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Assessing the Livelihood Impacts of a Livestock Disease Outbreak

An Alternative Approach

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ABSTRACT

Because of the substantive role played by livestock in the income and asset portfolios of the poor, livestock diseases can be an important threat to livelihoods. Yet for a variety of reasons, there are few applicable methods and consequently scant literature to assess the impacts of livestock diseases on livelihood outcomes. Existing literature comprises small-area studies and computable models with wider geographic focus, both of which have limitations in this specific context. We propose an alternative approach for estimating the impacts of livestock diseases on livelihoods. This proposed approach is an adaptation of a quasi-experimental impact evaluation method, namely propensity score matching, which uses features available in large-scale datasets with wide geographic coverage to create counterfactual scenarios that could mimic outcomes of a disease outbreak. By its construction the method is well suited for ex ante impact assessment. As an illustration we apply the method to the hypothetical case of an avian flu outbreak in Kenya.

Keywords: livestock disease, propensity score matching, livelihoods, impact assessment

1. INTRODUCTION

Livestock supports the livelihoods of 800 million to 1 billion of the world's poor and landless (Livestock in Development (LID) 1999; Thornton et al. 2000). It is not only an important income-generating asset but also an indicator of wealth status and a source of food and nutrition security as well as insurance against future shocks and stresses (see Randolph et al. 2007 for a review). However, livestock owned by the poor is particularly vulnerable to diseases because of poor people's lack of resources to cope with, and often knowledge regarding, disease prevention and mitigation. Livestock diseases can therefore potentially have significant impacts on the various livelihood outcomes of the poor.

Information on the magnitude of livelihood impacts of livestock diseases is crucial for the design of efficient and effective policies for disease prevention and control. Preferably such information should be available before the occurrence of an actual outbreak so as to help policymakers efficiently allocate scarce resources and design effective preparedness plans.

The literature on the evaluation of the livelihood impacts of livestock diseases is, however, scant. The most common methodologies employed for this purpose are techniques that simulate the effect of livestock mortality or price shocks following a disease outbreak on various livelihood outcomes, such as income, wealth, and employment. The simulation techniques could be at the economywide level, using computable general equilibrium models (see Diao 2009) or at sector or multisectoral levels using single-market (for example, Nin Pratt and Falconi 2006) or multi-market models (Rich and Winter-Nelson 2007).

In a few cases, the simulation-based techniques have links to a disaggregated set of households, such as those from different income groups, to assess the impact of livestock disease on livelihood outcomes of different demographic groups, especially on those of the poorest segments (for example, Diao 2009; Diao, Alpuerto, and Nwafor 2009). Though useful and well suited for this context, the simulation-based models have their limitations. The parameterization of such models in the case of a livestock disease outbreak is difficult, and in general these models cannot account for a comprehensive set of household characteristics that determine the coping possibilities for those households affected by the disease shocks.

Moreover, the standard methods of impact evaluation have not been used to estimate the impact of livestock diseases on livelihood outcomes. There are several reasons for this, mainly related to the implementability of these methods in this context. Consider the "gold standard" in impact evaluation, randomized controlled trials (RCTs). If we designate a livestock disease outbreak as "treatment," with pre- and post-treatment data on randomly selected treatment and control groups (households or communities), unbiased estimates of the effects of "treatment" could be obtained. It is obvious that RCTs, which randomly assign households or communities into treatment (affected by disease) or control (not affected by disease) groups, are neither practical nor ethical in the case of livestock disease outbreaks.

Another impact evaluation approach could be based on the collection of data before and after the outbreak of a livestock disease. This approach might be difficult to implement inasmuch as the occurrence of disease is random across space and time. The problem is compounded by the fact that the areas of disease incidence and disease impacts might not be congruent. This happens, for example, if consumer preferences change in response to the livestock disease outbreak, in other words if there is a demand shock (for poultry in the case of avian flu, for example, or for beef and other meats in the case of brucellosis). The resulting price shock would not necessarily be coincident with the place of disease outbreak.

In this paper we propose an alternative approach to estimating the impact of livestock disease outbreaks on livelihood outcomes. This is a quasi-experimental method, which is commonly used in impact evaluation literature, but its use is novel in the present context. It is based on the premise that large datasets, such as those from nationally representative household surveys, can provide variation in the states of the households' livestock ownership (such as whether or not they own livestock and the number and type of livestock owned) and in prices faced. Using such data, we can construct counterfactual scenarios of disease impact, by allocating households into "treatment" or "control" groups based on their livestock ownership status.

For example, in the case of a livestock disease outbreak resulting in a complete loss of livestock, "control" households could comprise those households who own livestock, whereas "treatment" households could comprise those who do not own any livestock, thereby mimicking households who may have lost their livestock to the disease. "Treatment" households could then be matched to their closest "neighbors" in the control group. Matching can be done based on different household-, infrastructure-, and location-specific attributes that jointly determine the livelihood outcome variables and the probability of being in a certain livestock ownership state. The significant differences between the livelihood outcomes of the matched treatment and control households would provide us with estimates of the livelihood impacts of livestock diseases on livelihood outcomes of focus, which are income and wealth in this case. The matching technique that we employ in this paper is based on the well-established method of propensity score matching (PSM), used in situations where assignment into a treatment or a control group is not random.

To illustrate the use of this approach, we applied it to estimate the impact of a potential highly pathogenic avian influenza (HPAI) outbreak in Kenya on poultry producers' livelihood outcomes. For this application we used the latest wave of the nationally representative Kenya Integrated Household Budget Survey (KIHBS) data (Kenya National Bureau of Statistics 2006). Our proposed approach proved to be particularly useful in this case since Kenya has not yet experienced an HPAI outbreak, though due to the circulation of the virus in the neighboring Sudan, timely information on the ex ante livelihood impacts is of paramount importance. Our results show that on average, the net effects of an HPAI outbreak on Kenyan poultry-producing households' income and wealth is small. There is, however, significant disparity across provinces and among poultry producers of different sizes.

Further, by drawing from some basic qualitative risk maps, we categorize regions of the country into high-, medium-, and low-risk areas for HPAI occurrence and assess the livelihood impacts when only some areas are affected. We believe that this mapping of the risk levels onto the livelihood impacts can be useful for ex ante policy responses. Areas of both high livelihood impact and high disease risk can clearly be considered important geographic targets for policy action. Where this congruence is lacking, a case can be made for prioritizing areas of high disease risk for action in order to prevent spread of disease to other areas and also because shortening the life span of a disease can be important for areas not affected by the outbreak but affected by demand shocks arising from consumer panic.

Though we have tailored the method to the case of ex ante assessment of livestock disease outbreak, which could encompass many types of diseases, we believe that the proposed method has applicability in cases beyond livestock diseases. These cases, characterized by the need for ex ante assessment and large geographic focus (for example, the effect of food prices or weather variation on household outcomes), can draw upon the approach proposed here directly.

The rest of the paper unfolds as follows: The next section describes the method used to assess the livelihood impacts of livestock disease outbreak. Section 3 presents the data used for the analysis and descriptive analysis results on the significance of poultry production in livelihoods. Section 4 discusses the results of the impact evaluation method employed, and the final section concludes the paper with some policy implications.

2. METHODOLOGICAL APPROACH

In this section we describe the methodology that can be used to estimate the potential livelihood impacts of a livestock disease outbreak, with a highly pathogenic avian influenza (HPAI) outbreak in Kenya as a case study. Since we would generally not have nationally representative data on the same households from before and after a disease outbreak and since randomized control trials (RCTs) cannot be used in this context, we use an ex ante evaluation method as proposed by Ichimura and Taber (2000) and Todd and Wolpin (2006). The main feature of this approach is that all the factual outcomes are about control households; in other words, none of these households has yet been exposed to the livestock disease outbreak, but are susceptible to livestock disease because they own livestock. In this study not owning livestock or owning smaller flocks (as a result of loss to disease outbreaks) is the "treatment" whose impact we would like to evaluate. The matching procedure is between a household *i* about whom we observe (or estimate) the outcome as control and a household *j* who mimics the outcome household *i* would have under the treatment. Then it must be $Y_i^1 = Y_j^0$; that is, the factual outcome for household *j* under the status quo situation must be equal to the one of household *i* under the treatment).

The estimation of an average treatment effect in observational studies can produce biased results when a non-experimental estimator is used. The typical problem in this type of study is that the assignment of subjects to the treatment and control groups is not random, and therefore the estimation of the average treatment effect is usually biased as a result of the existence of confounding factors. For that reason, the matching between treated and control subjects becomes difficult when there is an *n*-dimensional vector of characteristics. The matching approach is one possible solution to the selection problem and has become a popular approach to estimate causal treatment effects (Caliendo and Kopeinig 2005). Its basic idea is to find a large group of control households or households that are similar to the treatment households in all relevant pretreatment characteristics *X*. That being done, differences between the outcomes of this well-selected and thus adequate control group and of the treatment group can be attributed to the treatment.

Because conditioning on all relevant covariates is limited in the case of a high-dimensional vector *X* (the "curse of dimensionality"), Rosenbaum and Rubin (1983) suggest the use of so-called balancing scores *b*(*X*), that is, functions of the relevant observed covariants *X* such that the conditional distribution of *X* given *b*(*X*) is independent of assignment into treatment. This is the conditional independence assumption (CIA). One possible balancing score is the propensity score, that is, the probability of participating in a treatment given observed characteristics *X*. The matching procedures based on this balancing score are known as propensity score matching (PSM).

Besides CIA, a second assumption of matching requires that treatment observations have comparison observations "nearby" in the propensity score distribution. This common support or overlap condition ensures that persons with the same *X* values have a positive probability of being both control and treatment households (Heckman, LaLonde, and Smith 1999). The common support thus represents the area where there are enough of both control and treatment observations. The common support region allows effective comparisons of outcomes between the treatment and control groups.

Assuming the CIA holds and that there is overlap between both groups, the average treatment effect can then be estimated. One ideally wants to estimate $\Delta = Y_t^1 - Y_t^0$, which is the difference of the outcome variable of interest at time *t* between two groups, denoted by the superscripts 1 and 0. However, we are unable to estimate Δ in this way because a household cannot simultaneously be in the treatment and the control groups. We are thus forced to measure the average treatment effect (ATE) given the observable data:

$$ATE = E(Y_t^1 | T = 1) - E(Y_t^0 | T = 0) \tag{1}$$

When data are generated through a properly implemented random experimental design, such as an RCT, the expectations of the treatment and control groups are equal because the groups are composed of randomly allocated households, ensuring that the distribution of observable and unobservable characteristics of the two groups is equivalent in a statistical sense. With a randomized design, the selection bias equals zero, which establishes that the estimate of the ATE provides an unbiased estimate of its impact.

Since randomized experiments are not possible in this context, we use matching techniques to estimate treatment effects. We estimate the average treatment effect on the treated households (ATT), given a vector household characteristic, *X:*

$$ATT = E(\Delta | X, T = 1) - E(Y_t^1 - Y_t^0 | X, T = 1) = E(Y_t^1 | X, T = 1) - E(Y_t^0 | X, T = 0) \quad . \tag{2}$$

To estimate potential effects of a livestock disease outbreak, propensity scores are used to match households with similar observable characteristics, varying only the state of livestock ownership (such as whether or not they own livestock and the number of livestock owned) or prices faced. Households with different ownership status, such as those who own livestock and those who do not, are matched to each other conditional on a set of observable household-, infrastructure-, and location-specific characteristics. A probit model is estimated using a vector of these characteristics to obtain predictions of household propensity scores.

Heckman and others (1998) observe that the PSM has lower bias when X includes variables that affect both program participation and the outcome. The household-, infrastructure-, and location-specific characteristics (for example, household demographics, assets, regional characteristics such as location, poverty status, and number of income sources) included in the model are therefore those that have a high probability of influencing participation in livestock production, as well as outcome variables including livelihood indicators such as income and wealth. According to this method of matching, the two groups—the treatment group of households representing the result of the livestock disease outbreak and the control group representing the status quo of no outbreak—should differ only in their livestock ownership characteristics.

3. APPLYING THE METHOD TO THE CASE OF A POSSIBLE HPAI OUTBREAK IN KENYA: DATA AND DESCRIPTIVE RESULTS

In this section we present information on the data used and some descriptive information on the role of poultry in Kenyan households' livelihood outcomes. The data are used for application of the method discussed above to assess the impact on livelihoods from a highly pathogenic avian influenza (HPAI) outbreak.

Data

The data used for the analysis come from the Kenya Integrated Household Budget Survey (KIHBS) of 2005/06 (KNBS 2006). Collection of the KIHBS data started in May 2005 and lasted 12 months. The survey is based on the National Sample Survey and Evaluation Program (NASSEP-IV) sampling frame, which is composed of 1,800 clusters, of which 540 are urban and 1,260 are rural. KIHBS was conducted in 1,343 randomly selected clusters across all districts in Kenya and comprised 861 rural and 482 urban clusters. Ten randomly selected households with equal probability were interviewed in each one of the clusters. The yearlong survey was organized into 17 cycles of 21 days each, during which enumerators conducted household interviews in the clusters.

The districts were grouped into 22 zones. Seasonal variation was captured by randomizing visits to the selected clusters so that in each cycle at least one cluster was visited in each zone. In the first stage, 1,343 clusters were stratified by district (and by both urban and rural areas within each district). The objective was to make the total sample representative and descriptive of the distribution of the population across districts.

In the second stage, 10 households were randomly selected in each cluster to give a total sample of 13,430 households allocated into 136 explicit strata in urban and rural sections of Kenya's 69 districts and in Nairobi and Mombasa, which are mainly urban. Of the 13,430 households, 8,610 are located in rural areas and 4,820 in urban areas. This sample design makes possible representative estimates at national, provincial, and district as well as rural and urban levels. The KIHBS 2005/06 was designed to provide numerous indicators (pertaining to health, education, agriculture, etc.) and the data needed to measure living standards and poverty in Kenya.

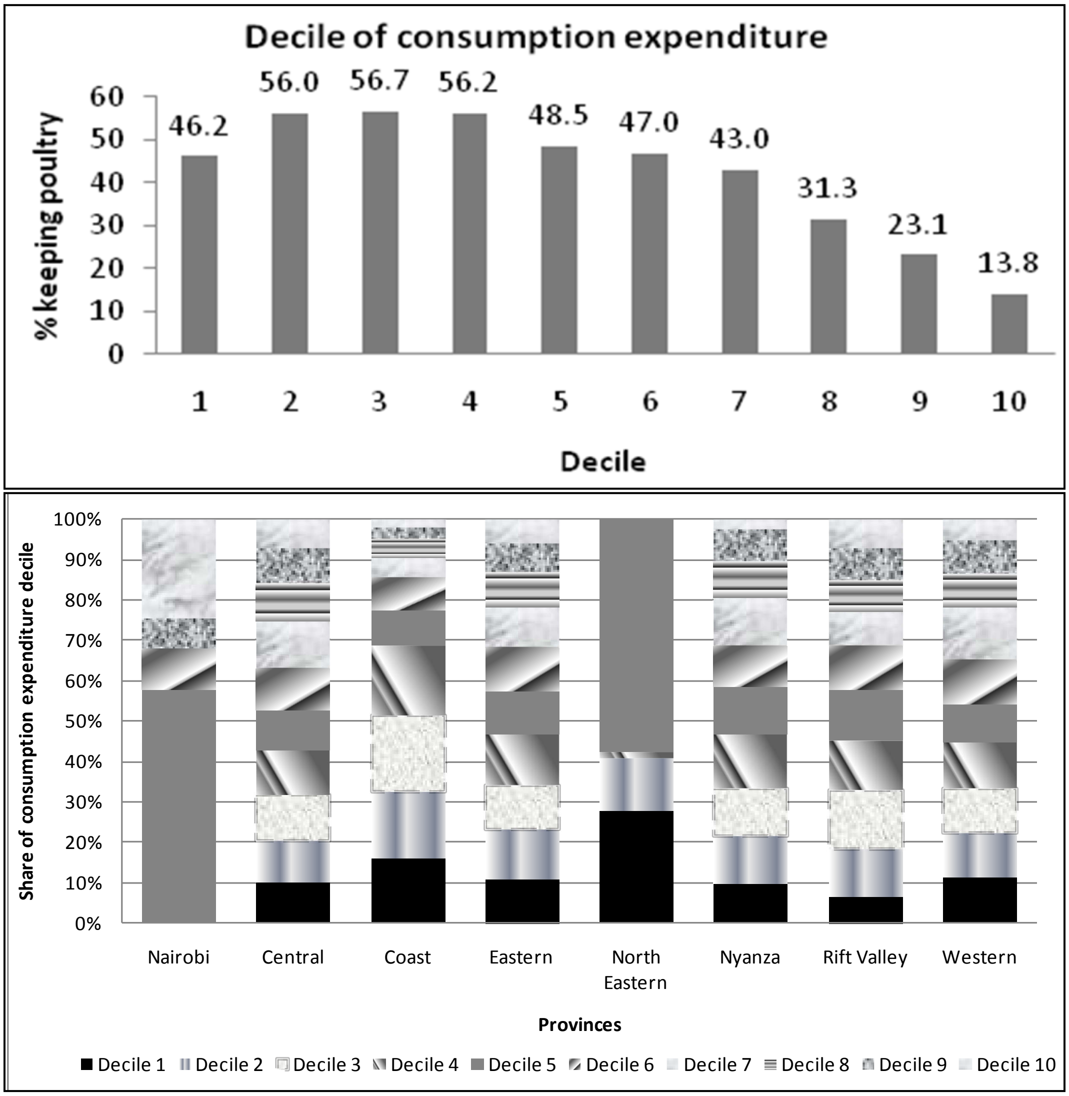
Household-level Poultry Production and Livelihoods in Kenya

According to the KIHBS data (KNBS 2006), about 50 percent of all Kenyan households keep poultry. Following Omiti and Okuthe (2008) in this study we consider household level poultry producers to manage maximum 500 birds in a year. About 95 percent of all poultry producers are in rural areas, and about 80 percent of all poultry producers are in four provinces: Eastern (23 percent), Nyanza (20 percent), Rift Valley (19 percent), and Western (18 percent), whereas less than one percent of all Kenyan household-level poultry producers are in Nairobi and North Eastern provinces. In terms of poultry production within each province, Western province has the highest percentage of households that keep poultry (72 percent), followed by Eastern and Nyanza (64 percent each). The provinces with the smallest proportion of poultry-producing households are Nairobi (0.6 percent) and North Eastern (2.4 percent).

The average flock size of poultry-producing households is small, with 14.6 birds. The few poultry-producing households in Nairobi manage the largest flocks in the country with an average of 158 birds, suggesting that distance to the densely populated market areas is an important determinant of flock size. This is followed by Coast province, with 31 birds, and Central and Nyanza provinces, each with an average flock size of about 19 birds. Poultry-producing households in North Eastern province manage the smallest flocks, with 6 birds.

Figure 3.1 shows the relationship between poultry keeping and household consumption expenditure (proxy for income). According to the top panel, a greater proportion of Kenya's households in the lower deciles for consumption expenditure (2nd, 3rd, and 4th) keep poultry compared to households in higher deciles (that is, 8th to 10th deciles). The distribution of poultry keepers across consumption deciles by province (bottom panel) reveals that in Nairobi province, where households keep the largest flocks, most of the poultry keepers are in the 5th consumption decile (that is, middle income) whereas in North Eastern province, where households keep the smallest flocks, most of the poultry producers are poorer, falling in the lowest two deciles for consumption expenditure.

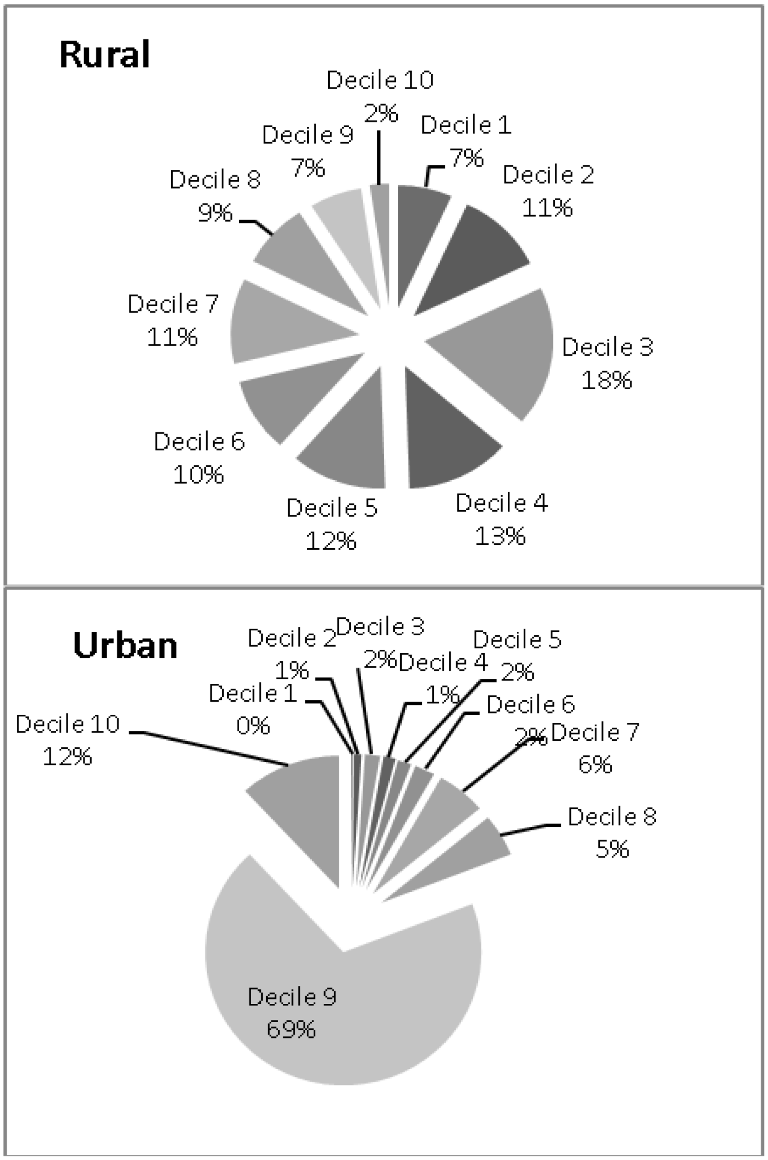
Figure 3.1—Distribution of poultry keepers across consumption deciles, Kenya (top) and by province (bottom)



Source: Authors' calculations from KIHBS 2005/06 (KNBS 2006).

Figure 3.2 presents the poultry population by deciles of consumption expenditure in rural and urban areas. This figure reveals that while in rural areas the wealthiest segments (9th and 10th deciles) manage the smallest proportion (9 percent) of rural poultry population, in urban areas it is the wealthiest segments that manage almost 75 percent of the urban poultry. In rural areas, the poultry population is fairly equally distributed across consumption deciles, with 75 percent of the poultry population being managed by households in the 2nd to 7th segments.

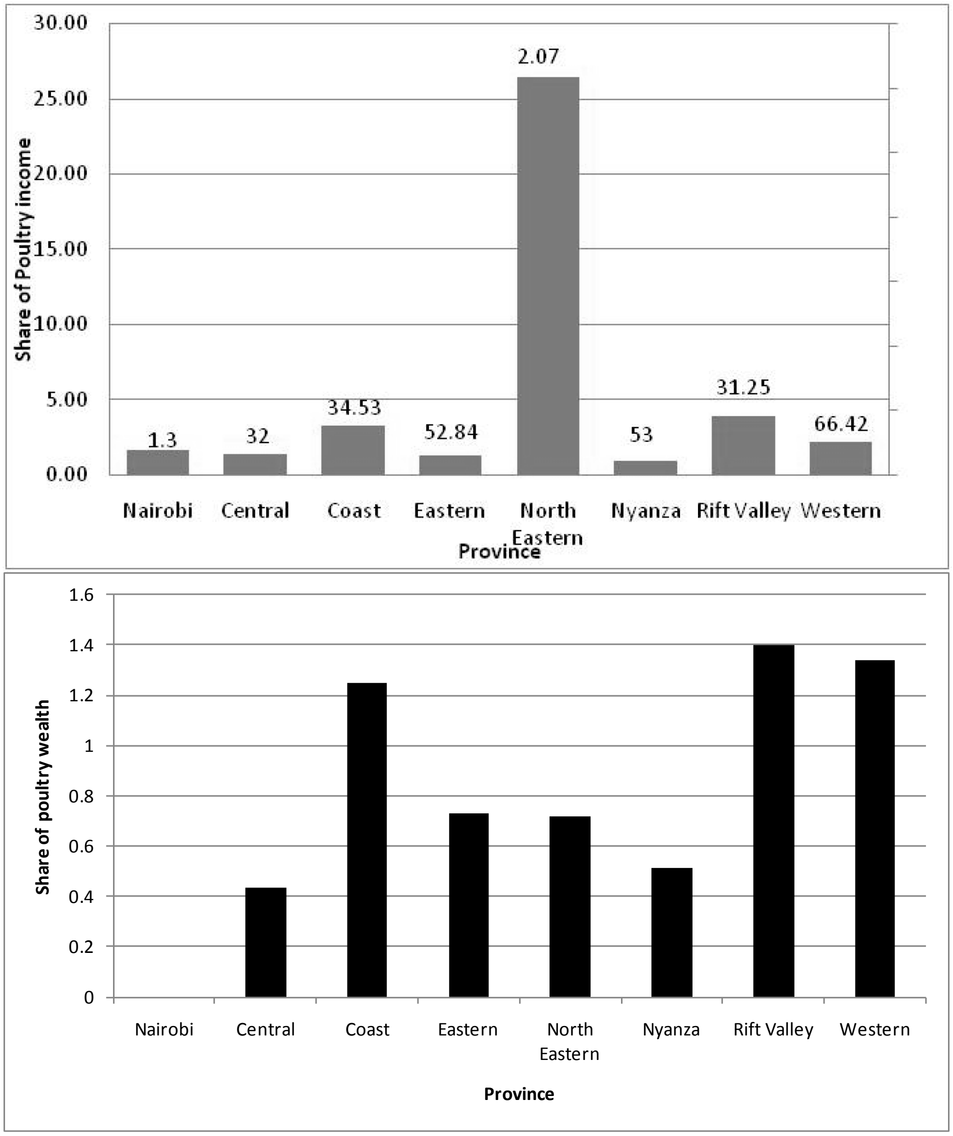
Figure 3.2—Proportion of poultry kept by consumption deciles in rural (top) and urban (bottom) areas



Source: Authors' calculations from KIHBS 2005/06 (KNBS 2006).

The contribution of poultry (live bird) and egg sales to the total annual household incomes of poultry-producing households is portrayed in Figure 3.3, top panel. The numbers on the columns represent the proportion of households that keep poultry in that province. In this study, total annual household income includes annual salaries from employment of the household members in various industries, income from livestock and crop sales, and income from remittances, rent, and other sources. On average, poultry contributes around 2 percent of the poultry producers' total annual household income. This figure varies across provinces, with the few households that produce poultry in North Eastern province obtaining the highest proportion of their income from poultry (about 27 percent), followed by those in Rift Valley (4 percent) and Coast (3.3 percent). Poultry-producing households located in Nyanza province rely the least on poultry income (less than 1 percent). As with the flock size distribution, there is significant variation within provinces. In some districts, there are only a few "larger" household-level poultry-producing households, who are more commercially oriented.

Figure 3.3—Share of poultry income (top) and wealth (bottom) in household income and wealth, by province



Source: Authors' calculations from KIHBS 2005/06 (KNBS 2006).

Finally, the proportion of total household wealth that comes from poultry ownership is reported in Figure 3.3, bottom panel. Household wealth includes the value of land, durable assets, house, and livestock owned. According to this figure poultry contributes very little to the average household's total wealth. This is not very surprising given that poultry is the livestock with the lowest value and households on average keep very small flocks. Poultry contributes the most to overall wealth in Rift Valley and Western provinces, at around 1.4 percent, followed by Coast with 1.2 percent. Contribution of poultry to overall household wealth is insignificant for poultry-keeping households in Nairobi.

4. RESULTS

With the background information on poultry and its role in the income and wealth portfolios of Kenyan households across regions, we now illustrate the use of the matching method to assess the impact of an HPAI outbreak on the livelihood outcomes of Kenyan poultry producers. In this study we simulated five counterfactual scenarios. In order to estimate the impact of HPAI on producers of different sizes, we categorized poultry producers into two groups, with "smaller" household-level poultry producers representing those households with 1 to 6 birds (6 being the 25th percentile of flock size), and more intensive, "larger" household-level poultry producers having more than 7 but fewer than 500 birds, where, as mentioned above, 500 is considered to be the maximum for household-level poultry production in Kenya (Omiti and Okuthe 2008).

Scenario 1 assumes a countrywide shock whereby all poultry-producing households in Kenya experience a total loss of their poultry flock due to an HPAI outbreak. For this scenario, outcomes of households with poultry are compared with outcomes of those without poultry. Scenario 2 assumes that only "larger" household-level poultry producers are adversely affected by an HPAI outbreak, and they lose some of their birds and are left with a flock size similar to that of the "smaller" household-level poultry producers.

Scenario 3 assesses the impact of a demand (price) shock caused by HPAI. We assume this shock would be countrywide. We look at the impact of a price shock on the livelihood outcomes of those producers who sell poultry. Of those households that sell, we compare households that get higher prices (above the median poultry price) with those that get lower (below-median) prices.

For scenarios 4 and 5 we use the disease spread map developed by Stevens and others (2009), which shows the likelihood for the spread of HPAI in Kenya, assuming that the disease has been introduced (see appendix). In scenario 4, all of the households located in the areas with a high risk that HPAI will break out are assumed to be affected by HPAI and to lose all of their birds. Similar to the first scenario, poultry-producing households are compared with those with no poultry; however, in this scenario only those households in the high-risk areas are matched.

Finally, in Scenario 5 we use the disease spread risk map to identify medium-risk areas in Kenya (Stevens et al. 2009). Similar to Scenario 2, this scenario assumes that only "larger" household-level poultry producers are adversely affected by HPAI and that they lose some of their birds and are left with a flock size similar to that of the "smaller" household-level poultry producers; however, in this scenario only those households in the medium-risk areas are matched. These scenarios are summarized in Table 4.1.

Table 4.1—Description of HPAI scenarios for treatment and control households

	Scenario 1	Scenario 2	Scenario 3	Scenario 4*	Scenario 5*
Description of simulated impact	100% loss of poultry flock	85% loss in large-scale poultry flock	50% reduction in poultry price	100% loss of poultry flock in high-risk areas	85% loss in large-scale poultry flock in medium-risk areas
Treatment group	All households without poultry	Small-scale poultry keepers (1 to 6 birds)	Poultry keepers who sold at low prices	All households without poultry	Small-scale poultry keepers (1 to 6 birds)
Control group	All households with poultry	Large-scale poultry keepers (7 to 500 birds)	Poultry keepers who sold at high prices	All households with poultry	Large-scale poultry keepers (7 to 500 birds)

Source: Authors.

Note: *For scenarios 4 and 5, Kenya disease spread map (Stevens et al. 2009) was used to allocate districts into areas of high and medium risk for spread of HPAI. According to this map, Western and Nyanza provinces contain mainly high-risk districts and Coast and Rift Valley provinces contain medium-risk districts.

In each of the scenarios, the propensity scores for matching are obtained using a probit model. Table 4.2 reports the results of the probit models for each of the five scenarios where the binary dependent variable equals 1 for being in the respective treatment, as described in Table 4.1. Table 4.2 presents the results of these probits for each scenario with only those covariates that satisfy the balancing property and common support requirements in each case, since only these variables have been used to generate propensity scores. The balancing property condition requires that the observed variables used to generate the propensity scores are not significantly different across slices of the propensity score distribution. Common support distribution of the propensity scores overlaps, as reported in Figure 4.1 (the kernel density plots for each of the scenarios).

Table 4.2—Determinants of being in the treatment groups as defined in Table 4.1, by scenario

Household- and location-specific characteristics	**Scenario 1**	**Scenario 2**	**Scenario 3**	**Scenario 4**	**Scenario 5**
Number of people in household	-0.015** (0.007)	-0.062*** (0.009)	0.018 (0.015)		-0.024* (0.014)
Female-headed household (1 = yes, 0 = no)			-0.230** (0.115)		0.112 (0.071)
Head of household education	-0.077*** (0.010)	-0.033*** (0.006)			-0.032** (0.014)
Head of household education squared	0.004*** (0.001)		0.000 (0.002)		
Age of the head of the household			-0.041 (0.055)	0.002 (0.019)	
Age of the head of the household squared			-0.000 (0.000)	0.000 (0.000)	0.000* (0.000)
Skill (agehead-eduhead-5l)	-0.018*** (0.004)	-0.020*** (0.005)	0.039 (0.041)	-0.025** (0.012)	-0.020* (0.011)
Skill squared	0.000* (0.000)	0.000*** (0.000)	0.000 (0.000)	0.000 (0.000)	
(Max) age of the spouse			-0.002 (0.003)		
Proportion of household members under 18 years old	-0.543*** (0.075)			-0.642*** (0.085)	
Proportion of female household members 15 years and older	-0.246*** (0.077)	0.204* (0.122)		-0.097 (0.099)	
Number of income sources	-0.524*** (0.014)		-0.021 (0.033)	-0.545*** (0.018)	-0.212*** (0.027)
Current value of livestock owned (excluding poultry)	-0.000** (0.000)		-0.000 (0.000)		
If obtained credit(1 = yes, 0 = no)	-0.051 (0.032)	-0.049 (0.042)	0.141* (0.074)	-0.127*** (0.042)	
Hardcore poor (1 = yes, 0 = no)	0.098** (0.040)		-0.038 (0.287)		
Food poor		0.331*** (0.083)		-0.055 (0.041)	0.056 (0.069)
Rural (1 = yes, 0 = no)	-0.911*** (0.037)			-0.904*** (0.046)	

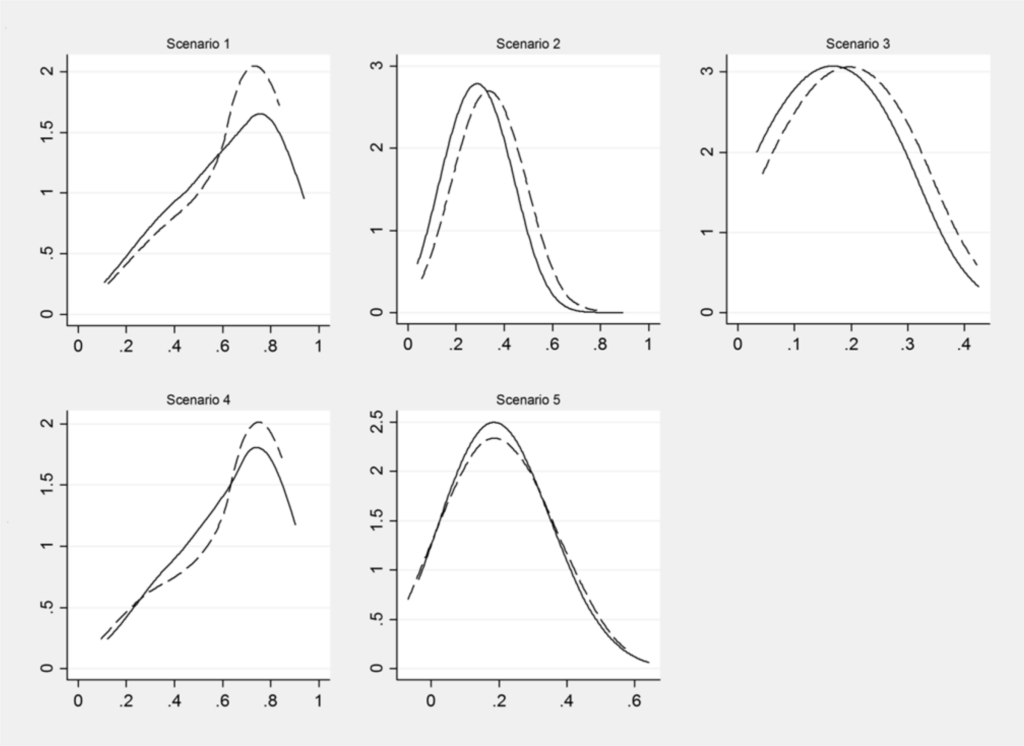
Table 4.2—Continued

Household- and location-specific characteristics	Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5
Province dummies	Yes	Yes	Yes	Yes	Yes
Share of total population of households in the district owning poultry	-0.444*** (0.066)	-0.352*** (0.095)	0.005 (0.180)	-0.371*** (0.090)	-0.474*** (0.154)
Proportion of household members 6–14 years old		0.032 (0.114)			-0.245 (0.180)
Constant	3.245*** (0.105)	0.132 (0.140)	-0.799 (0.691)	3.325*** (0.285)	1.176*** (0.269)
Observations	12089	4829	1896	6922	1962

Source: Estimated from KIHBS 2005/06 (KNBS 2006).

Note: *** significance level $p < 0.001$, ** significance level $p < 0.01$, * significance level $p < 0.5$

Figure 4.1—Matching distributions from treatment and control groups, all scenarios



Source: Estimated from KIHBS 2005/06 (KNBS 2006).

To illustrate the interpretation of the results reported in Table 4.2, consider scenario 1, which depicts the incidence where all poultry producers could lose 100% of their poultry. The probit model for this scenario reveals that smaller households with lower proportions of children and adult females are less likely to keep poultry. This is in line with the findings of previous research in Sub-Saharan African countries, which found that poultry are mainly managed by the children and women of the household (Alders 1996; Guèye 1998, 2000; Hailemariam et al. 2006; Kimani, Obwayo, and Muthui 2006; Sonaiya 2007; Aklilu et al. 2008). The impacts of the household head's education and skill levels on the household's likelihood of not keeping poultry are negative. Highly educated and skilled people are unlikely to be associated with a livelihood activity such as poultry that does not require human, physical, or financial capital. This finding is also in line with previous studies, which found that household-level poultry keeping is a low-input, low-output activity that does not require high levels of skill and education (Kimani, Obwayo, and Muthui 2006; Omiti and Okuthe 2008).

Further, households with less diversified income sources are less likely to keep poultry. For poultry-producing households, poultry production is one of the many livelihood activities in their portfolios. Households that have at least one member in off-farm employment are less likely to be engaged in poultry production. Overall, participation in off-farm employment reduces the probability of being a poultry keeper by about 27 percent.

Geographically, the estimated probability that a household located in a rural area will *not* be a poultry keeper is 46 percent. An urban household has only a 3 percent probability of *being* a poultry keeper. Taking Nairobi as the excluded category, households in all other provinces, except North Eastern, are more likely on average to keep poultry. As expected, a household in Western province has the lowest probability of *not* being a poultry producer, with a likelihood of 30 percent. This is closely followed by Eastern (31 percent) and Nyanza (32 percent). These results are similar to those presented in Omiti and Okuthe (2008).

The variables affecting the probability of being in a certain state of livestock ownership and those affecting outcomes (income or wealth) are used to generate propensity scores. Hence, regional characteristics and several household characteristics meet this requirement.

Once the two requirements of common support and balancing of propensity scores are met, the next step is to choose the matching estimator. Following Abadie and Imbens (2008), we chose the single nearest-neighbor matching estimator with replacement. This is our preferred estimator as it provides analytical standard errors for the estimator. We do test for robustness using a kernel-based matching estimator where the standard errors are obtained by bootstrapping. Table 4.3 presents the results of the differences between the livelihood outcomes of the control and treatment households with different livestock ownership status corresponding to possible outcomes under an HPAI outbreak.[1]

Table 4.3—Estimated impact of an HPAI outbreak on livelihood outcomes under different scenarios

Scenarios	Livestock Income	Livestock Wealth
1. All Kenya: Lose all poultry		
Loss in percentage	-*	-
Loss in Kenyan shillings (KES)	-	-
2. All Kenya: Large flocks become small flocks		
Loss in percentage	- 34 %	- 31 %
Loss in KES	- 3527.4 (1204.2) **	- 13402.9 (2672.4)
3. Poultry Sellers: High price falls to low price		
Loss in percentage	-	-
Loss in KES	-	-
4. High HPAI risk: Lose all poultry		
Loss in percentage	- 67 %	- 46 %
Loss in KES*	- 2352.2 (716.9)	- 13105.4 (3688.3)
5. Medium HPAI risk: Large flocks become small flocks		
Loss in percentage	-	- 41 %
Loss in KES*	-	- 20688.1 (7481.3)

Source: Authors' calculations from KIHBS 2005/06 (KNBS 2006).
Note: * insignificant estimated impact ; ** standard errors in parentheses

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[1] For robustness, we also estimated ATTs using kernel-based matching estimators. Results are available upon request.

These results reveal that under scenarios 2 and 4, HPAI may cause significant reductions in poultry-producing households' income from livestock. According to scenario 2, if an average poultry-producing household that manages a "larger" flock lost 85 percent of its birds due to HPAI, its total annual livestock income would decrease by KES 3,527 (US$45), from its pre-HPAI average annual livestock income of KES 12,742. This represents a 34 percent reduction in livestock income on average, which translates to a 7 percent reduction in total annual household income on average for the matched households. According to the results from scenario 4, if all poultry-producing households in the areas at high risk for HPAI lost 100 percent of their flocks, on average they would lose as much as KES 2,352 (US$30) of their annual livestock income, from their pre-HPAI average annual livestock income of KES 3,500. This translates to a 67 percent loss of their annual income from livestock on average and an 8 percent reduction in total annual household income on average.

In terms of its impact on wealth, HPAI is found to result in significant reductions in livestock wealth under scenarios 2, 4, and 5. According to scenario 2, if an average poultry-producing household that manages a "larger" flock lost 85 percent of its flock due to HPAI, its total livestock wealth would decrease by KES 13,403 (US$171). This represents a 31 percent reduction to its pre-HPAI livestock wealth of KES 43,989 and a 6 percent reduction in its total household wealth on average. According to scenario 4, if all poultry-producing households in the high-risk areas lost 100 percent of their flocks, on average they would lose as much as KES 13,105 (US$167) worth of their livestock wealth, representing a 46 percent reduction of their pre-HPAI livestock wealth of KES 28,370 and a 4 percent reduction of their total household wealth on average.

Finally, according to scenario 5, if "larger" household-level poultry producers in areas at medium risk for HPAI (Western, Nyanza, and parts of Eastern provinces) lost 85 percent of their flocks due to HPAI, their total livestock wealth would decrease by KES 20,688 (US$264), from the pre-HPAI average livestock wealth of KES 50,119. This represents a 41 percent decrease in wealth from livestock and a 9 percent decrease in total household wealth on average.

These results point to a few important considerations that should be kept in mind while assessing the livelihood impacts of a livestock disease outbreak. There is likely to be non-linearity in the impacts across flock or herd sizes. In the case of HPAI in Kenya, for example, on average those farmers who keep smaller flocks tend to have much less stake in poultry because it barely contributes to their income or wealth portfolio. The households that keep sizable flocks de facto constitute the most vulnerable households, whose livelihoods are likely to be affected significantly. This is because these households are more likely to derive significant portions of their income or wealth from poultry. Hence, in scenarios 2 and 5 the significant impact on livelihood outcomes can be observed once comparatively large flocks are projected to turn into smaller ones.

In the extreme case of total loss of flocks (scenario 1), the average effect is insignificant because of the low average share of income or wealth being derived from poultry. The significance of the effect of a complete loss of flock in high-risk areas can be explained by the congruence in the areas of high HPAI risk identified by Stevens and others (2009) and the areas where a high share of income, wealth, or both comes from poultry. Hence, these are the areas where shocks to the poultry sector are likely to result in significant livelihood impacts.

The estimated effects of a demand shock (scenario 3) obtained through matching of poultry producers that face high prices with those that face low prices yields insignificant effects. There are two main reasons for this result. First, since demand shocks are assumed to be nationwide, the average effect becomes diminished owing to inclusion in the sample of households with low poultry dependence. Moreover, KIHBS data on prices come from a question that asks for the price (value) that the household would receive if it sold its poultry (KNBS 2006). The price dispersion in the sample based on this type of question tends to be small. In effect, the spatial integration of the market would determine the extent of price dispersion, and less integrated markets would provide greater dispersion to enable researchers to capture greater price shocks in the household data. Seasonality could further provide another possibility of variation in prices that could be used. In reality, in many developing countries, markets are not spatially integrated and could exhibit greater spatial difference in prices than what was exhibited in KIHBS data based on the type of question asked.

5. CONCLUSIONS

In this paper we present an application of a well-established impact evaluation approach to the specific context of estimating the livelihood impacts of a livestock disease outbreak. We argue that the specific needs of impact evaluation in the context of livestock disease outbreaks require incorporating the spatial dimension of the incidence and effect of the disease in a setting that constrains creation of counterfactuals. Therefore neither randomized control trials (RCTs) nor reliance on before and after data for the same households would be suitable in this context. Moreover, other methods, such as partial or general equilibrium models with micro-simulations, are limited by their inability to account for a comprehensive set of household characteristics that determine the coping possibilities for those affected by the disease shocks. Our proposed approach is particularly useful in ex ante impact assessment. In most instances, policymakers require such ex ante assessment of the impacts in order to be able to develop efficient and targeted preparedness plans.

For this purpose we propose the use of the quasi-experimental matching methods. This approach is based on the premise that large datasets, such as those from nationally representative household surveys, can provide variation in the state of households regarding their livestock ownership characteristics (such as whether or not they own livestock or the number of livestock owned) and prices faced. In such a situation, we can construct counter-factual scenarios of disease impact for households. This can be done by matching households to their closest “neighbors” in terms of different household-, infrastructure-, and location-specific characteristics that jointly determine the probability of being in a certain state (for example, owning livestock or owning large flocks or herds) as well as the livelihood outcomes (such as income or wealth levels). Any significant differences between the livelihood outcomes of the matched households would provide us with estimates of the livelihood impacts of livestock diseases.

The estimation of livelihood impacts requires taking into account the whole income and asset portfolios. Focusing merely on the income from the livestock affected by the disease or the asset value of that livestock can portray a misleading picture. Therefore datasets that provide information on the income and asset portfolio as a whole (such as the Living Standards Measurement Study [LSMS] Survey or the Household Budget Survey) should be used. In the specific application of the matching approach, such data is needed by design. The application of the matching methodology rests on the use of large-scale datasets that have wide geographic coverage resulting in information that can map into households’ being in different states related to livestock ownership that can then be marked as pre– and post–disease outbreak states.

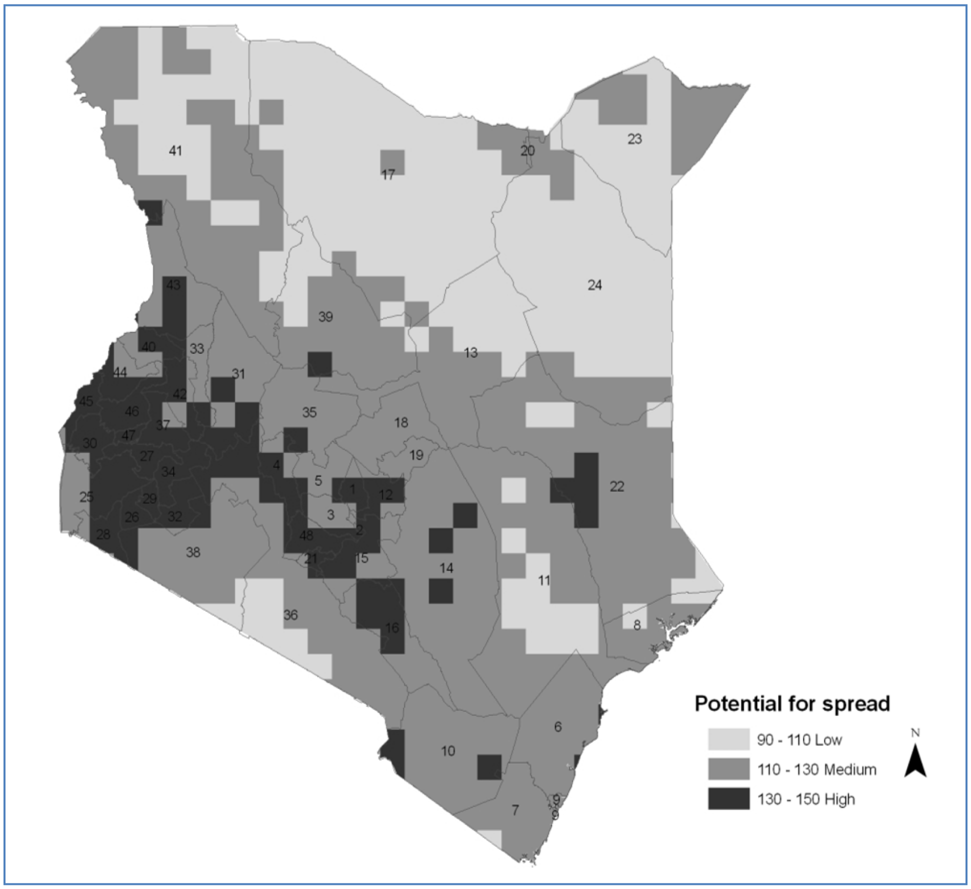
As an illustration of this approach we applied the method to the hypothetical case of a highly pathogenic avian influenza (HPAI) outbreak in Kenya. The fact that an HPAI outbreak has not yet occurred in Kenya, though the country is in constant threat due to the circulation of the virus in neighboring Sudan, made it an ideal case to study as an application of the method. The results of the application clearly point to the importance of including the spatial dimension of disease spread as well as the flock sizes kept by the households. This follows from significant differences in the risk of disease spread and in the stakes of the households in the poultry sector. Our findings reveal that given the magnitude of loss in total wealth (4.1 to 9.4 percent, depending on the scenario) and total annual household income (7 to 8 percent) that the “larger”-scale poultry-producing households and the households in high-risk areas for HPAI stand to sustain, they should be the primary targets for HPAI prevention and mitigation measures.

Even though in this paper we focused on the case of a livestock disease outbreak, that situation is inherently similar to several shocks that can affect livelihoods. Consider for example the effect of a food price shock. How households might be affected by a food price shock is a very important question for researchers and development practitioners alike. The same inabilities as in the case of livestock disease outbreaks would undermine impact assessment of such a shock. Our proposed method, relying on matching, can be clearly seen to have applicability in this context.

Finally, a note on the external validity of the exercise conducted here. RCTs, or target area studies, have often been criticized owing to the questions they raise about external validity. In this study the use of the nationally representative data has at one level mitigated the concern for external validity. Yet at another level, the method suffers from its inability to deal with the bias that follows from not accounting for unobservables. A well-designed RCT clearly dominates the method proposed here on this count, the impracticability of RCTs in this context notwithstanding. When external validity is desired, the competition between matching approaches, such as the one presented here, and methods that account for unobservables, such as RCTs, is not clear cut. To quote Deaton (2009, page 46), “Running RCTs to find out whether a project works is often defended on the grounds that the experimental project is like the policy that it might support. But the ‘like’ is typically argued by an appeal to similar circumstances, or a similar environment, arguments that can only be mounted for observable variables. Yet controlling for observables is the key to the matching estimators that are the main competitors for RCTs, and that are typically rejected by their advocates on the grounds that RCTs control, not only for things that we observe, but things that we cannot.”

APPENDIX: SUPPLEMENTARY FIGURE

Figure A.1—Map showing the likelihood of the spread of HPAI H5N1 virus in Kenya assuming that the disease has been introduced



Source: Stevens et al. (2009).

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