease transmission. The nature of relationship between herd introductions and disease incidents has policy implications for animal and human health under emerging disease environments and threat of zoonotic outbreaks, especially in areas where livestock exchange as gifts and loans is ubiquitous.

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## Figures

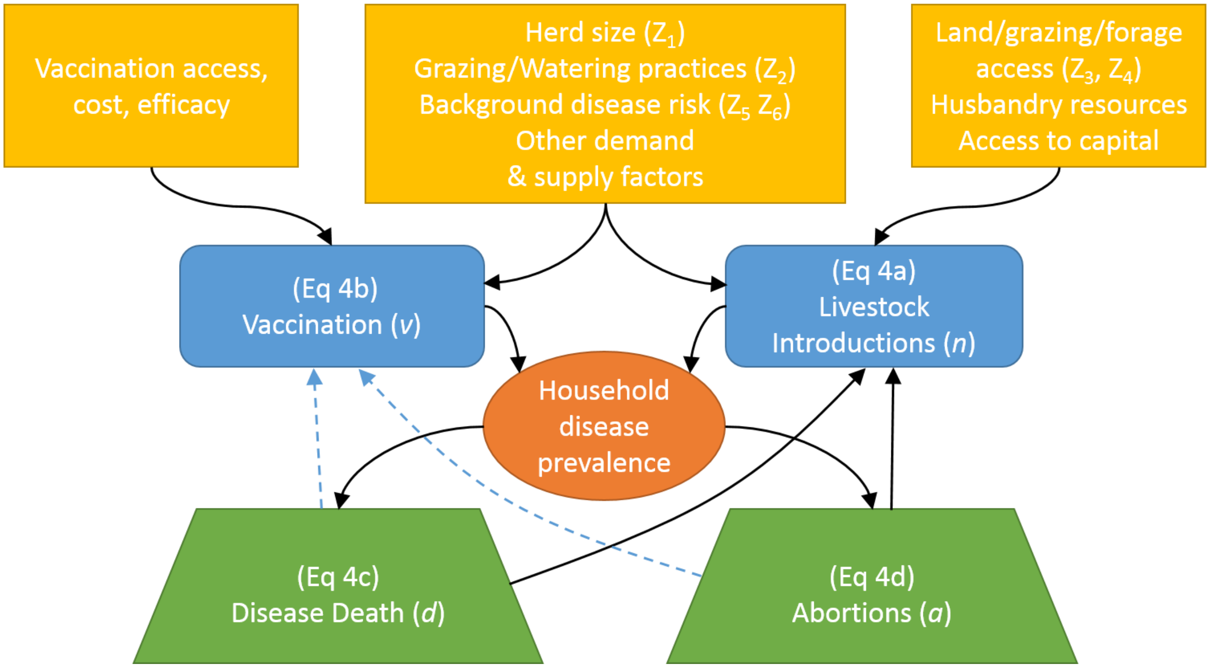

Figure 1: Feedback Mechanisms between Vaccinations, Disease Losses and Introductions

## Tables

Table 1: Data Description

| Variable | Definition |
|---|---|
| *Vaccinations* | Count of different vaccinations applied to the herd in the past 12 months |
| *Total Disease Deaths* | Number of cattle, sheep or goats reported dead due to disease in the past 12 months. |
| *[Stock] Disease Deaths* | Number of *[Stock]* reported dead due to disease in the past 12 months. |
| *Livestock Abortions* | Number of cattle, sheep or goats that reported abortions in the past 12 months. |
| *[Stock] Abortions* | Number of *[Stock]* that reported abortions in the past 12 months. |
| *Cattle Introductions* | Number of cattle introduced into a household through market or non-market transactions in the past 12 months |
| *Shoats Introductions* | Number of sheep and goats introduced into a household through market or non-market transactions in the past 12 months. |
| *Cattle* | Number of cattle present in the household net of introductions. |
| *Shoats* | Number of sheep and goats present in the household net of introductions. |
| *Land Owned* | Number of acres owned by the household. |
| *Transhumance Distance* | Euclidean distance between household's home and seasonal grazing camp. Measured in Kilometers. |
| *Grazing Time* | Time taken by livestock keepers and animals to walk to grazing points, measured in minutes. |
| *Watering Time* | Time taken by livestock keepers and animals to walk to water points, measured in minutes. |
| *Sub-Village Vaccinations* | Sub-village level leave-out mean of vaccinations, calculated as $\overline{v_i} = \frac{\sum_{j \neq i} v_j}{N-1}$, where $v_i$ is vaccination number of each household and $N$ is the number of households in the sub-village. |
| *Sub-Village Disease Death* | Sub-village level leave-out mean of total livestock disease mortality calculated as $\overline{m}_i = \frac{\sum_{j \neq i} m_j}{N-1}$, where $m_i$ is mortality number of household $i$ and $N$ is the number of households in the subvillage. |
| *Sub-Village Abortions* | Sub-village level leave-out mean of livestock abortions calculated as $\overline{q_i} = \frac{\sum_{j \neq i} q_j}{N-1}$, where $q_i$ is livestock abortion number of household $i$ and $N$ is the number of households in the sub-village. |
| *Goat Drought Death* | Number of goats died during the last drought. |
| *Sheep Drought Death* | Number of sheep died during the last drought. |
| *Cattle Drought Death* | Number of cattle died during the last drought. |
| *Household Size* | Number of household members including children. |
| *Compound Size* | Number of households in a compound. |
| *Maasai Ethnicity* | Dummy variable = 1 if ethnicity of household is Maasai, 0 otherwise. |

*[Stock]* refers to Cattle or Shoats

Table 2: Summary Statistics (N = 386)

| | Mean | Standard Deviation | Min | Max |
|---|---|---|---|---|
| *Vaccinations* | 0.218 | 0.483 | 0 | 3 |
| *Total Disease Death* | 11.15 | 31.73 | 0 | 350 |
| *Cattle Disease Death* | 1.51 | 6.31 | 0 | 100 |
| *Shoats Disease Death* | 9.65 | 28.11 | 0 | 250 |
| *Livestock Abortions* | 3.04 | 8.15 | 0 | 90 |
| *Cattle Abortions* | 0.59 | 2.71 | 0 | 40 |
| *Shoats Abortions* | 2.78 | 6.84 | 0 | 52 |
| *Cattle Introductions* | 1.61 | 7.25 | 0 | 94 |
| *Shoat Introductions* | 2.17 | 9.23 | 0 | 120 |
| *Cattle* | 53.57 | 122.7 | 0 | 1,200 |
| *Shoats* | 95.27 | 246.5 | 1 | 2,500 |
| *Land Owned* | 9.40 | 20.38 | 0 | 320 |
| *Transhumance Distance (km)* | 10.34 | 25.36 | 0 | 281.58 |
| *Watering Time (minutes)* | 3.36 | 1.19 | 0 | 6.39 |
| *Grazing Time (minutes)* | 69.7 | 123.22 | 0 | 1,440 |
| *Sub-Village Vaccinations* | 0.215 | 0.254 | 0 | 1.33 |
| *Sub-Village Abortions* | 0.80 | 2.18 | 0 | 20 |
| *Sub-Village Disease Death* | 1.59 | 2.89 | 0 | 17.85 |
| *Goat Drought Death* | 2.61 | 14.15 | 0 | 200 |
| *Sheep Drought Death* | 2.38 | 16.21 | 0 | 260 |
| *Cattle Drought Death* | 2.78 | 15.2 | 0 | 200 |
| *Household Size* | 7.02 | 5.03 | 1 | 37 |
| *Compound Size* | 1.79 | 2.06 | 1 | 15 |
| *Maasai ethnicity* | 0.24 | 0.43 | 0 | 1 |

Table 3: Vaccination Equation Results - Poisson Regression

| Dependent Variable<br>*Vaccinations* | Coefficient<br>(S.E) | Elasticities |
|---|---|---|
| *Sub-Village Vaccination* | 1.59***<br>(0.427) | 0.31***<br>(0.08) |
| *Transhumance Distance* | 0.176*<br>(0.096) | 0.034*<br>(0.019) |
| *Cattle*[a] | 0.907<br>(0.67) | 0.176<br>(0.131) |
| *Shoats*[a] | -0.62<br>(0.44) | 0.12<br>(0.087) |
| *Cattle Introductions* [a] | 0.028<br>(0.088) | 0.032<br>(0.10) |
| *Shoats Introductions* [a] | 0.044<br>(0.08) | 0.093<br>(0.17) |
| *Watering Time* | -0.036<br>(0.12) | -0.007<br>(0.024) |
| *Grazing Time* | -0.019<br>(0.15) | -0.003<br>(0.028) |
| *Disease Death* [a] | -0.005<br>(0.012) | -0.067<br>(0.153) |
| *Intercept* | -3.24***<br>(0.85) | |
| Vuong Test Statistic: | | 0.007 |
| LR Test: NB vs Poisson (P-Value): | | 0.45 |

***, **, * indicate significance at 1, 5 and 10% levels respectively.

[a] Predicted values from a first stage regression.

*N* = 314

Table 4: Cattle and Shoats Introduction Regressions (Negative Binomial Regressions)

| | *Cattle Introductions* | Elasticities | *Shoats Introductions* | Elasticities |
|---|---|---|---|---|
| *Total Disease Death*[b] | 0.020 | 0.23 | 0.039* | 0.45* |
| | (0.03) | (0.22) | (0.02) | (0.24) |
| *Livestock Abortions*[b] | 0.78*** | 0.52*** | 0.34* | 0.23* |
| | (0.21) | (0.14) | (0.17) | (0.12) |
| *Cattle*[b] | 1.58** | 4.33** | -0.03 | -0.08 |
| | (0.77) | (2.11) | (0.73) | (2.01) |
| *Shoats*[b] | -0.09 | -0.24 | 1.65*** | 4.43*** |
| | (0.47) | (1.26) | (0.42) | (1.11) |
| *Shoats Drought Death* | -0.52** | -0.15** | -0.42*** | -0.13*** |
| | (0.23) | (0.067) | (0.15) | (0.04) |
| *Cattle Drought Death* | 0.23 | 0.064 | 0.17 | 0.04 |
| | (0.22) | (0.061) | (0.25) | (0.07) |
| *Household Size* | -2.22** | -1.85** | -2.93*** | -3.26*** |
| | (0.949) | (0.72) | (0.80) | (0.66) |
| *Land Owned* | -0.31 | -0.58 | -0.55** | -1.01** |
| | (0.27) | (0.50) | (0.25) | (0.45) |
| *Intercept* | -2.89*** | | -0.82 | |
| | (0.81) | | (0.88) | |
| LR Test: NB vs Poisson (P-Value): | 0.000 | | 0.000 | |

[b] Predicted values from first stage regressions.

***, **, * indicate significance at 1, 5 and 10% levels respectively.

*N* = 313

Table 5: The Effect of Vaccinations and Introductions on Livestock Disease Death - Zero-Inflated Poisson Regression

| Dependent Variable: *[Stock]* Disease Death | Shoats Disease Death[a] | Shoats Disease Death # | Elasticities | Cattle Disease Death | Cattle Disease Death # | Elasticities |
|---|---|---|---|---|---|---|
| *Vaccinations*[b] | -0.81 | -0.904*** | -0.11 | -0.12 | 1.24 | 0.27 |
| | (1.13) | (0.12) | (0.19) | (1.13) | (1.52) | (0.35) |
| *Cattle Introductions*[c] | - | - | - | -0.22* | 0.109* | 0.21* |
| | | | | (0.12) | (0.058) | (0.13) |
| *Shoat Introductions*[c] | 0.04 | -0.13 | -0.18 | - | - | - |
| | (0.06) | (0.18) | (0.14) | | | |
| *Cattle*[d] | - | - | - | 0.31 | 0.50** | 0.86 |
| | | | | (0.29) | (0.19) | (0.62) |
| *Shoats*[d] | -0.38** | 0.51*** | 1.88*** | - | - | - |
| | (0.18) | (0.02) | (0.21) | | | |
| *Transhumance Distance* | 0.007 | 0.15** | 0.17* | -0.11 | 0.17 | 0.29* |
| | (0.09) | (0.07) | (0.09) | (0.09) | (0.12) | (0.16) |
| *Grazing Time* | -0.107 | 0.23* | 0.95** | -0.13 | 0.13 | 0.76** |
| | (0.11) | (0.12) | (0.45) | (0.13) | (0.09) | (0.36) |
| *Watering Time* | -0.204 | -0.17 | -0.28 | -0.02 | 0.14 | 0.51 |
| | (0.127) | (0.12) | (0.18) | (0.13) | (0.10) | (0.37) |
| *Sub-Village Disease Death* | -0.133 | 0.027 | 0.11** | -0.06 | 0.001 | 0.06 |
| | (0.087) | (0.025) | (0.05) | (0.05) | (0.028) | (0.05) |
| *Intercept* | 2.25*** | 0.925* | | 0.88 | -1.42 | |
| | (0.55) | (0.50) | | (0.78) | (1.05) | |
| Vuong Test (P-Value) | 5.90 | | | 4.00 | | |
| | (0.000) | | | (0.000) | | |

[a] The model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no mortality in the herd.

[b] Predicted values from a first-stage regression of *Vaccinations* on exogenous variables in the system.

[c] The predicted values from the first-stage regressions of *Cattle* and *Shoats Introductions* on exogenous variables in the system.

[d] The predicted values from the first-stage regressions of *Cattle* and *Shoat* herd sizes.

*, **, *** indicate statistical significance at 10, 5 and 1% respectively.

*N* = 314

Table 6: The Effect of Introductions on Livestock Abortions – Negative Binomial Regression

| Dependent Variable: *[Stock]* Abortions | Shoats Abortion | Elasticities | Cattle Abortions | Elasticities |
|---|---|---|---|---|
| *Shoats Introductions*[a] | 0.005 | 0.008 | - | - |
| | (0.06) | (0.12) | | |
| *Cattle Introductions*[a] | - | - | 0.22 | 0.20 |
| | | | (0.17) | (0.2) |
| *Shoats*[a] | 0.55*** | 1.45*** | - | |
| | (0.17) | (0.49) | | |
| *Cattle*[a] | - | - | 0.53 | 1.46 |
| | | | (0.41) | (1.11) |
| *Transhumance Distance* | 0.037 | 0.04 | 0.06 | 0.07 |
| | (0.095) | (0.08) | (0.10) | (0.13) |
| *Grazing Time* | 0.26** | 0.88** | 0.23 | 0.79 |
| | (0.12) | (0.42) | (0.17) | (0.61) |
| *Watering Time* | 0.40*** | 1.34*** | 0.27 | 0.91 |
| | (0.11) | (0.44) | (0.17) | (0.59) |
| *Sub-Village Abortions* | 0.176 | 0.09 | 0.56** | 0.32*** |
| | (0.20) | (0.09) | (0.24) | (0.11) |
| *Intercept* | -3.62*** | | -5.37*** | |
| | (0.59) | | (1.00) | |
| LR Test: NB vs Poisson (P-Value) | 0.000 | | 0.000 | |

[a] The predicted values from the first-stage regressions of *Cattle* and *Shoat Introductions* and *Cattle* and *Shoats* herd sizes on exogenous variables.

*, **, *** indicate statistical significance at 10, 5 and 1% respectively.

*N* = 265

**Appendix**

Table A1: Cattle and Shoat Introductions – Negative Binomial Regressions

| | Cattle Introductions | Shoats Introductions |
|---|---|---|
| *Intercept* | -2.03***<br>(0.53) | -1.00*<br>(0.52) |
| *Shoats Drought Death* | 0.032<br>(0.16) | 0.08<br>(0.16) |
| *Cattle Drought Death* | -0.13<br>(0.17) | 0.01<br>(0.26) |
| *Household Size* | 1.36***<br>(0.41) | 1.01**<br>(0.40) |
| *Land Owned* | 0.38*<br>(0.20) | 0.31*<br>(0.18) |
| F-Statistics (regression) | 27.9 | 26.7 |

*, **, *** indicate statistical significance at 10, 5 and 1% respectively.

Table A2: First-Stage Reduced Form Vaccination Regression - Poisson Regression

| Dependent Variable: *Vaccinations* | Coefficient | Standard Errors |
|---|---|---|
| *Sub-Village Vaccination* | 1.79*** | 0.39 |
| *Transhumance Distance* | 0.15* | 0.074 |
| *Watering Time* | -0.038 | 0.116 |
| *Grazing Time* | -0.04 | 0.107 |
| F-Statistic | 25.9 | |

***, **, * indicate significance at 1, 5 and 10% levels respectively.

Table A3: First-Stage Reduced Form Livestock Disease Death and Livestock Abortions Regressions – Negative Binomial Regressions

| | Disease Deaths | Livestock Abortions |
|---|---|---|
| *Transhumance Distance* | 0.21***<br>(0.07) | 0.25***<br>(0.09) |
| *Grazing Time* | 0.191*<br>(0.11) | 0.002<br>(0.12) |
| *Watering Time* | 0.04<br>(0.10) | 0.36***<br>(0.14) |
| *Sub-Village Disease Death* | 0.19***<br>(0.05) | - |
| *Sub-Village Abortions* | - | 0.37**<br>(0.17) |
| F-Statistic for excluded instruments | 59.6 | 36.7 |

Table A4: First-Stage Reduced Form Herd Size Regression - OLS Regression

| | Cattle Herd Size | Shoats Herd Size |
|---|---|---|
| *Household Size* | 0.42*** | 0.05 |
| | (0.09) | (0.15) |
| *Compound Size* | 1.18*** | 1.72*** |
| | (0.13) | (0.23) |
| *Land Owned* | 0.25*** | 0.46*** |
| | (0.06) | (0.11) |
| *Maasai Ethnicity* | 0.55*** | 1.40*** |
| | (0.13) | (0.23) |
| *Electricity* | 0.03 | 0.30* |
| | (0.10) | (0.17) |
| | | |
| F-Statistic | 49.6 | 39.9 |

***, **, * indicate significance at 1, 5 and 10% levels respectively.