Copyright is owned by the Author of the thesis. Permission is given for a copy to be downloaded by an individual for the purpose of research and private study only. The thesis may not be reproduced elsewhere without the permission of the Author.

# Development of a method for optimal detection of emerging disease incursions

A thesis presented in partial fulfilment of the requirements for the degree of Doctor of Philosophy at Massey University

Shiyong Wang

2016

Submitted 29 January, 2016

Institute of Veterinary, Animal and Biomedical Sciences

Massey University

Palmerston North, New Zealand

#### **Abstract**

Emerging and re-emerging infectious diseases (ERID) are capable of generating sizable economic loss, and causing loss of life and social instability. To prevent and mitigate the negative impacts of ERID, it is imperative to have a sensitive surveillance system for early disease detection. Furthermore, from the economic perspective, resources are always scarce and have opportunity cost, so investment in surveillance programs has to demonstrate that it can maximize the utility of available resources. The thesis was focused on development and application of a software toolbox, **H**uman and **An**imal **Di**sease **Response** Program (HandiResponse), designed for (i) visualizing the disease risk landscape and representing spatial variation in the expected occurrence of a zoonotic disease both quantitatively and visually; (ii) evaluating economic benefit and costs of a single surveillance activity or a multi-component portfolio; (iii) identifying optimal use of resources for surveillance. It comprises four modules: (i) risk map development – HandiMap; (ii) surveillance portfolio development – HandiSurv; (iii) economic impact assessment – HandiEcon and (iv) surveillance optimization – OptiSurv.

The modules developed were tested on a number of data sets from various countries. The experience demonstrated that using satellite-derived data in combination with national statistical data to produce a disease risk map improved spatial prediction of avian influenza H5N1 outbreaks in southern Vietnam. Development of a risk map from satellite data for Crimean Congo Haemorrhagic Fever for Mongolia guided a field surveillance program which provided the first evidence that this disease is present in both animals and people in Mongolia. Finally an invented disease affecting pigs and people was used to investigate the likely consequences of an incursion of such a novel disease into Australia, involving both domestic and feral pigs and transferring to people. Risk-based and classical disease surveillance options were then tested for disease detection, and modelling work confirmed that a portfolio consisting of different options was the most technically and economically appropriate.

HandiResponse is a practical tool that could promote the implementation of risk-based surveillance approaches, and improve both technical and economic efficiency of surveillance programs for infectious diseases, particularly those affecting both people and animals.

#### Acknowledgements

This study was carried out at the EpiCentre of Massey University with data from Mongolia, Vietnam and Australia. It was a byproduct of my many years involvement in the World Bank supporting emergency operations in response to the emerging infectious diseases such as HIV/AIDS, SARS, HPAI H5N1, human pandemic influenza (H1N1, 2009) and Ebola Virus Disease outbreaks. I dedicate this thesis to the health workers and others who fought against these diseases, and even gave their lives. I appreciate the understanding, trust and support from my World Bank colleagues, Trina Haque, Nicole Kligen, Enis Baris, Toomas Palu, Olusoji Adeyi and Timothy Evans and the opportunities you gave me to join the responses to various infectious disease outbreaks and pandemics through the involvement of the World Bank over the last fifteen years.

I am deeply indebted to my supervisor Dr. Joanna McKenzie and co-supervisor Dr. Peter Jolly for keeping me on schedule, and helping me navigating through the administrative procedures at the University. The extensive and perhaps unusual nature of this project meant that I needed to involve a wide variety of people in providing me with the tools and the data I needed to undertake the development and application of HandiResponse. It would have been impossible for me to accomplish this thesis without generous support from my colleagues and friends. Sincere thanks to all of you in the spirit of One Health. These include Dr. Eric Neumann, Mr. Bryan O'Leary, Mr. Masood Sujau, Mr. Simon Verschaffelt and Dr. Masako Wada from the Epicentre, Dr. Robert Cannon from Australia, Ms. Min Wang and Ms. Xiaohua Wang from China, Dr Bolortuya Purevsuren from Mongolia; Mr. Mark Stern from Switzerland and Ms. Birgit Schauer from Germany.

I express my sincere gratitude to my fatherly Emeritus Professor Roger Morris, who has set a role model that I have to learn and emulate in my whole life. Thanks for your inspiration to me. Countless debates and discussions which have taken place between us during the years have helped me grow as a seasoned one health professional. I am deeply indebted to you and your beloved wife, Dr. Anne Harvey for training me on how to be a student after many years away from school, and to grow as a father and a person. Without you, this thesis, and my life would never have been the same.

I also wish to thank my parents and my parents in law for their love and always available support. Last but not least, I want to thank my family. Thank you, my dear wife Yue and my son Minkun (Moe) for being with me for the journey this far. I promise to spend more time with you when it is done.

Shiyong Wang, Washington DC, January 29, 2016

## **Table of Contents**

Abstract		i
Acknowledge	ements	iii
Table of Con	itents	v
List of Figure	es	xi
List of Table	S	XV
Abbreviation	18	xix
1. Introduc	ction	1
1.1. Re	ferences	3
2. Review	of Risk-based Surveillance for Infectious Diseases	5
2.1. Int	roduction	5
2.2. Me	ethods	6
2.2.1.	Literature search strategy	6
2.2.2.	Inclusion criteria	7
2.3. Re	sults	7
2.3.1.	General information on the review	7
2.3.2.	Definition and objectives of risk-based surveillance	9
2.3.3.	Typology of RBS	9
2.4. Dis	scussion: key observations on RBS	33
2.4.1.	Key assumptions for RBS	33
2.4.2.	Benefits from RBS	34
2.4.3.	Challenges related to RBS	35
2.4.4.	Evolution in risk-based disease surveillance	37
2.5. Co	nclusion	39
2.6 Re	ferences	41

3. F	From S	cience to Application: Development of a User-friendly Program to Facilitate Risk-ba	sed
Appro	oaches	for Disease Surveillance -HandiResponse	59
3.1.	. Al	ostract	59
3.2.	. In	troduction	60
3.3.	. M	aterials and methods	60
3	3.3.1.	Program description	60
3	3.3.2.	Program flow	67
3.4.	. In	plementation	67
3.5.	. Di	scussion	68
3	3.5.1.	Program design	68
3	3.5.2.	Risk mapping	69
3	3.5.3.	Models for disease introduction and spread	76
3	3.5.4.	Optimization of surveillance program	77
3.6.	. Co	onclusion	78
3.7.	. Re	eferences	79
4. I	Develo	pment of a generic system for creating a digital disease risk landscape – HandiMap	87
4.1.	. Al	ostract	87
4.2.	. In	troduction	88
4.3.	. M	ethod	88
4	.3.1.	Login to HandiResponse	88
4	1.3.2.	HandiMap operation	92
4.4.	. Re	esults	112
4.5.	. Di	scussion	119
4	1.5.1.	Rationale for development of HandiMap	119
4	1.5.2.	Selection of risk layers and environmental descriptors for genuinely novel diseases	s 120
4	1.5.3.	Standardization of risk values	123
4	1.5.4.	Relative importance of risk factors and environmental descriptors	123
4	1.5.5.	Challenges and limitations	124
4.6.	Co	onclusions	126

4	.7.	Refe	erences	. 127
5. Path			ng the benefit of risk mapping to predict temporal and spatial distribution of Highly vian Influenza (H5N1) outbreaks in southern Vietnam	. 133
5	.1.	Abs	tract	. 133
5	.2.	Intro	oduction	. 134
5	.3.	Met	hods	. 136
	5.3.	1.	Overall technical approach	. 136
	5.3.	2.	Risk map development	. 136
	5.3.	3.	Development of avian influenza H5N1 outbreak model for Southern Vietnam	. 137
	5.3.	4.	Statistical analysis	. 140
	5.3.	5.	Identifying good fit model(s)	. 140
5	.4.	Res	ults	. 140
5	.5.	Disc	cussion	. 150
	5.5.	1.	Rationale for the selection of Wave II HPAI H5N1 outbreak in Southern Vietnam.	. 150
	5.5.	2.	Identification of the best fit model(s)	. 151
	5.5.	3.	Relative importance of risk factors and environmental predictors	. 152
	5.5.	4.	The benefit of using a risk map for modelling H5N1 avian influenza	. 152
	5.5.	5.	Future direction	. 154
5	.6.	Con	clusion	. 154
5	.7.	Refe	erences	. 155
6.	Han	diMa	ap Assisted Risk-based Survey on Crimean Congo Haemorrhagic Fever in Mongolia	159
6	.1.	Abs	tract	. 159
6	.2.	Intro	oduction	. 160
6	.3.	Met	hods and Data	. 161
	6.3.	1.	Study area	. 161
	6.3.	2.	Investigation approach	. 161
	6.3.	3.	Development of CCHFV suitability map	. 162
	6.3.	4.	Field investigation	. 164
	6.3.	5.	Concordance analysis	. 164

	6.4.	Res	ults	. 165
	6.5.	Dis	cussion	. 169
	6.5.	1.	CCHF infection exists in Mongolia	.169
	6.5.	2.	Selection of risk factors	. 169
	6.5.	3.	Selection of sheep for the CCHF survey	. 170
	6.5.	4.	Inconsistency in CCHF occurrence between people and animals	. 170
	6.5.	5.	Timing for field investigation	. 172
	6.5.	6.	Interpretation of the risk landscapes	. 172
	6.5.	7.	Limitation of the study and future directions	. 173
	6.6.	Cor	nclusion	. 173
	6.7.	Ref	erence	. 174
7.	. Mo	dellir	ng alternative surveillance methods to detect incursion of an exotic zoonotic disease.	. 179
	7.1.	Abs	stract	. 179
	7.2.	Intr	oduction	. 180
	7.3.	Met	thods and data	. 181
	7.3.	1.	The example disease - Austeria	.181
	7.3.	2.	Data needed for modelling	. 182
	7.3.	3.	Surveillance components for the disease	. 193
	7.4.	Res	ults	. 196
	7.4.	1.	Temporal and spatial distribution of Austeria	. 196
	7.4.	2.	Number of days taken for Austeria detection	. 197
	7.4.	3.	Number of infected properties by the time of detection	. 199
	7.4.	4.	Number of Austeria outbreaks detected	.202
	7.5.	Dis	cussion	. 204
	7.5.	1.	Selection of disease and location for modelling	. 204
	7.5.	2.	Epidemiological performance of surveillance approaches	. 206
	7.5.	3.	Contributions and limitations of our approach	.209
	7.6.	Cor	nclusion	.210
	7.7.	Ref	erences	.211

8.	. Sele	ection of optimal surveillance portfolios for detecting the incursion of an emerging	
Z	oonotio	c disease affecting pigs and human beings	.215
	8.1.	Abstract	.215
	8.2.	Introduction	.216
	8.3.	Method and materials	.217
	8.3.	1. Details of the disease and populations	.217
	8.3.	2. Surveillance components	.217
	8.3.	3. Simulation modelling of Austeria and surveillance components/sub-components	.218
	8.3.	4. Estimation of economic effect of an Austeria outbreak and benefit of surveillance .	.219
	8.3.	5. Surveillance optimization approach	.224
	8.4.	Results	.226
	8.4.	1. Portfolios with the shortest expected 'number of days to detection'	.226
	8.4.	2. Portfolios with the highest net benefit	.227
	8.4.	3. Portfolios with the highest benefit cost ratio	.230
	8.4.	4. Portfolios with both early detection and high net benefit	.232
	8.4.	5. Portfolios with speedy detection and high benefit cost ratio	.234
	8.4.	6. The final set of optimal surveillance portfolios	.236
	8.5.	Discussion	.238
	8.5.	Feasibility of optimizing zoonotic disease surveillance	.238
	8.5.	2. Comparison of a surveillance portfolio with a single surveillance component	.240
	8.5.	3. Practical consideration of different criteria for surveillance decision making	.240
	8.6.	Conclusions	.244
	8.7.	References	. 245
9.	. Gen	neral discussion	.247
	9.1.	Goal of the thesis	.247
	9.2.	Studies undertaken in the thesis	. 247
	9.3.	Classification of diseases	.250
	9.4.	Steps in the HandiResponse surveillance planning process	.251
	9.5	Development of a risk man	251

9.6.	Using risk mapping to inform surveillance	256
9.7.	Development of optimal surveillance portfolios	257
9.8.	Practical value of HandiResponse	260
9.9.	Limitations and future direction	261
9.10.	Conclusion	262
9.11.	References	263

## **List of Figures**

Figure 2-1. Publications on RBS by year	8
Figure 2-2. Publications on RBS by source	8
Figure 2-3. Publications on RBS by continent	8
Figure 2-4. Publications on RBS by approach	8
Figure 2-5. Focus of Risk-based Surveillance	8
Figure 2-6. Algorithm for Prioritization of Disease Surveillance	11
Figure 2-7. Primary steps and key considerations in the collection and analysis of animal social	al
networks	14
Figure 2-8. A schematic overview of the process of predicting spatial disease risk	19
Figure 2-9. The Sentinel Framework in Context	24
Figure 2-10. Stylized scenario tree	26
Figure 2-11. Standardized approach for demonstration of freedom from disease by using scena	ario tree
modelling	27
Figure 3-1. Structure of HandiResponse and linkage between different modules	62
Figure 3-2. Algorithm for constructing a surveillance portfolio	65
Figure 3-3. Results of weight elicitation by different methods	75
Figure 3-4. Example: AHP result of weight elicitation by risk component and layer for HPAI	in
southern Vietnam	76
Figure 4-1. Login to IRIS	89
Figure 4-2. Entering HandiResponse	91
Figure 4-3. HandiResponse main screen.	93
Figure 4-4. Report details on the risk map of HPAI H5N1 outbreak for southern Vietnam	95
Figure 4-5. Selection of risk groups, layers	97
Figure 4-6. List of risk layers for selection under affected species.	98
Figure 4-7. Results of standardization of duck density layer	103
Figure 4-8. Risk layer weight assignments of M-Map for HPAI H5N1 outbreak, southern Viet	tnam 105
Figure 4-9. Group weight assignments of M-Map for HPAI H5N1 outbreak, southern Vietnam	1 106
Figure 4-10. A sample of risk level categorization	109
Figure 4-11. Selection of map presentation	111
Figure 4-12. Kernel smoothed P-Map for HPAI H5N1 outbreak, southern Vietnam (open street	et map)
	113

Figure 4-13. Non-kernel smoothed P-Map for HPAI H5N1 outbreak, Southern Vietnam (open st	reet
map)	114
Figure 4-14. Options for map presentation by HandiResponse	115
Figure 4-15. Selected individual risk layers for HPAI H5N1 outbreak in southern Vietnam	116
Figure 4-16. E-Map for HPAI H5N1 outbreak in southern Vietnam	117
Figure 4-17. M-Map for HPAI H5N1 outbreak in southern Vietnam	118
Figure 4-18. The structure and content of a sample risk file produced by Handimap	119
Figure 4-19. Comparison of results from weight elicitation methods for M-map	124
Figure 5-1. Approach for Screening best fit model for HPAI H5N1 outbreak in southern Vietnam	1.136
Figure 5-2. Adjustment procedure for transmission probabilities based on risk level	137
Figure 5-3. Plan of risk-adjusted disease modelling process	138
Figure 5-4. Comparison of four base models with the actual cumulative epidemic curve	142
Figure 5-5. Kernel smoothed E-map.	143
Figure 5-6. Kernel smoothed P-Map	143
Figure 5-7. Kernel smoothed M-map.	143
Figure 5-8. Comparison of spatial distribution of the good fit risk adjusted model with the actual	
outbreak in southern Vietnam, 2004/5	145
Figure 5-9. Comparison of daily cumulative number of infected communes of model 4-m-r-3-10	with
that of the actual outbreak in Southern Vietnam, 2004/5	146
Figure 5-10. Comparison of number of daily infected communes under model 4-m-r-3-10 with the	nat of
the actual outbreak in Southern Vietnam, 2004/5	147
Figure 5-11. Result of Kolmogorov Smirnov Test	148
Figure 5-12. Epidemic Waves of HPAI H5N1 in Mekong River Delta, Vietnam	151
Figure 6-1. Habitat suitability map for tick distribution (CCHFV I map)	165
Figure 6-2. Risk map for CCHF occurrence (CCHFV II-1 map)	165
Figure 6-3. Risk map for CCHF occurrence (CCHFV II-2 map)	166
Figure 6-4. Number of sheep by district in Mongolia, 2013	166
Figure 6-5. Districts selected for field investigation of CCHF in Mongolia, 2013	167
Figure 7-1. Estimated relative density of feral pigs in Queensland, Australia	186
Figure 7-2. Infection transmission routes between herd types for pigs in Queensland, Australia	187
Figure 7-3. Number of daily cumulative infected farms of an uncontrolled Austeria outbreak in	
Queensland, Australia	196
Figure 7-4. Spatial distribution of Austeria infected pig herds in a median outbreak overlaid on to	op of
the feral pig zones in Queensland, Australia.	197
Figure 7-5. Number of days taken for Austeria detection by surveillance approach	199
Figure 7-6. Median number of herds infected by the day of detection, by surveillance approach	201

Figure 7-7. Percentage of the 99 simulated Austeria outbreaks detected by each surveillance appr	oach
within 365 days	203
Figure 7-8. Estimated density of backyard pig herds in Australia <sup>1</sup>	205
Figure 7-9. Estimated density of feral pigs in Australia based on habitat	205
Figure 7-10. Weekly cumulative Austeria epidemic curves by pig production sector	207
Figure 8-1. Optimization process under OptiSurv Program	224
Figure 8-2 Summary screen of OptiSurv	226
Figure 8-3. Optimal performance of a surveillance strategy	241
Figure 8-4. The weekly count of infected farms caused by a medium sized Austeria outbreak in	
Queensland, Australia	242
Figure 8-5 Generic form of economic analysis of zoonoses being developed -beyond the scope of	f this
project	243
Figure 9-1 Thesis structure	248
Figure 9-2. Structure of HandiResponse and linkage between different modules	249

### **List of Tables**

Table 2-1. Key vectors, relevant environmental/climatological predictors and diseases	20
Table 2-2. Contextual factors for evaluation of methods for space-time analysis of disease	
surveillance	25
Table 2-3. Suggested framework for simplified sampling scheme for Trichinella in European Unio	n30
Table 2-4. Summary on when likelihood and consequence need to be used for different RBS	32
Table 2-5. Summary on technical efficiency improvement by RBS	34
Table 2-6. Summary on economic efficiency improvement by RBS	35
Table 2-7. Development of output based surveillance for demonstration of freedom from disease	38
Table 3-1. Essential Steps for Risk Mapping by Using HandiMap	63
Table 3-2. Key Parameters Used for Estimating Performance of Surveillance Subcomponent	65
Table 3-3. Typology of risk map	70
Table 3-4. Epitypes of Zoonoses	72
Table 3-5. Categorization of risk factors related to emerging infectious diseases	73
Table 3-6. Selected key risk factors, environmental predictors and their proposed relationship with	l
HPAI H5N1 outbreaks in South East Asia	74
Table 4-1. Summary of selected putative risk factors, environmental predictors and their relationsh	nip
with HPAI H5N1 outbreaks in South East Asia	.100
Table 4-2. Selected putative risk factors and environmental predictors for HPAI H5N1 Outbreaks is	in
Vietnam	.101
Table 4-3. AHP for weight assignment for risk layers for the P-Map estimating the risk of HPAI	
H5N1 outbreak, southern Vietnam	.104
Table 4-4. Final weight assignments for selected risk factors and environmental descriptors	.107
Table 5-1. Key parameters needed for HPAI H5N1 outbreak model	.139
Table 5-2. Criteria for assessing fit of HPAI model(s) to actual epidemic data	.140
Table 5-3. Summary of goodness of fit of models to actual epidemic	.144
Table 5-4. ROC association statistics for Model 4-m-r-3-10	.149
Table 5-5. Weight assignments under three additional hypotheses	.152
Table 5-6. Average AUC under three additional hypotheses	.152
Table 5-7. Epidemiological contribution of different transmission routes under m4-m-r-3-10	. 153
Table 6-1. Putative environmental and climatological factors for CCHFV suitability mapping	.162
Table 6-2. Selected putative environmental/climatological predictors for CCHF mapping in Mongo	olia
	163

Table 6-3. Assumed relationship between a selected environmental and climatological descriptor	and
tick distribution, human CCHF infection risk	163
Table 6-4. Weight assignment for selected environmental/climatological descriptors for CCHF	
mapping in Mongolia	164
Table 6-5. Anti-CCHFV IgG prevalence among human and sheep by district surveyed	168
Table 6-6. Districts in disagreement in CCHF status between human and sheep	171
Table 6-7. CCHFV antibody test results for sheep samples in selected districts by ELISA and IFA	. 171
Table 7-1. Number of feral pig and commercial pig herds in Queensland, Australia, 2013	183
Table 7-2. Estimated distribution of feral families by risk zone in Queensland, Australia	185
Table 7-3. Number of owned herds of each type in the feral pig density zones	185
Table 7-4. Movement type 1: Simulates routine movements within and among the types of	
commercial and backyard pig holdings	188
Table 7-5. Movement type 1: distance matrix	188
Table 7-6. Movement type 2: Simulates movement of commercial and backyard pig holdings to s	ale
yards	189
Table 7-7. Movement type 2: movement distance matrix	189
Table 7-8. Movement type 3: simulates movement from sale yards to commercial and backyard p	ig
holdings	190
Table 7-9. Movement type 3: distance matrix	190
Table 7-10. Movement type 4: Long distance movements among feral pigs	191
Table 7-11. Movement type 4: distance matrix	192
Table 7-12. Local spread 1: probability of transmission	192
Table 7-13. Adjustment in probability of transmission for specific farm class destinations	192
Table 7-14. Local spread type 2: probability of transmission	192
Table 7-15. Local spread type 2: adjustment in probability of transmission for specific farm class	
destinations	193
Table 7-16. Local spread type 3: probability of transmission	193
Table 7-17. Local spread type 3: adjustment in probability of transmission for specific farm class	
destinations	193
Table 7-18. Subjects for each Austeria surveillance component	194
Table 7-19. Description of surveillance components for Austeria	195
Table 7-20. Two examples of defining surveillance intensity and probability of detection for the h	nigh
intensity sub-component	195
Table 7-21. Mean number of days taken for each surveillance component to detect Austeria over	up to
99 iterations, Queensland, Australia (summarized for 9 sub-components)	197
Table 7-22. Mean number of farms infected by the day of detection over up to 99 iterations,	200

Table 7-23. Mean Percentage of Austeria outbreaks detected over 99 iterations for each surveillance
component in Queensland, Australia (summarized for 9 sub-components)
Table 7-24. Comparison of HCR and RB2 by the day of onset and the day of detection208
Table 7-25. Comparison of number of infected farms under different surveillance approaches209
Table 8-1. The nine surveillance components evaluated in the study and the populations in which they
were applied
Table 8-2. Description of surveillance components and sub-components for Austeria218
Table 8-3. Terminology and definitions used in the economic evaluation of surveillance
components/sub-components
Table 8-4. Diet specifications and ingredient costs for Australian pig budgeting model220
Table 8-5. Key performance metrics influencing cost of production and net revenue per pig in herds
with and without Austeria
Table 8-6. Economic net loss per pig due to Austeria under different production systems in Australia
Table 8-7. Top ten surveillance portfolios for Austeria in Australia with the shortest days to detection
Table 8-8. Top ten surveillance portfolios for Austeria in Australia with the highest net benefit229
Table 8-9. Top ten surveillance portfolios for Austeria in Australia with high benefit cost ratio231
Table 8-10. Top ten surveillance portfolios for Austeria in Australia with fast detection and high net
benefit
Table 8-11. Top ten surveillance portfolios for Austeria in Australia with fast detection and high
benefit cost ratio
Table 8-12. A summary of the best surveillance portfolios for Austeria in Australia
Table 8-13 Comparison of the optimal surveillance portfolios with single components for two
different surveillance decision rules
Table 9-1 The purpose and output of different modules of HandiResponse 250

#### **Abbreviations**

**Abbreviation** Explanation

ACF Autocorrelation Function
AHP Analytic Hierarchy Process

ARIMA Autoregressive Integrated Moving Average

AUC Area Under Curve bTB bovine Tuberculosis

CAC Codex Alimentarius Commission
CCHF Crimean Congo Haemorrhagic Fever

COS Consequence of spread
CV Coefficient of Variation
CWD Chronic Wasting Disease
DALY Disability Adjusted Life Year

DR Direct Rating

EBL Enzootic Bovine Leucosis

ELISA Enzyme-linked Immunosorbent Assay

ERID Emerging and Re-emerging Infectious Diseases

GARP Genetic Algorithm for Rule-set Prediction

GIS Geographic Information System
GLM Generalized Linear Model

HandiEcon Human and Animal Disease Economic Module
HandiMap Human and Animal Disease Mapping Module
HandiResponse Human and Animal Disease Response Program
HandiSpread Human and Animal Disease Spread Program
HandiSurv Human and Animal Disease Surveillance Module
HandiView Human and Animal Disease View Program

HIV Human Immunodeficiency Virus
HPAI Highly Pathogenic Avian Influenza
IFA Indirect Immunofluorescence Assay
IPPC International Plant Protection Convention

LOS Likelihood of Spread

MADM Multi-Attribute Decision Making

MARP Most at Risk Population

MCDA Multiple-criteria Decision Analysis
NDVI Normalized Difference Vegetation Index
OIE World Organization of Animal Health

OptiSurv Optimal Surveillance Module

PA Point Allocation

PACF Partial Autocorrelation Function
PCR Polymerase Chain Reaction
POE Probability of Exposure

PRRS Porcine Reproductive and Respiratory Syndrome

RBS Risk-based Surveillance
RDS Respondent Driven Sampling

ROC Rank Order Centroid

ROC Receiver Operating Characteristic

RS Remote Sensing

SNA Social Network Analysis

SPS Sanitary and Phytosanitary Measures/Agreement

SSC Surveillance System Component

TLS Time Location Sampling
WHO World Health Organization
WLC Weighted Linear Combination
WTO World Trade Organization
WTP Willingness To Pay