

EVALUACION DE ESTRATEGIAS DE CONTROL Y PREVENCION DE ENFERMEDADES TRANSFRONTERIZAS MEDIANTE EL USO DE MODELOS MATEMATICOS

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<https://www.spablo-temporal.network>

SECCIONES

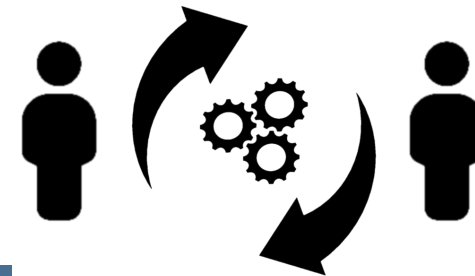
- Introducción
- Modelos para introducción de enfermedades
- Modelos de dispersión de enfermedades

QUE ES UN SISTEMA COMPLEJO?

Numero de elementos
y estructuras jerarquicas

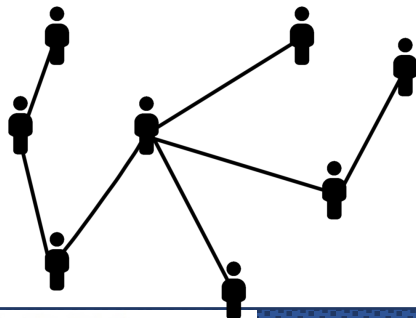


Interdependencia



Que es un sistema
complejo?

Conectividad



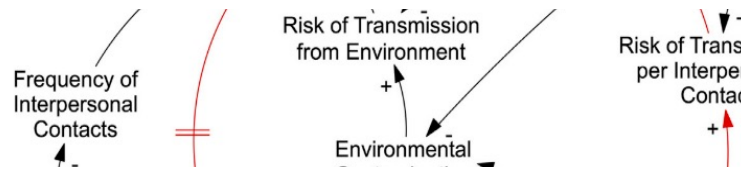
Autonomia



Epidemics on dynamic networks

Jessica Enright^a, Rowland Raymond Kao^{b,*}

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Social Network Analysis. Review of General Concepts and Use in Preventive Veterinary Medicine

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² Center for Animal Disease Modeling and Surveillance, VM: Medicine and Epidemiology, UC Davis, Davis, CA, USA; and CONICET, Facultad de Ciencias Veterinarias UNR, Casilda, Santa Fe, Argentina

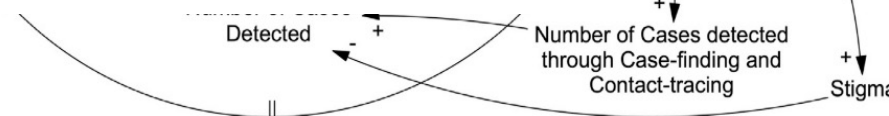


Fig. 1. An example causal loop diagram illustrating some of the interacting components in a society responding to the threat of COVID-19.

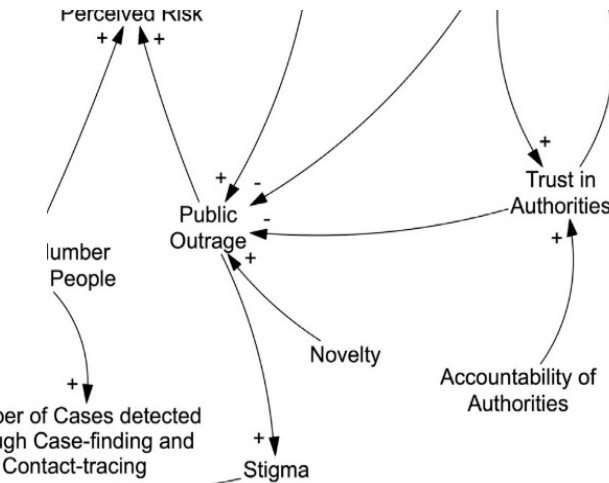
Heterogeneities in the transmission of infectious agents: Implications for the design of control programs

(basic reproduction number/HIV/AIDS/leishmaniasis/malaria/schistosomiasis)

M. E. J. WOOLHOUSE^{*†}, C. DYE[‡], J.-F. ETARD^{§¶}, T. SMITH^{||}, J. D. CHARLWOOD^{||}, G. P. GARNETT^{*}, P. HAGAN^{**}, J. L. K. HUI^{††}, P. D. NDHLOVU^{‡‡}, R. J. QUINNELL[‡], C. H. WATTS^{§§}, S. K. CHANDIWANA^{‡‡}, AND R. M. ANDERSON^{*}

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Communicated by Robert May, University of Oxford, Oxford, United Kingdom, October 7, 1996 (received for review March 2, 1996)



Bradley 2020

Que es un modelo?

Que sabemos?

Lo que pensamos que sabemos

Que pararía si?...

Observaciones
Literatura



Experiencia



Hipótesis



Nueva información

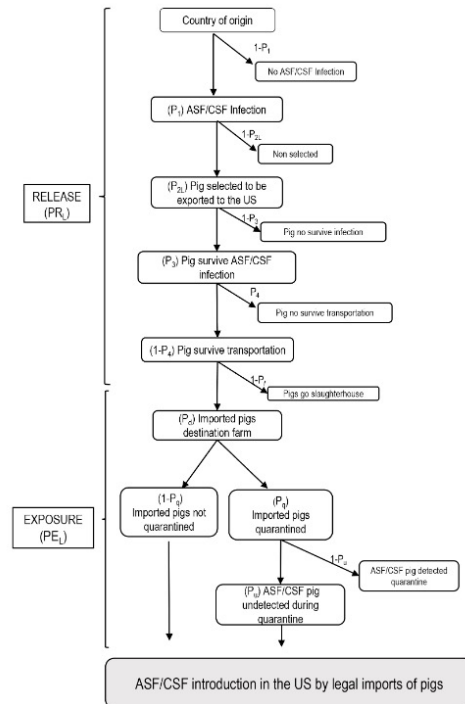


Fig 1. Event tree of ASF/CSF introduction into the US by the legal imports of live pigs.

<https://doi.org/10.1371/journal.pone.0182850.g001>

Table 2. Description of input parameters and probabilities used in the quantitative models for the release and exposure assessment of the risk of ASF/CSF introduction into the US through legal imports of live pigs.

Notation	Definition	Parametrization	Source	Values
P_i	Probability of ASF ^a /CSF ^b infection in the country of origin	Free countries: Pert (min, most likely, max)	Free- countries: SI model results	
P_{sel}	Probability of selecting an ASF ^a /CSF ^b infected pig from country c before the detection of the infection	Beta (α_1, α_2) • $\alpha_1 = NI + 1$ • $\alpha_2 = N_c \cdot (NI + 1)$	• NI = $O_u \cdot T_o \cdot H_p$ • No = pig population in c	
O_u	Number of ASF ^a /CSF ^b undetected outbreaks before official notification	Pert (min, most likely, max)	^a Outbreaks in Europe (2007–2016) [14] ^b World outbreaks (2006–2016) [14]	^a Pert (1, 1.28, 6) ^b Pert (1, 2, 3)
T_o	Average herd size in country c	Normal = N_h/S_o	[24]	
N_h	Pig population in country c	Normal (0078, σ)	[14] [24]	
S_o	Number of pigs establishments in country c	Normal (μ, σ)	[14]	
H_p	Intra-herd prevalence ^a ASF/CSF	Pert (min, most likely, max)	^a Data from outbreaks in Europe (cases/susceptible) [14] ^b [30]	^a Pert (0.05, 0.15, 0.32) ^b Pert (0.05, 0.4, 1)
P_t	Probability of pigs survival to ASF/CSF infection	Pert (min, most likely, max)	about 100%	^a Pert (0.05, 0.2, 0.9)

$$PLF = (W_R * LF_R + R_{RTE} * LF_{RTE} + W_H * LF_H) * FP_A * LF_{FP}$$

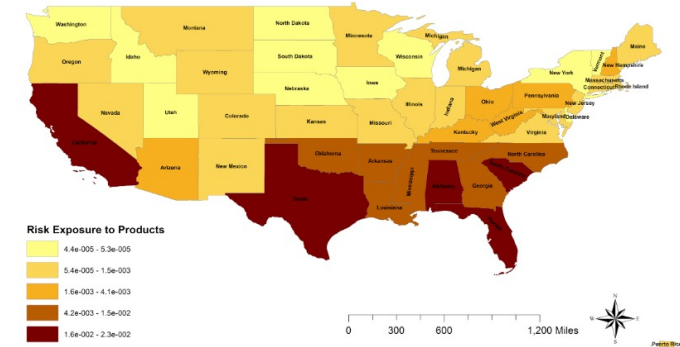


Fig 5. Risk of exposure to legal imports of swine products. The graduated color map represents the risk from the highest (darker) to the lowest (lighter) of US susceptible swine populations being exposed to the legally imported swine products.

<https://doi.org/10.1371/journal.pone.0182850.g005>

EVALUACION DEL RIESGO DE INTRODUCCION

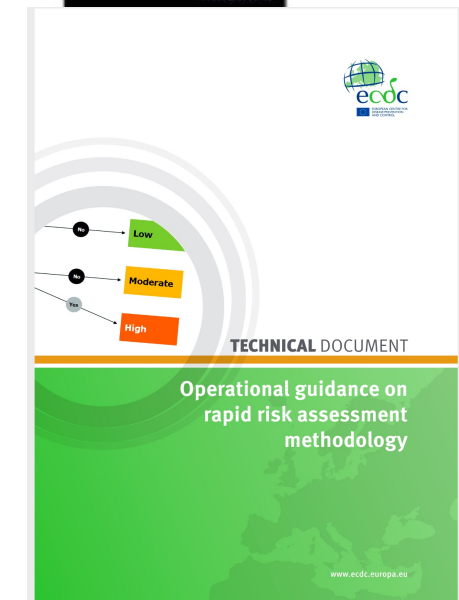
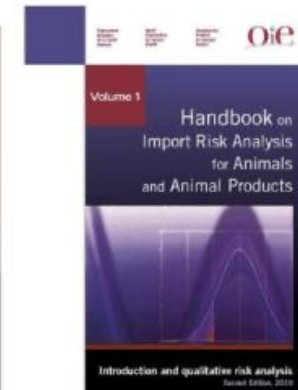
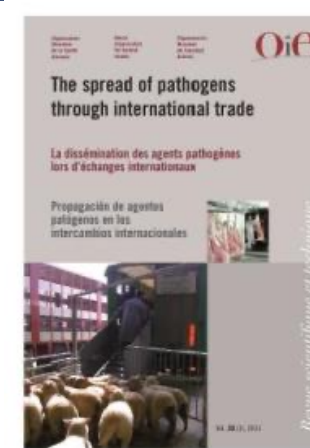
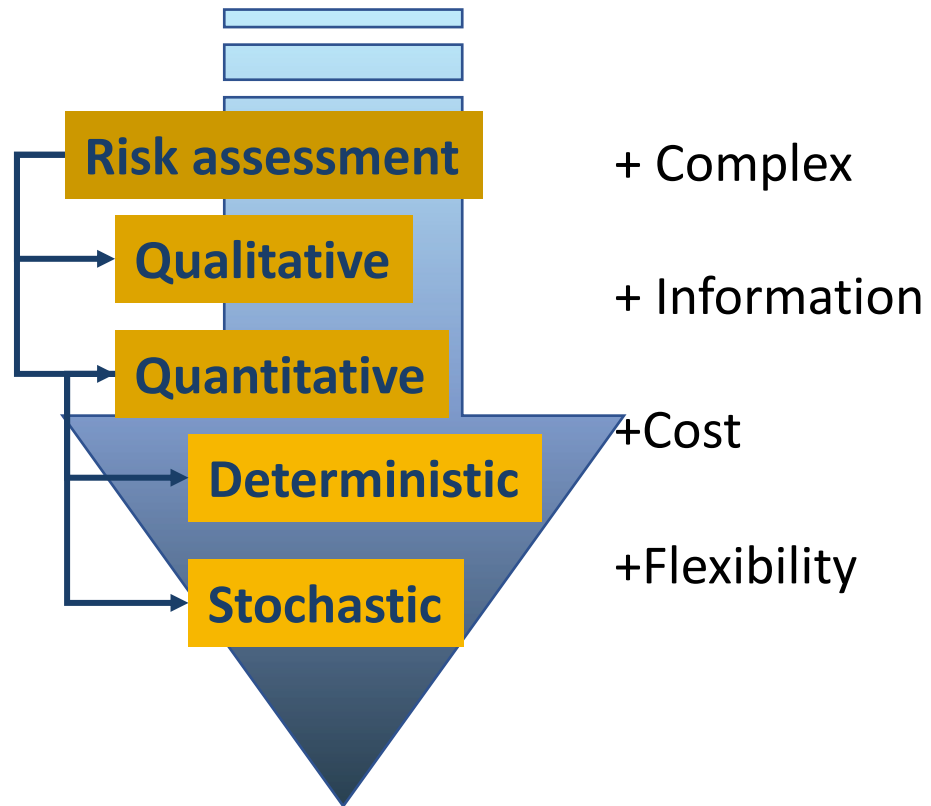
INTRODUCCIÓN

Risk analysis



OIE 2021

INTRODUCCIÓN



INTRODUCCIÓN

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Step 1

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\$2,038 /yr

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BUY NOW

1 Year

\$2,595 /yr

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Step 2

- ✓ All the benefits of the Professional Edition, PLUS:
- ✓ Time-series functions that represent values which change over time
- ✓ Fast simulation speeds with multiple, unlimited processors
- ✓ RISKOptimizer for combining Monte Carlo simulation with optimization, for budgeting, resource allocation, scheduling, and more
- ✓ Efficient Frontier analysis to determine the optimal return at a given level of risk



```
391     psm = psmpt(x),
392     pst = pstz(x)
393   ) %>%
394   pt_MeatProducts(.)
395 } %>%
396 do.call(rbind, .) %>%
397 data.frame() %>%
398 mutate(Introduced = round(pt * input$Nanimals),
399        p01 = p01,
400        piv = piv)
401 }
402 }
403
404 ## OUTPUTS
405 output$Pop2 <- renderValueBox({
406   p <- Pt_MeatProd[1]
407   # paste0(round(Pt_MeatProd[1]*input$Nprod2), ' ', round(Pt_MeatProd[1]*100, 4), '%')
408
409   ci <- ifelse(between(x = p, left = 0, right = 0.05), 'green',
410              ifelse(between(p, 0.05, 0.4), 'orange', 'red'))
411
412   ti <- ifelse(between(x = p, left = 0, right = 0.05), 'Low',
413              ifelse(between(p, 0.05, 0.4), 'Medium', 'High'))
414
415   valueBox(value = paste0(round(p*input$Nprod2), ' ', round(p*100, 4), '%'),
416           color = ci,
417           icon = icon('exclamation-triangle'),
418           subtitle = ti)
419 })
420
421
422 output$StochPlot2 <- shiny::renderPlot({
423   Pt_MeatProd$() %>%
424   ggplot() +
425   geom_density(aes(pt), fill = 'red', alpha = 0.5) +
426   labs(x = 'Probability of introduction') +
427   Pablove::Theme1()
428 })
429
430 output$StochDesc2 <- renderValueBox({
431   p <- median(Pt_MeatProd$pt)
432   ci <- ifelse(between(x = p, left = 0, right = 0.05), 'green',
433              ifelse(between(p, 0.05, 0.4), 'orange', 'red'))
434   ti <- ifelse(between(x = p, left = 0, right = 0.05), 'Low',
435              ifelse(between(p, 0.05, 0.4), 'Medium', 'High'))
436 }
```

OBJETIVO

Desarrollar una plataforma para
evaluacion de riesgo que permita un
 analisis mas transparente y
reproducible

HERRAMIENTAS

{QuantRRA}

{QuantRRA} is a package for rapid risk assessment developed for the statistical software R.



Installing QuantRRA

You can install `QuantRRA` development version from [GitHub](#) (if you have R > 3.5):

```
# make sure you have the package devtools installed
devtools::install_github("jpablo91/QuantRRA")
```

id	label	type	level	distribution	formula
1	P0	Prevalence	In	1	Pert(0.01, 0.1, 0.15)
2	P1	Vaccine Efficacy	In	1	Pert(0.7, 0.8, 0.9)

- Sample distribution
- Fitting distributions
- RRA: Main function
- Sensitivity analysis
- Shiny interface

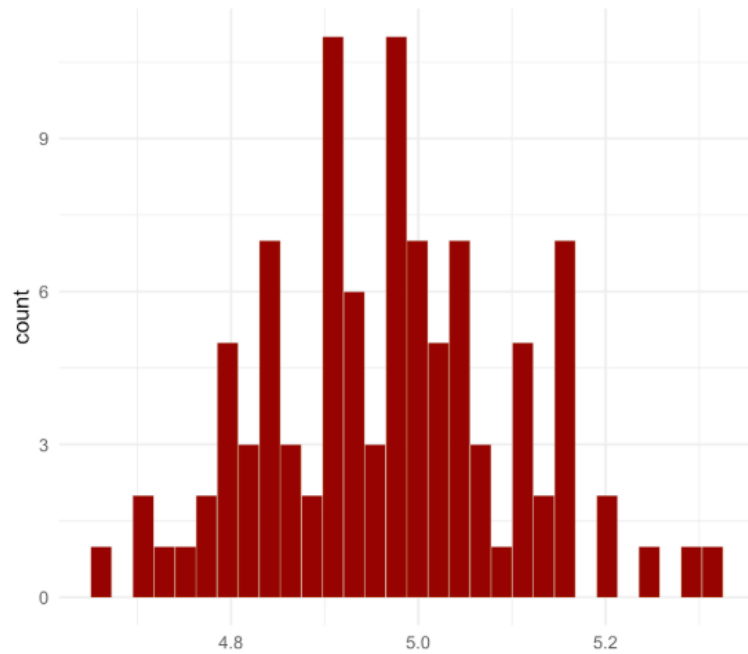
HERRAMIENTAS

```
n <- 100 # number of observations
d <- 'Normal(5, 0.12)' # Distribution to sample

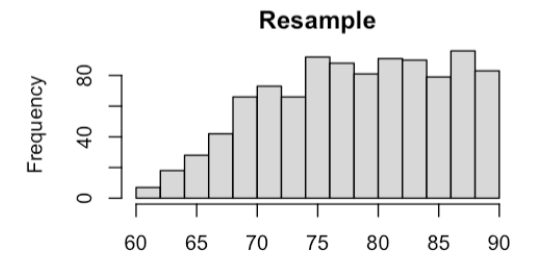
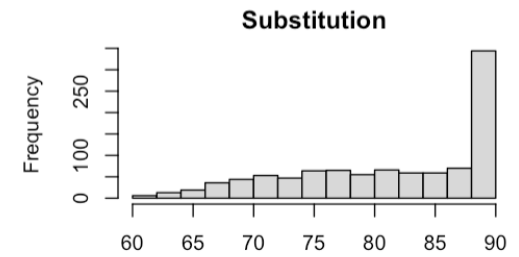
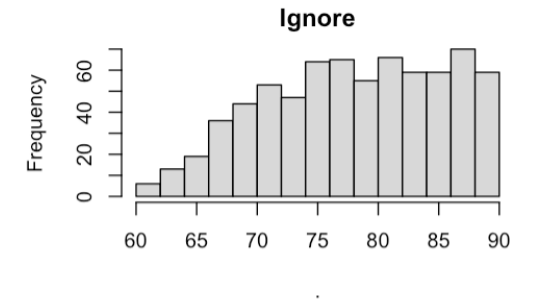
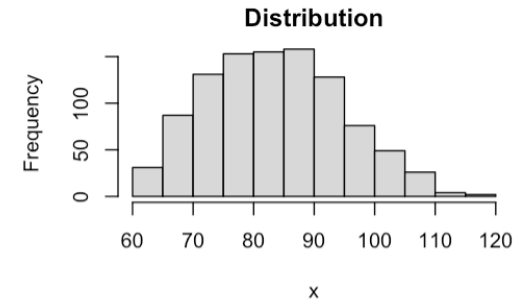
x <- SampleDist(x = d, n = n) # Function to sample the distribution

# We can use the function plotDist() from the package QuantRRA to get a more familiar output:
plotDist(x, # the values sampled
         main = 'Distribution of x') # A title for our plot
```

Distribution of x

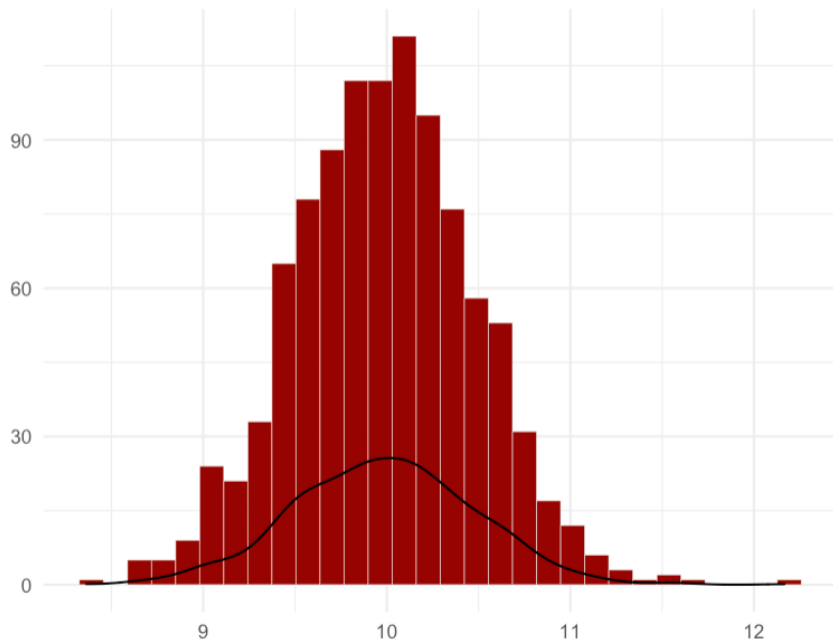


Value	
<i>min</i>	4.662
<i>max</i>	5.315
<i>mean</i>	4.969
<i>StdDev</i>	0.134



HERRAMIENTAS

NORMAL(9.99, 0.5)



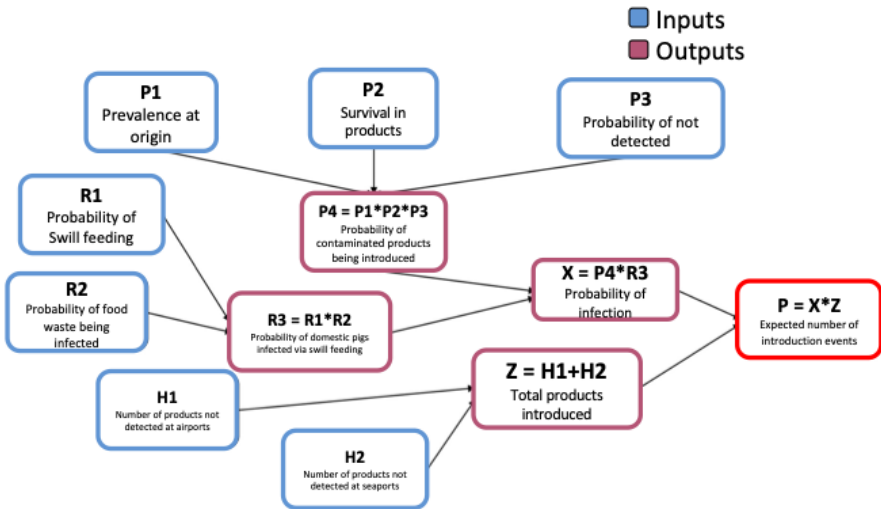
	Value
<i>min</i>	8.36357
<i>max</i>	12.1656
<i>mean</i>	9.986204
<i>StdDev</i>	0.4954982
<i>OLS</i>	1.3

```
WhichDist(x, distributions = dists)
```

Description: df [5 × 2]

distribution <chr>	value <dbl>
NORMAL(10, 1.32)	9.40
TRIANGLE(6.03, 10.97, 14.18)	336.40
PERT(6.02, 11.02, 14.21)	570.23
UNIFORM(7.53, 14.19)	1358.33
POISSON(9.34)	3004.24

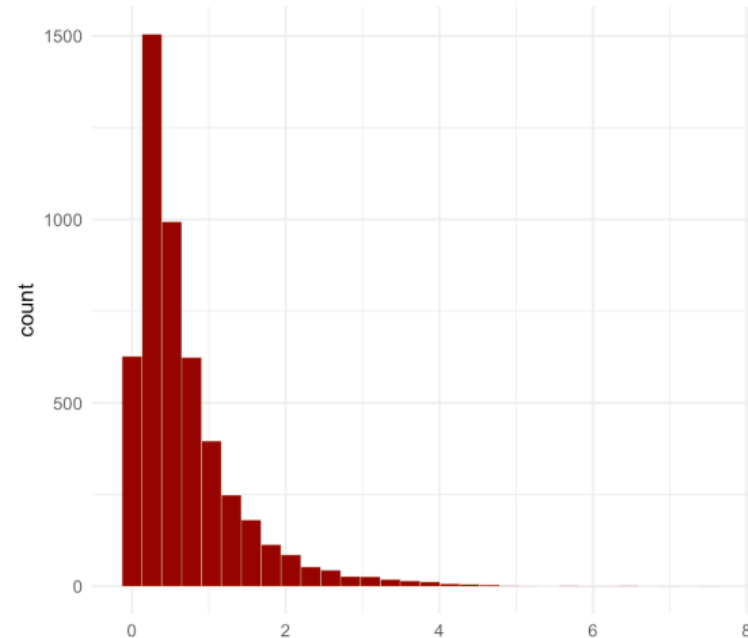
HERRAMIENTAS



id	label	type	level	distribution	formula
<chr>	<chr>	<chr>	<int>	<chr>	<chr>
P1	Prevalence	In	1	Pert(0.1, 0.54, 0.75)	NA
P2	Survival	In	1	Pert(0.01, 0.1, 0.6)	NA
P3	Detection	In	1	Pert(0.1, 0.25, 0.55)	NA
P4	Introduction	Out	2	NA	P1*P2*P3
R1	Swill feeding	In	1	Pert(0.1, 0.8, 0.95)	NA
R2	Food contamination	In	1	Pert(0.1, 0.55, 0.96)	NA
R3	Ingestion prob	Out	2	NA	R1*R2
X	Infection Probability	Out	3	NA	P4*R3
H1	Airport introduction	In	1	Pert(0, 32, 160)	NA
H2	Seaports intro	In	1	Pert(0, 22, 90)	NA

1-10 of 12 rows Previous 1 2 Next

```
# Save the model file to an object
M <- QuantRRA::OIRSA_M
# Run the model 5000 times
Mo <- RRA(M = M, nsim = 5000)
# Visualize the results:
plotDist(Mo$P)
```

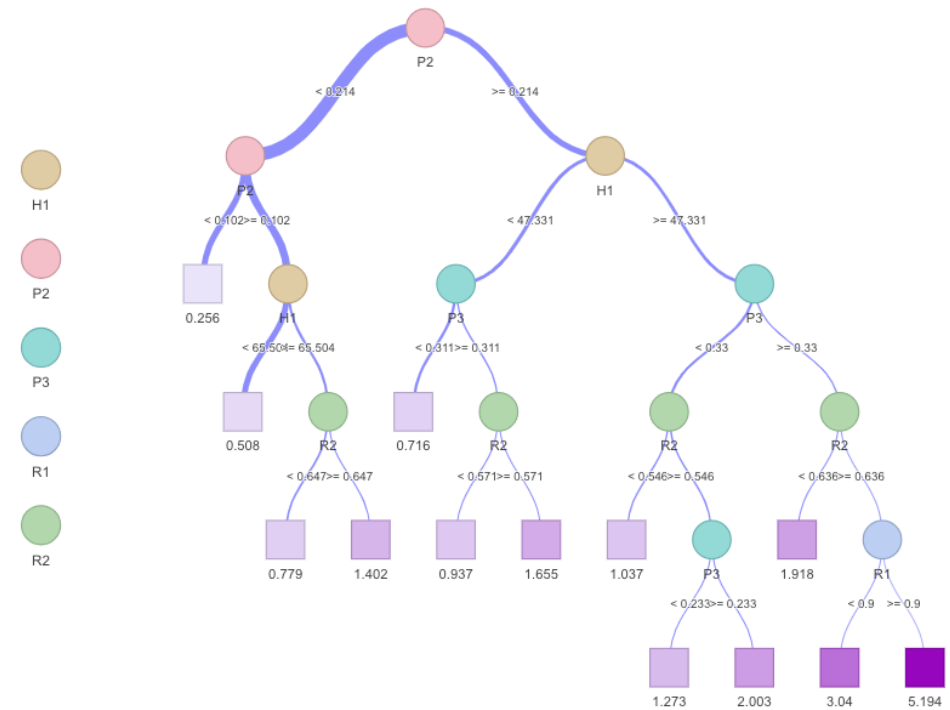
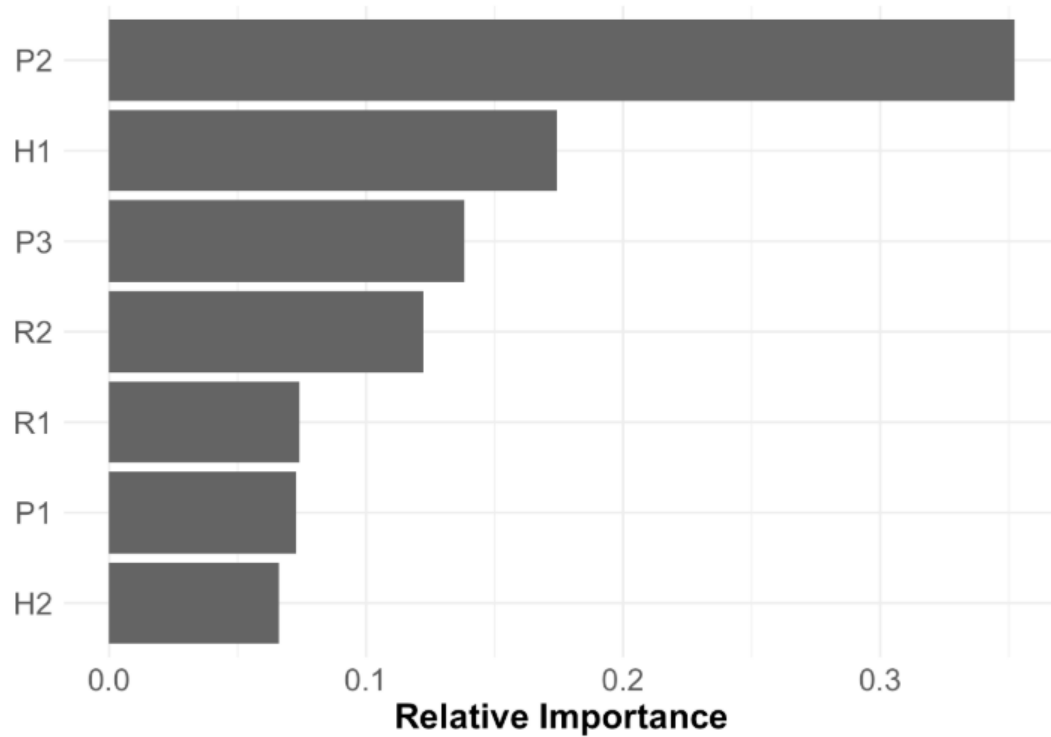


Value
min 0.00659
max 7.50472
mean 0.69834
StdDev 0.72703

$$P(a < x < b)$$

HERRAMIENTAS

```
# First we specify the formula:  
f <- P ~ P1 + P2 + P3 + R1 + R2 + H1 + H2  
# Then we use the function with our results  
SA <- RFCART(data = Mo, f = f, tree = 'interactive')
```



MODELOS ESTRATIFICADOS

```
# Run the model for all the states
rabRR <- QuantRRA::RRA_s(M = M, Tbl = rbts, nsim = 5000)
```

	State	I1	I2	I3	I4	I5	I6
1	AGUASCALIENTES	Pert(207178, 229628, 233325)	Pert(830762, 872284, 913173)	Pert(187, 359, 472)	Pert(0.936449158898532, 0.94634257999594, 0.948298987928301)	Pert(0.01, 0.1, 0.15)	Pert(0.1, 0.3, 0.5)
2	BAJACALIFORNIA	Pert(213802, 304764, 349926)	Pert(2192229, 2304488, 2414741)	Pert(367, 689, 807)	Pert(0.9087063215014, 0.911744825504325, 0.9212947880409)	Pert(0.01, 0.1, 0.15)	Pert(0.1, 0.3, 0.5)
3	BAJACALIFORNIASUR	Pert(98523, 99893, 110438)	Pert(475014, 503531, 531689)	Pert(166, 240, 291)	Pert(0.90517968463513, 0.921114675139385, 0.961146128315216)	Pert(0.01, 0.1, 0.15)	Pert(0.1, 0.3, 0.5)
4	CAMPECHE	Pert(77553, 163240, 178096)	Pert(591801, 621328, 650365)	Pert(188, 376, 491)	Pert(0.970475752513228, 0.984592579283083, 0.993474269718067)	Pert(0.01, 0.1, 0.15)	Pert(0.1, 0.3, 0.5)
5	CHIAPAS	Pert(47769, 344045, 460400)	Pert(3060969, 3201316, 3339960)	Pert(854, 1247, 1412)	Pert(0.973162511252067, 0.99161156244096, 0.998004471184864)	Pert(0.01, 0.1, 0.15)	Pert(0.1, 0.3, 0.5)

Showing 1 to 5 of 32 entries

Previous **1** 2 3 4 5 6 7 Next



INTERFAZ INTERACTIVA

QuantRRA

- Model
- Model**
- Stratified Model
- Sensitivity Analysis
- Distribution Fitting
- Documentation
- Examples

QuantRRA: Quantitative rapid risk assesment

This application is still under development, documentation will be shortly added, for any questions please contact the developer: [Jose Pablo Gomez](#)

The following application was developed for the implementation of rapid risk assesment. A model tree file can be uploaded or specified in the app, and the risk is estimated using a stochastic probabilistic model.
Example model files can be found in the library of exmaples tab in this application

Model table

To start, you need to specify the model. Models can be constructed directly from the app using the network tools in the following section, or can be uploaded from a model file previously created.

Upload a model file

Browse... No file selected

Show entries Search:

	id	label	type	level	distribution	formula
1	P0	Prevalence	In	1	Pert(0.01, 0.1, 0.15)	
2	P1	Vaccine Efficacy	In	1	Pert(0.7, 0.8, 0.9)	

INTERFAZ INTERACTIVA

The screenshot displays the QuantRRA RStudio interface. The main editor shows an R Markdown file with the following content:

```
1 ---
2 title: "QuantRRA: Quantitative Risk assessment with R"
3 output:
4   html_document:
5     df_print: paged
6     toc: true
7     toc_float: true
8     number_sections: true
9 ---
10
11 ```{r gloabl options, include = F}
12 knitr::opts_chunk$set(warning = F, message = F)
13 ```
14
15
16 # Objectives
17
18 In this vignette we will be using R, which is an open access software developed for
19 statistical analysis (but can do some data manipulation, simulation and modeling). We will
20 be using the package `QuantRRA` for rapid risk assessment (still under development). Make
```

The environment pane on the right shows the Global Environment with the following data objects:

Object Name	Description
Documen...	List of 3
Examples	List of 3
init_ed...	4 obs. of 3 variab...
init_no...	4 obs. of 8 variab...
M	12 obs. of 8 varia...
Mo	5000 obs. of 12 va...
SA	List of 3

The console at the bottom shows the R prompt and the current directory path: `R 4.1.3 ~ /Library/CloudStorage/Box-Box/Tools/Packages/QuantRRA/`.

Ejemplo

RESEARCH ARTICLE

Quantitative approach for the risk assessment of African swine fever and Classical swine fever introduction into the United States through legal imports of pigs and swine products

Diana María Herrera-Ibatá¹, Beatriz Martínez-López², Darla Quijada³, Kenneth Burton³, Lina Mur^{1*}

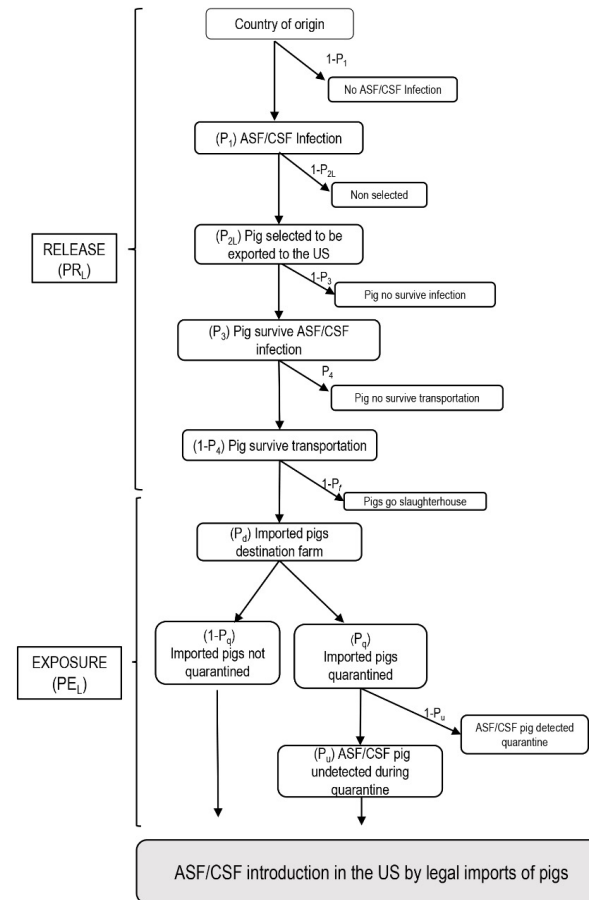
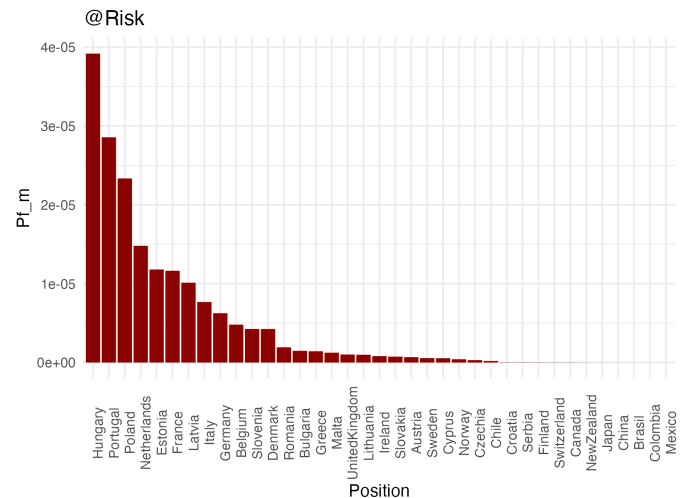
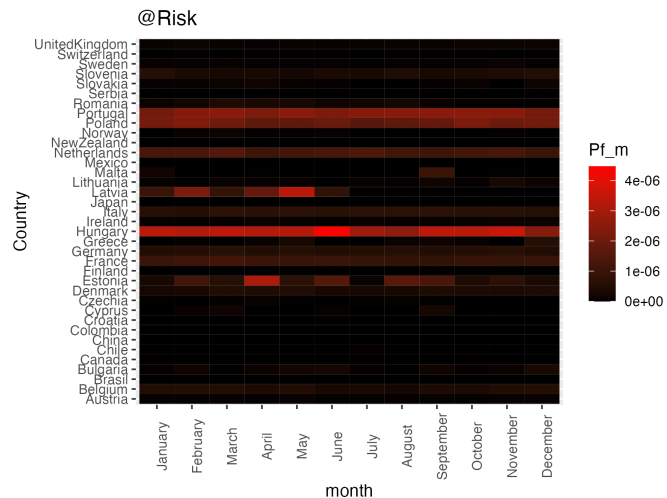
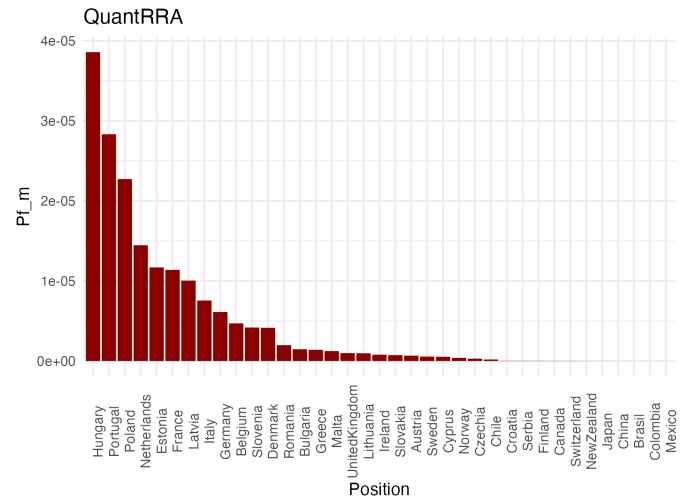
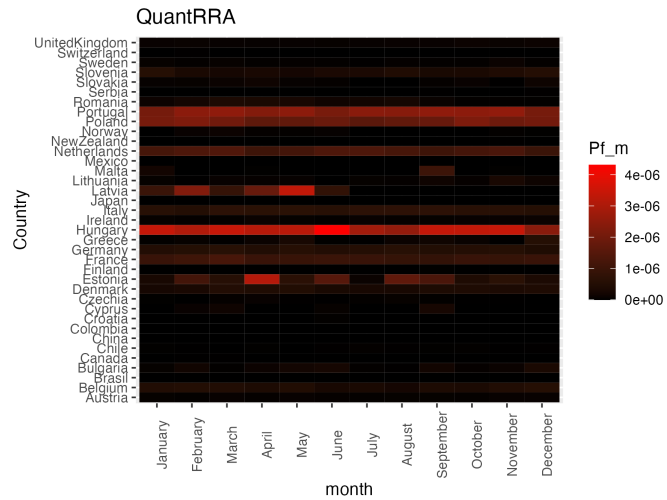


Fig 1. Event tree of ASF/CSF introduction into the US by the legal imports of live pigs.

<https://doi.org/10.1371/journal.pone.0182850.g001>



EJEMPLOS

Resultados del reporte

Diagrama 17.
Probabilidad de ingreso de mercancía porcina potencialmente contaminada

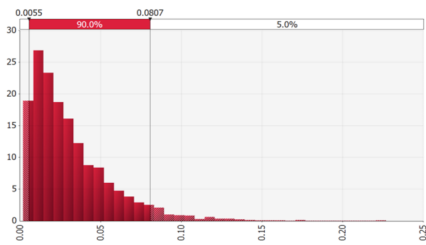


Diagrama 20.
Probabilidad de que cerdos domésticos sean alimentados con desperdicios de alimentos contaminados con vPPA

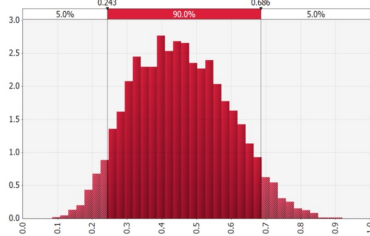


Diagrama 21.
Probabilidad de infección de cerdos domésticos con vPPA

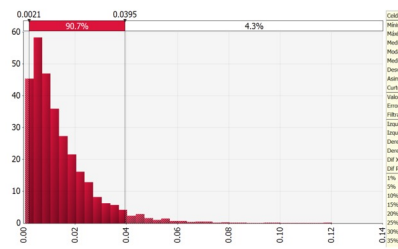
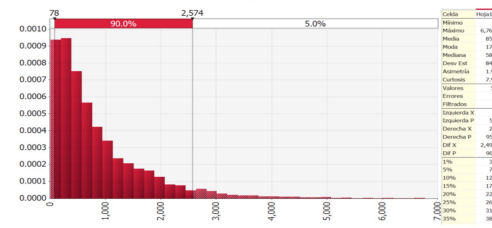
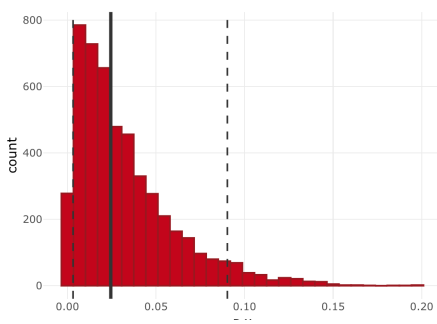


Diagrama 24.
Cantidad (Kg) probable de productos contaminados no decomisados en puertos y aeropuertos

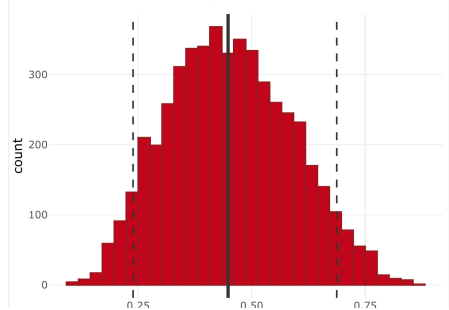


Resultados de QuantRRA

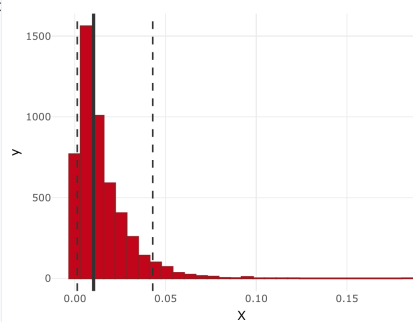
P4: Probabilidad de mercancía contaminada



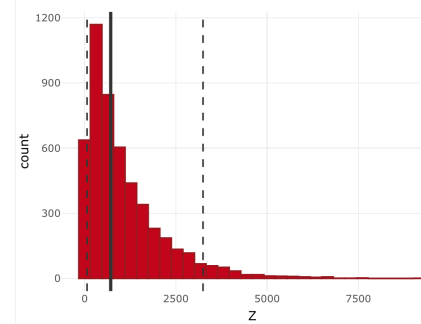
R3: Probabilidad de que cerdos sean alimentados con vPPA



X: Probabilidad de infección de cerdos domésticos con vPPA



Z: Cantidad (kg) probable de productos contaminados no decomisados en puertos y aeropuertos



Análisis de riesgo

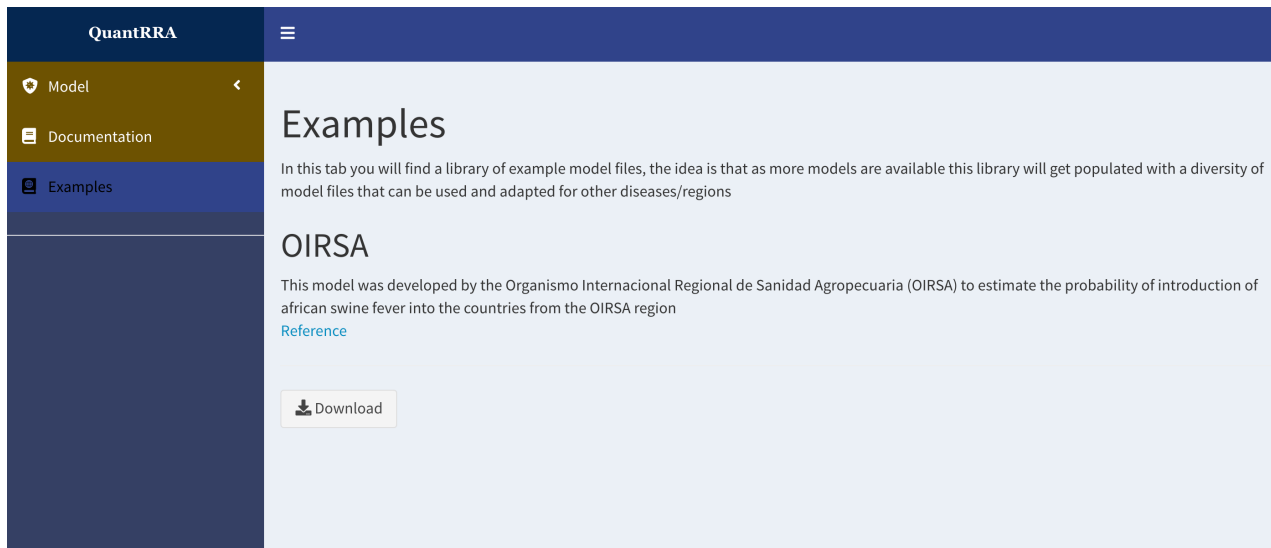
sobre la probabilidad de ingreso, establecimiento y diseminación del virus de la peste porcina africana en la porcicultura de los países de la región del OIRSA



Junio de 2020

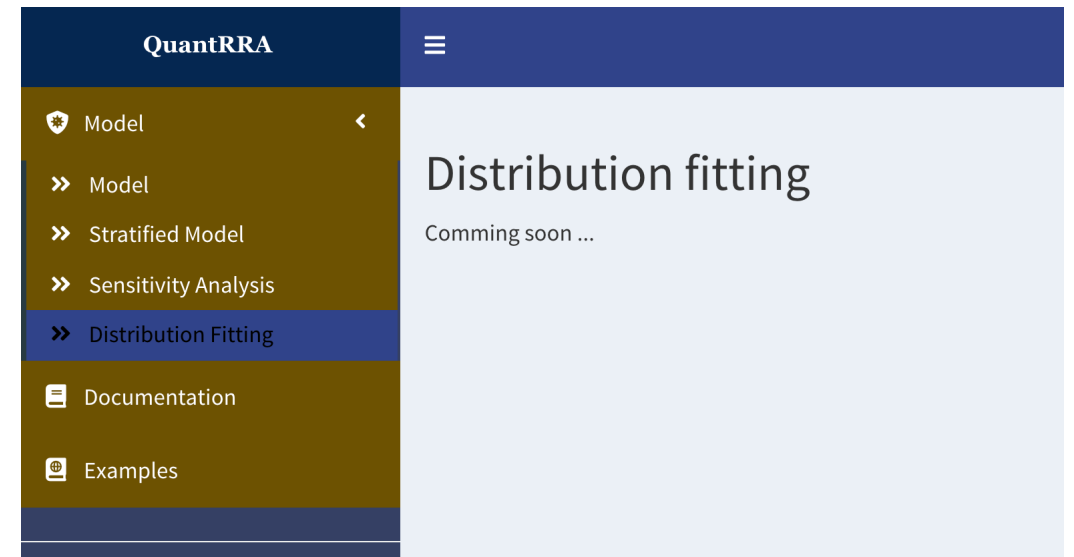
DIRECCIONES FUTURAS

Libreria de modelos



The screenshot shows the QuantRRA website interface. The top navigation bar is dark blue with the 'QuantRRA' logo and a hamburger menu icon. A left sidebar contains three items: 'Model' (with a shield icon), 'Documentation' (with a document icon), and 'Examples' (with a folder icon). The main content area is titled 'Examples' and contains a paragraph: 'In this tab you will find a library of example model files, the idea is that as more models are available this library will get populated with a diversity of model files that can be used and adapted for other diseases/regions'. Below this is a section for 'OIRSA' with a description: 'This model was developed by the Organismo Internacional Regional de Sanidad Agropecuaria (OIRSA) to estimate the probability of introduction of african swine fever into the countries from the OIRSA region'. A blue 'Reference' link is provided. At the bottom of the section is a 'Download' button with a download icon.

Distribution fitting



The screenshot shows the QuantRRA website interface with the 'Distribution fitting' page selected. The top navigation bar is dark blue with the 'QuantRRA' logo and a hamburger menu icon. The left sidebar now has five items: 'Model' (with a shield icon), 'Model' (with a double arrow icon), 'Stratified Model' (with a double arrow icon), 'Sensitivity Analysis' (with a double arrow icon), 'Distribution Fitting' (with a double arrow icon and highlighted in dark blue), 'Documentation' (with a document icon), and 'Examples' (with a folder icon). The main content area is titled 'Distribution fitting' and contains the text 'Comming soon ...'.

MODELOS DE DISPERSION DE ENFERMEDADES

Introducción

Estimar el impacto

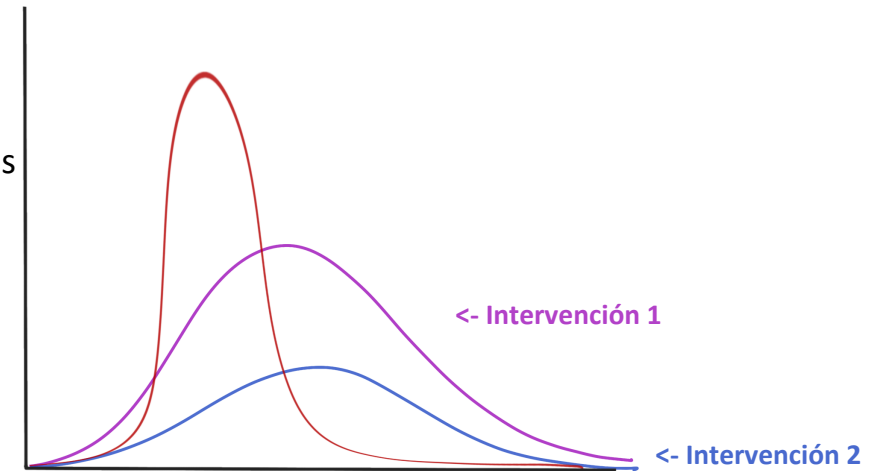
Áreas vulnerables
Potenciales super diseminadores

Probar intervenciones

Efecto de intervenciones
Donde y cuando pueden ser mas efectivas



Cuantos son afectados



Cuando es mas critica la enfermedad?

$$\frac{dS}{dt} = -\frac{\beta IS}{N}$$
$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

Población

S : Susceptible
I: Infectado
R: Recuperado

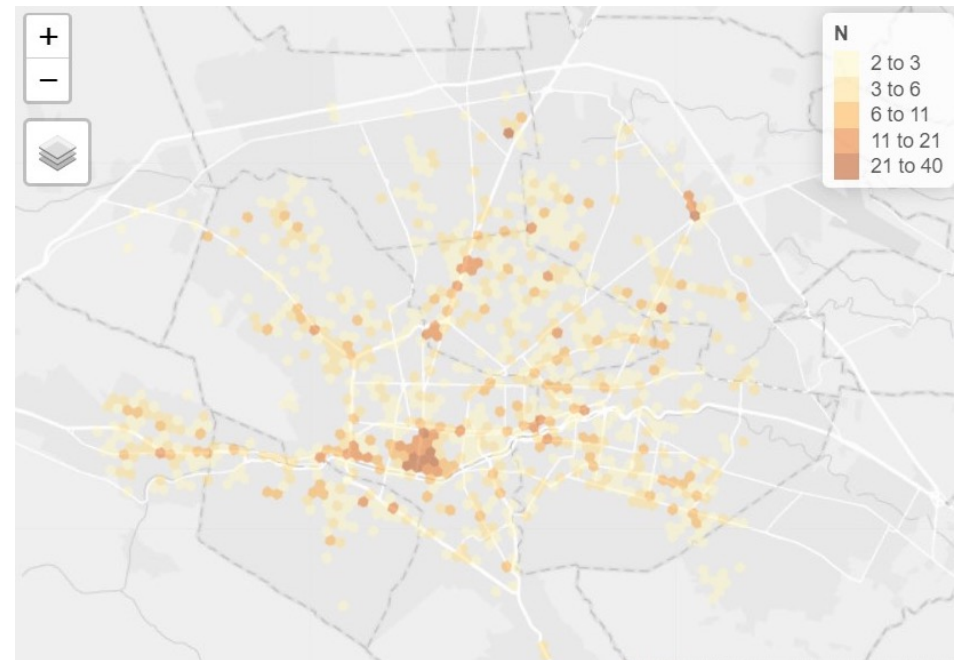
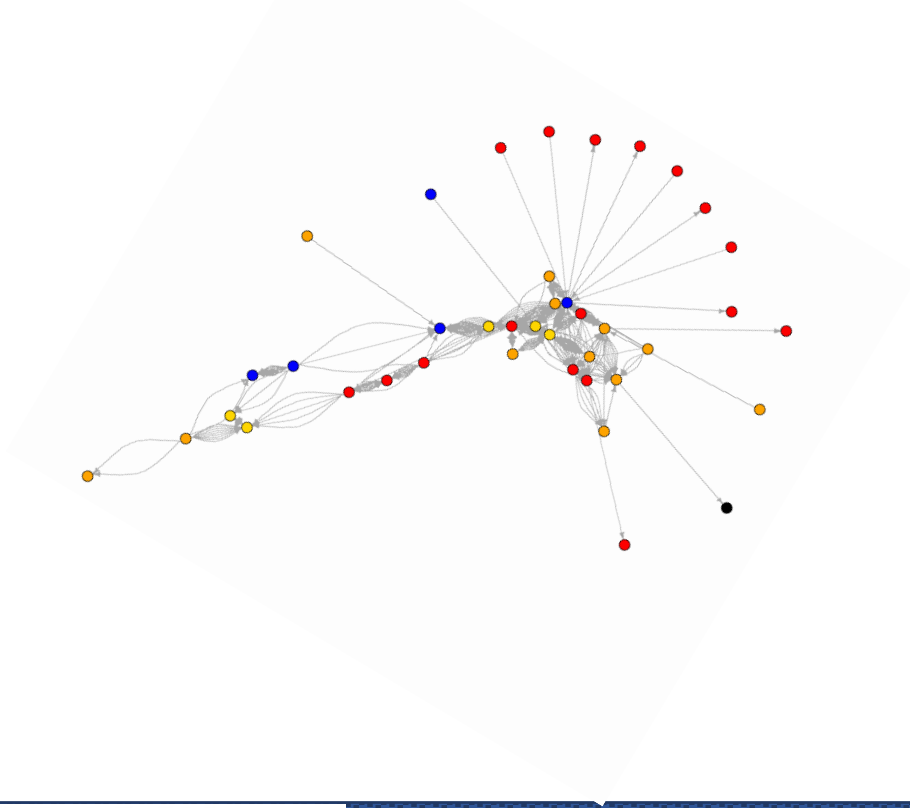
Tasa de cambio:

β : Tasa de transmisión
 γ : Tasa de recuperación

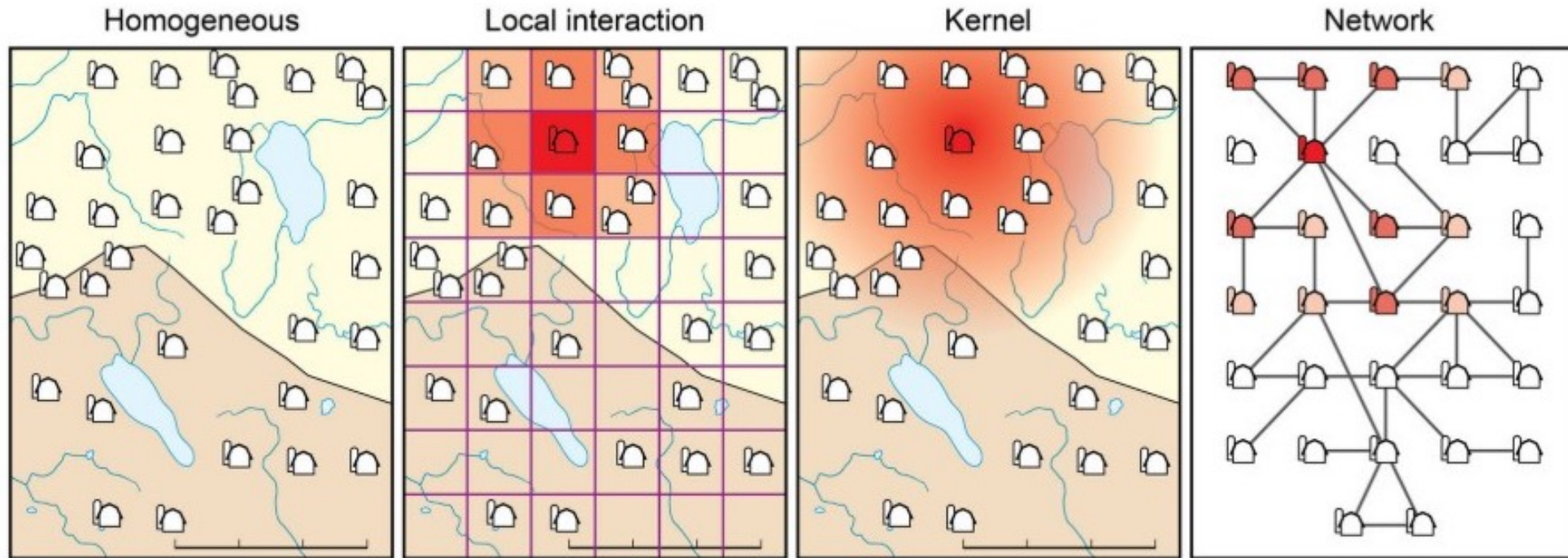
Introducción



- Sencillos de calibrar
- Buenos para poblaciones homogéneas



Introducción



Pomeroy LW et. al 2017

Modelo basado en agentes

Cada individuo (agente) tiene sus propias características que definen como interactúa con el sistema

- Localización espacial
- Patrones de movimiento
- Estatus de la enfermedad

Mientras mas características agregamos el tiempo de computación puede incrementar considerablemente

Objetivo

Desarrollar un modelo de simulación que nos permita:

- Estimar el impacto de la diseminación de PPA bajo distintos escenarios de introducción.
- Identificar regiones vulnerables.
- Estimar el efecto de las intervenciones y estrategias de control

Datos

Catastro ganadero

- Localización de las granjas
- Numero de animales

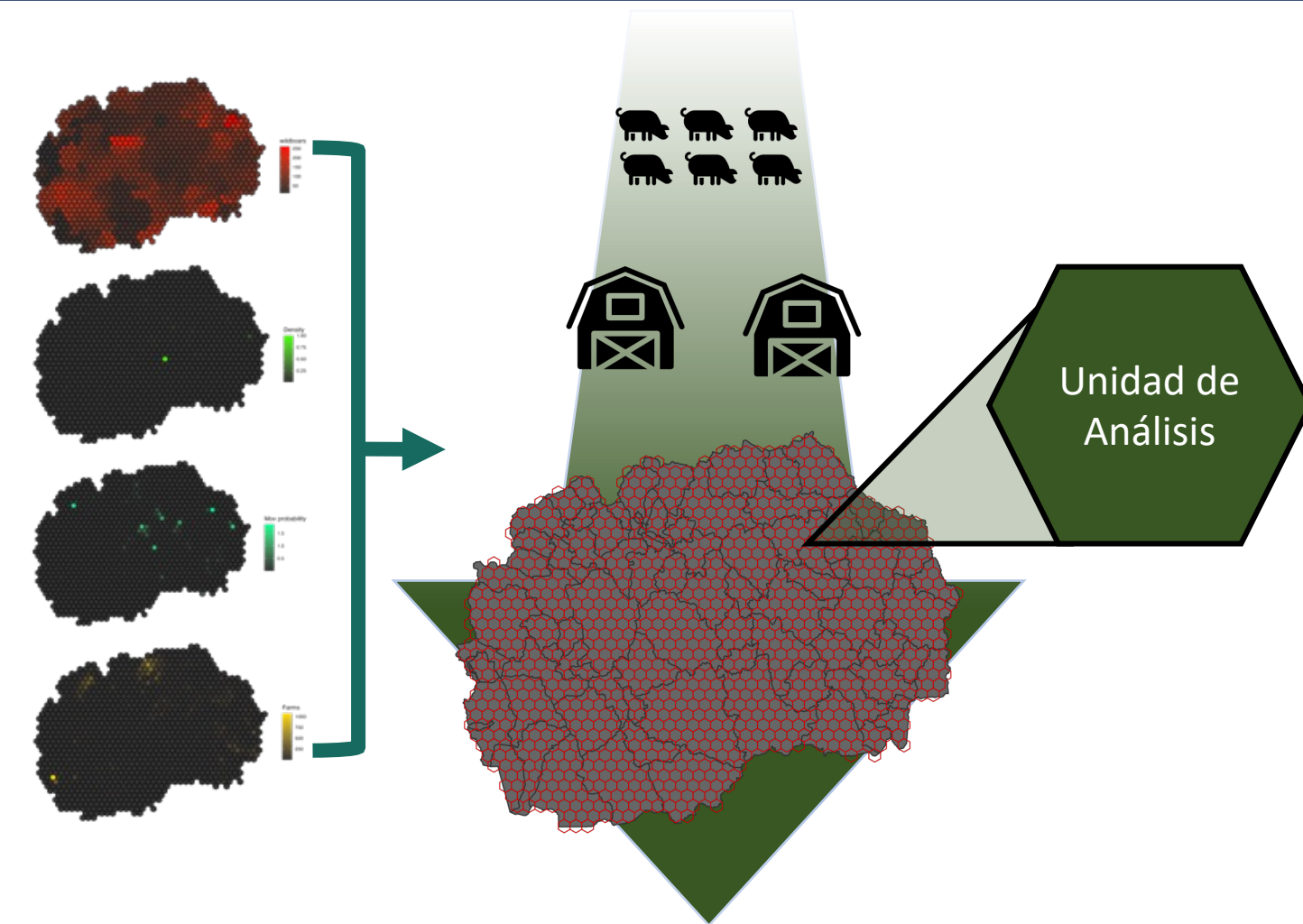
Movimientos

- Patrones de movimientos
 - Probabilidad de movimiento
 - Redes de comercio

Wildboars

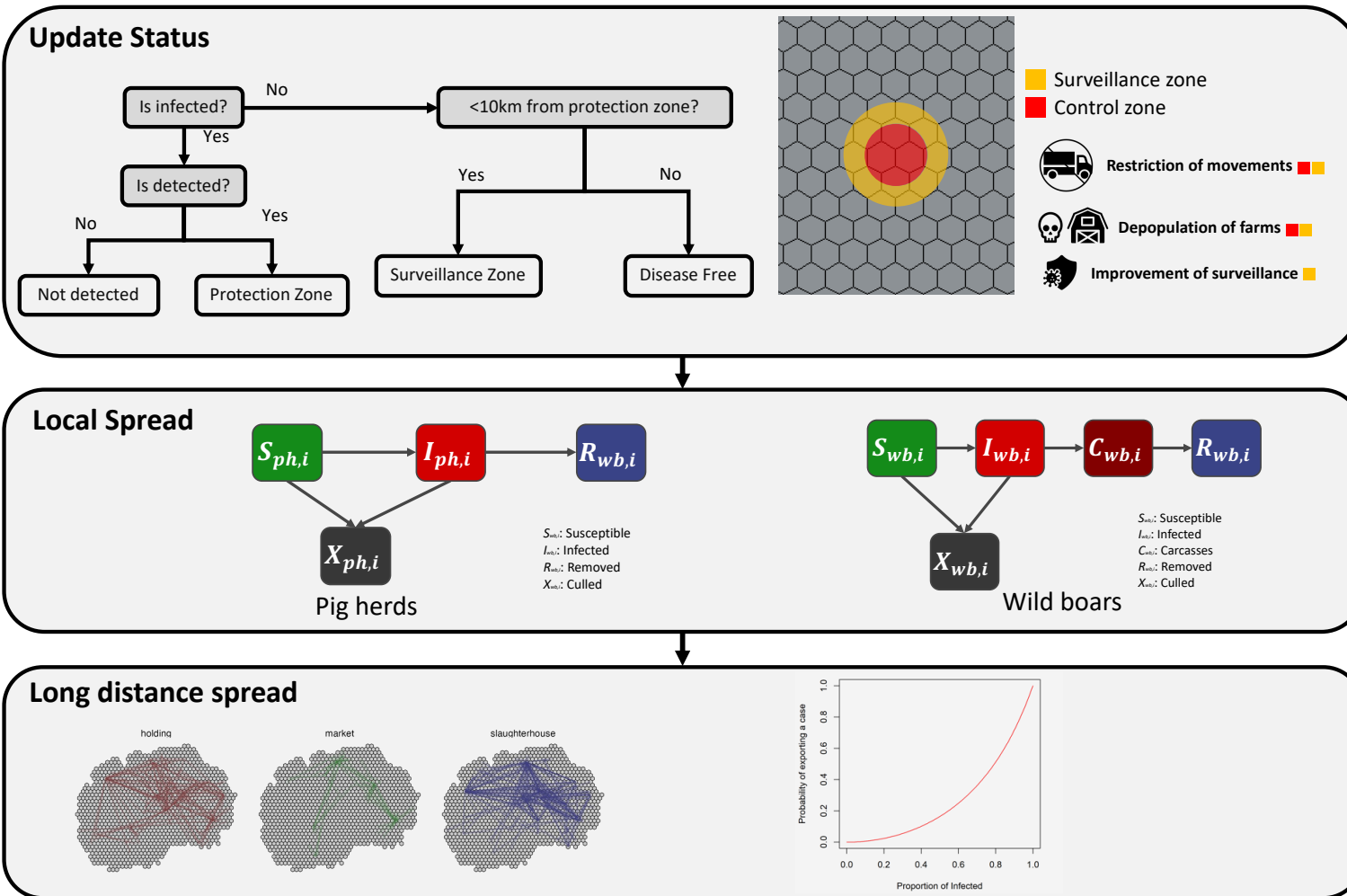
- Densidad estimada

Datos

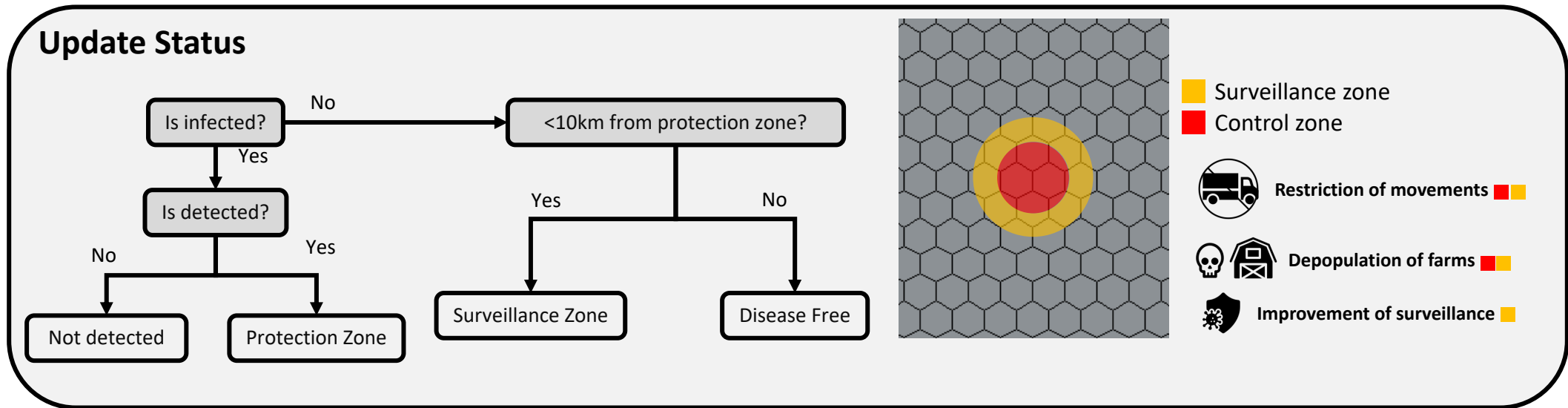


Características:

- Distribución de tipo de granjas
- Demografía de los animales
- Vecinos espaciales
- Movimientos internos
- Movimientos externos

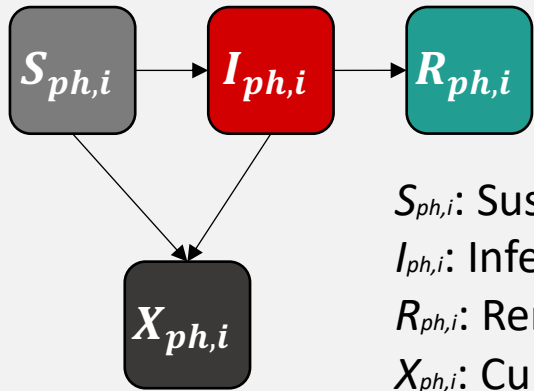


Estatus de la enfermedad



Model framework

Local spread PH



$S_{ph,i}$: Susceptible
 $I_{ph,i}$: Infected
 $R_{ph,i}$: Removed
 $X_{ph,i}$: Culled

$$\beta_i = \beta\omega_1\omega_2\omega_3(1 - v_p)$$

$$S_{ph,i} = \frac{\beta_{ph,i} I_{ph,i} S_{ph,i}}{N_{ph,i}} - \frac{\mu S_{ph,i}}{N_{ph,i}}$$

$$I_{ph,i} = \frac{\beta_{ph,i} I_{ph,i} S_{ph,i}}{N_{ph,i}} - \frac{\mu I_{ph,i}}{N_{ph,i}}$$

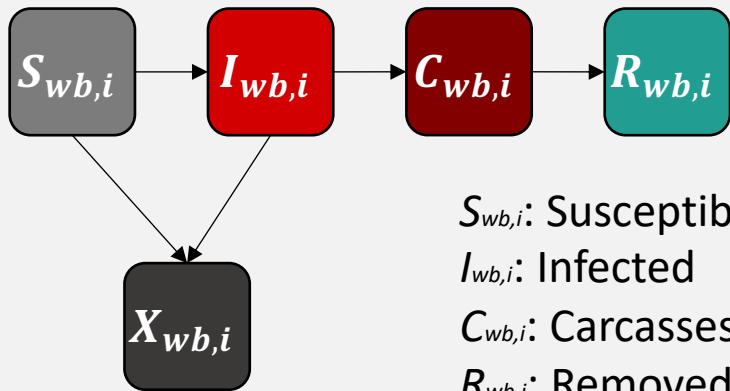
$$R_{ph,i} = \gamma C_{ph,i}$$

$$X_{ph,i} = \frac{\mu S_{ph,i}}{N_{ph,i}} + \frac{\mu I_{ph,i}}{N_{ph,i}}$$

$\gamma = 1/\text{days to detection and removal of infected herds}$
 Removed infected herds
 $\mu = \text{Speed of culling}$
 Culled pig herds

Model framework

Local spread WB



$S_{wb,i}$: Susceptible
 $I_{wb,i}$: Infected
 $C_{wb,i}$: Carcasses
 $R_{wb,i}$: Removed
 $X_{wb,i}$: Culled

$$\begin{aligned}
 S_{wb,i} &= -\frac{\beta_{wb,i} I_{wb,i} S_{wb,i}}{N_{wb,i}} - \frac{\nu_{wb,i} C_{wb,i} S_{wb,i}}{N_{wb,i}} - \frac{\mu S_{wb,i}}{N_{wb,i}} \\
 I_{wb,i} &= \frac{\beta_{wb,i} I_{wb,i} S_{wb,i}}{N_{wb,i}} + \frac{\nu_{wb,i} C_{wb,i} S_{wb,i}}{N_{wb,i}} - \frac{\mu I_{wb,i}}{N_{wb,i}} \\
 C_{wb,i} &= \gamma_1 I_{wb,i} \\
 R_{wb,i} &= \gamma_2 C_{wb,i} \\
 X_{wb,i} &= \frac{\mu S_{wb,i}}{N_{wb,i}} + \frac{\mu I_{wb,i}}{N_{wb,i}}
 \end{aligned}$$

New infections by carcasses

ν = Contribution of infected carcasses to new infections

Long distance spread

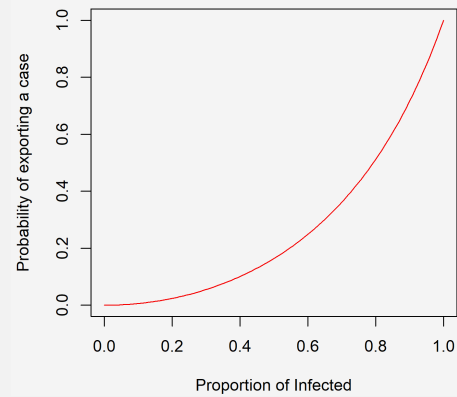
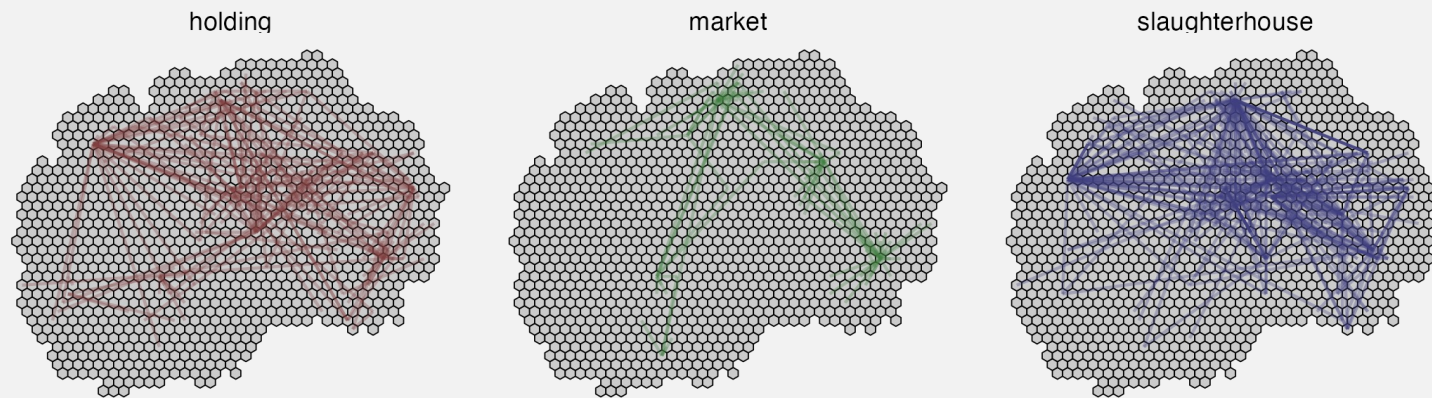


Table 2: Parameters explored for global sensitivity analysis.

Parameter	Definition	Sample space
GBetaPh (β_{ph})	Global transmission rate for pig herds	(0.2, 0.25, 0.3, 0.35)
GBetaWb (β_{wb})	Global transmission rate for wild boars	(0.2, 0.25, 0.3, 0.35)
AnmlDnsB	Effect of the animal density on the local transmission rate	(0.1, 0.2, 0.3)
loopsB	Effect of the number of internal movements on the local transmission rate	(0.1, 0.2, 0.3)
HuntingPressure	How much does the hunting increases	(1, 5, 10)
SurvGamma	Effect of increased surveillance after the detection of an infected pig herd	(1.0, 1.5, 2.0)
IndexCaseType	Type of farm where the index case was simulated	(Backyard, Family, Commercial)
Movement restrictions	Whether or not movement restrictions are implemented after the detection of a case	(yes, no)

Cumulative infected

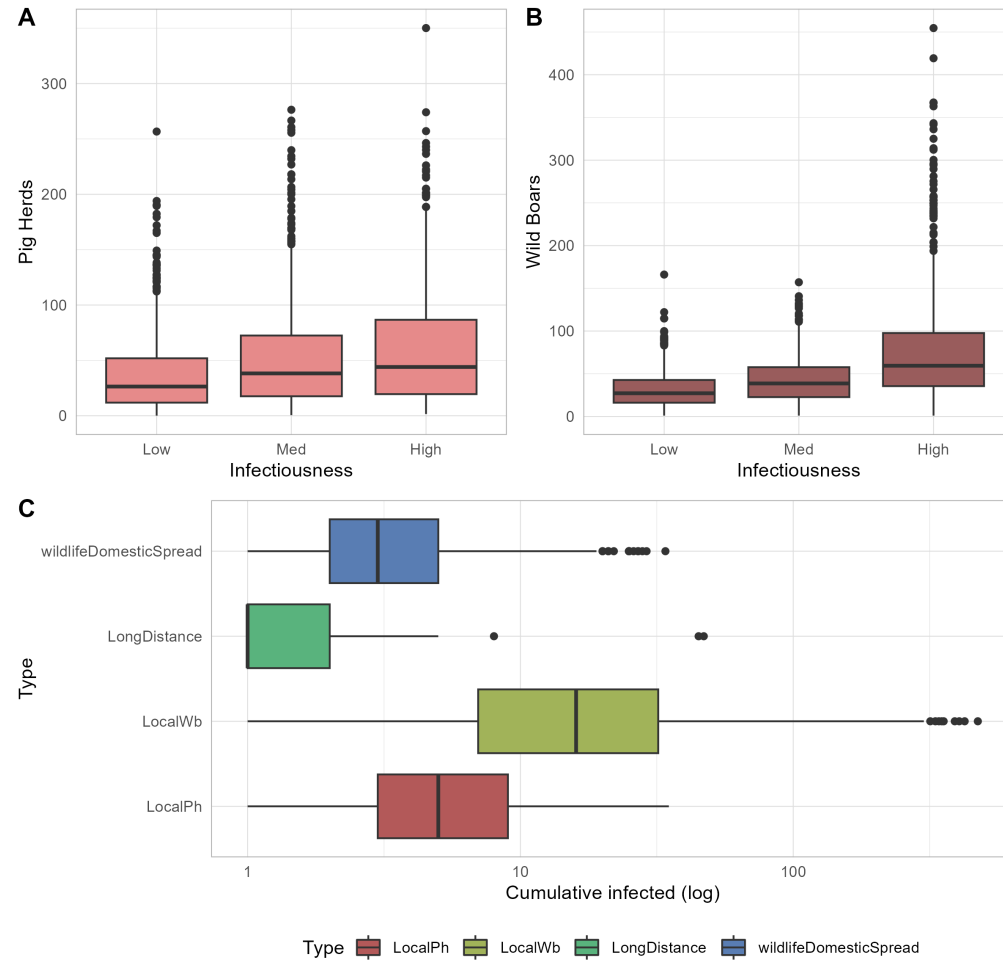
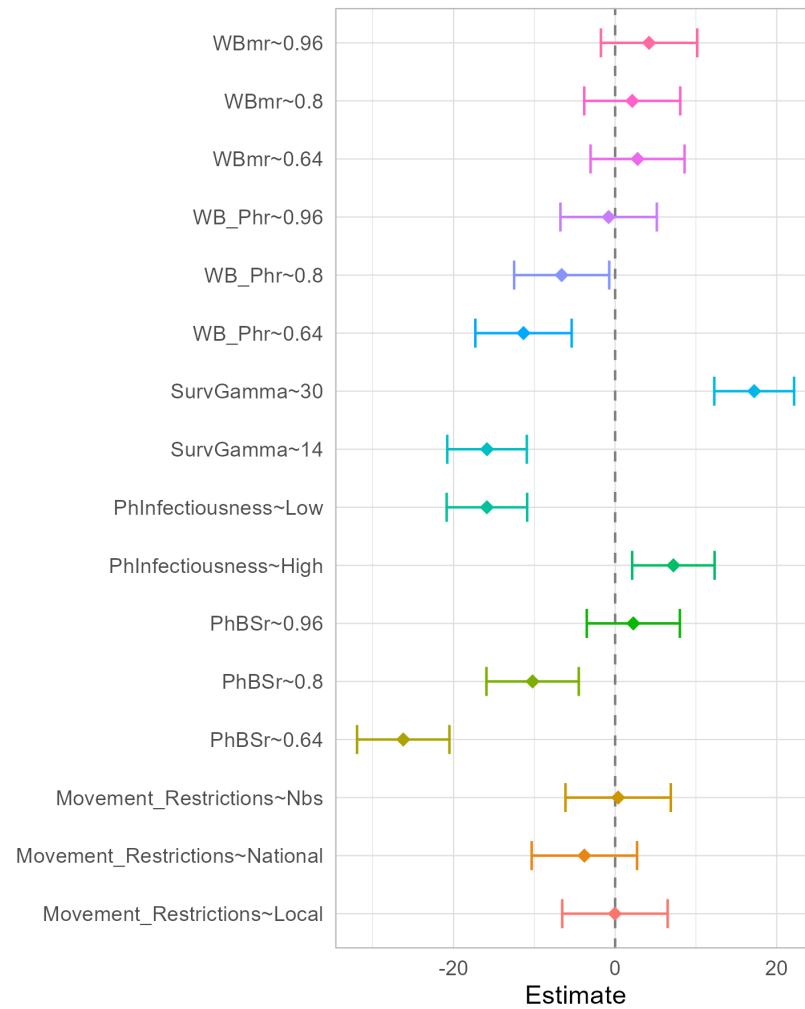


Table 3: Difference in simulation outcomes estimated by regression when compared to baseline. * Significant effect

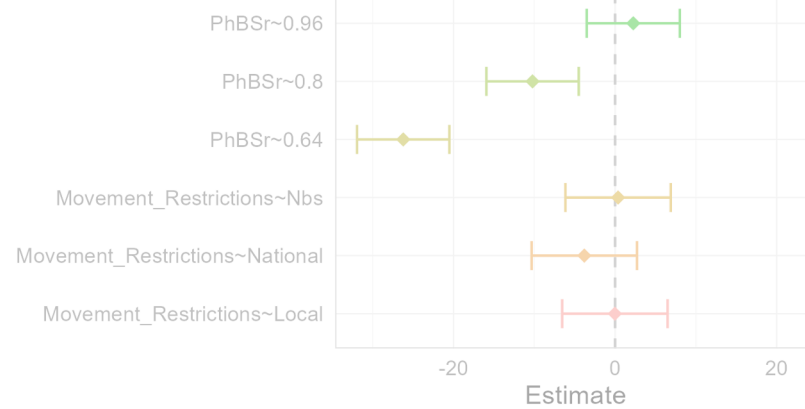
	Infected Pig Herds	Infected wild boars
Baseline	67.41(2.22,93.6)	134.08(30.01,196.16)
Movement Restrictions		
Yes	-1.29(-9.9,7.32)	-27.51(-113.87,58.86)
Average days to detection		
14-days	-44.31(-56.79,-31.82)*	35.19(-93.05,163.44)
21	-35.66(-47.91,-23.41)*	-66.64(-192.44,59.16)
Preventive culling		
Yes	-41.92(-50.09,-33.75)*	-35.15(-121.46,51.15)
Hunting pressure		
Yes	-14.64(-25.02,-4.27)*	-185.63(-289.02,-82.24)*



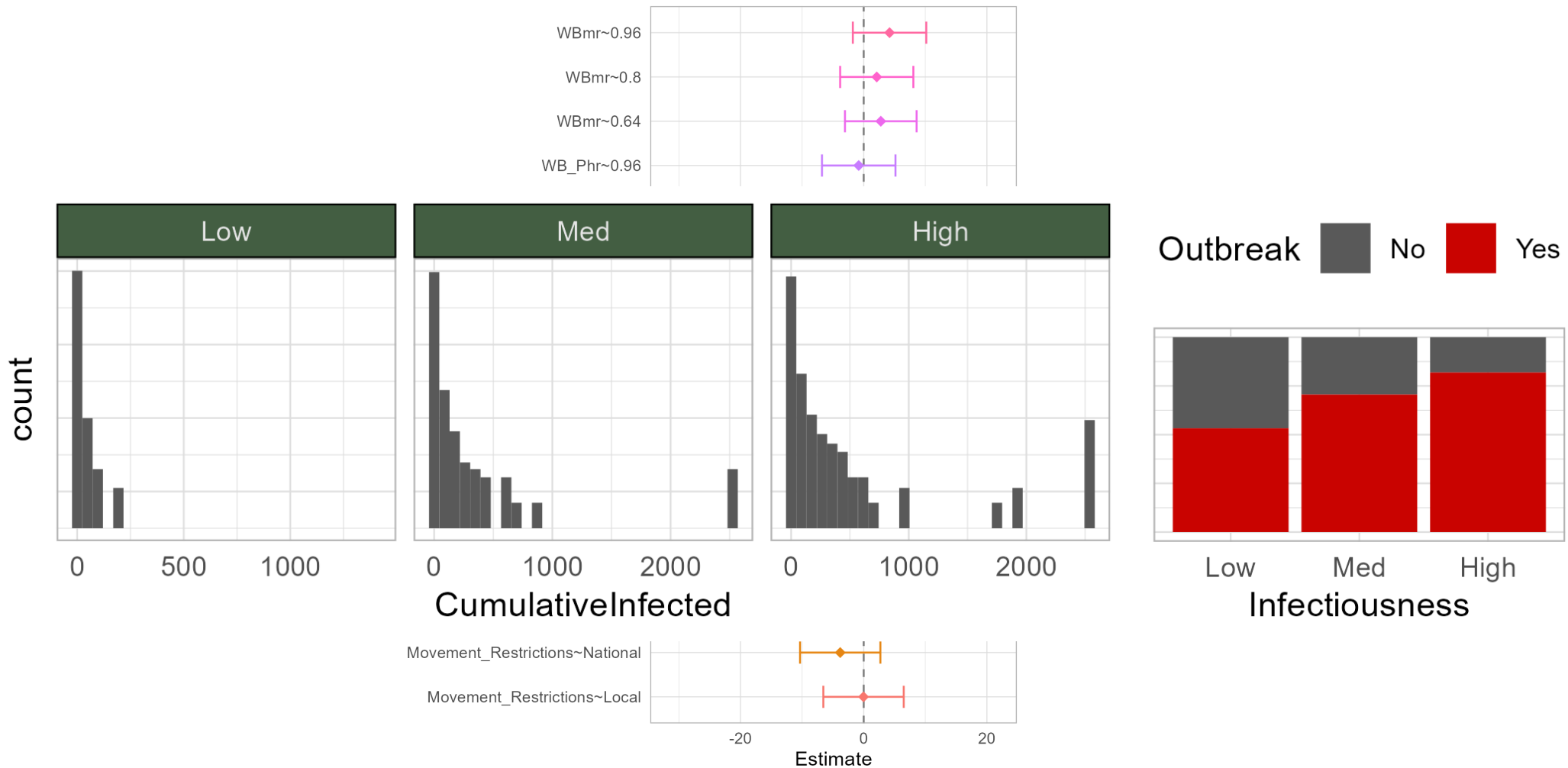


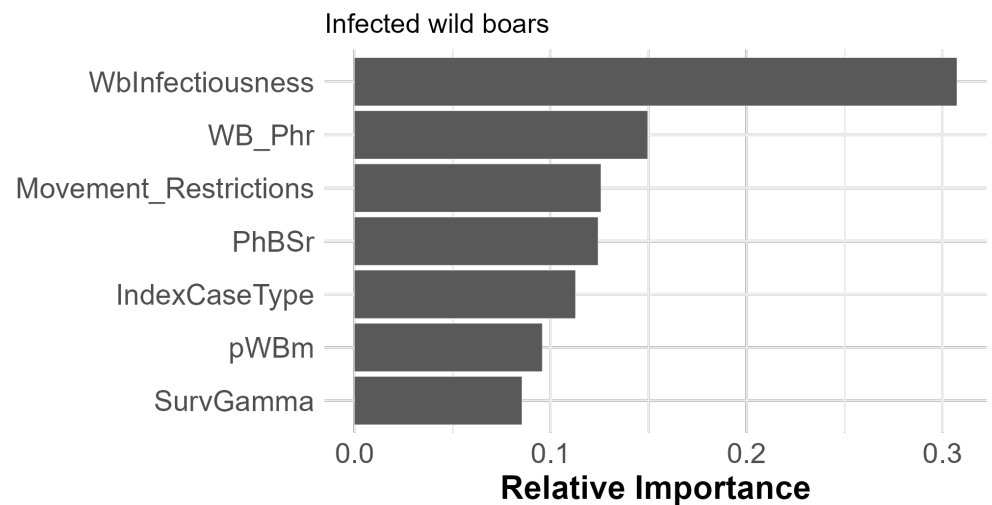
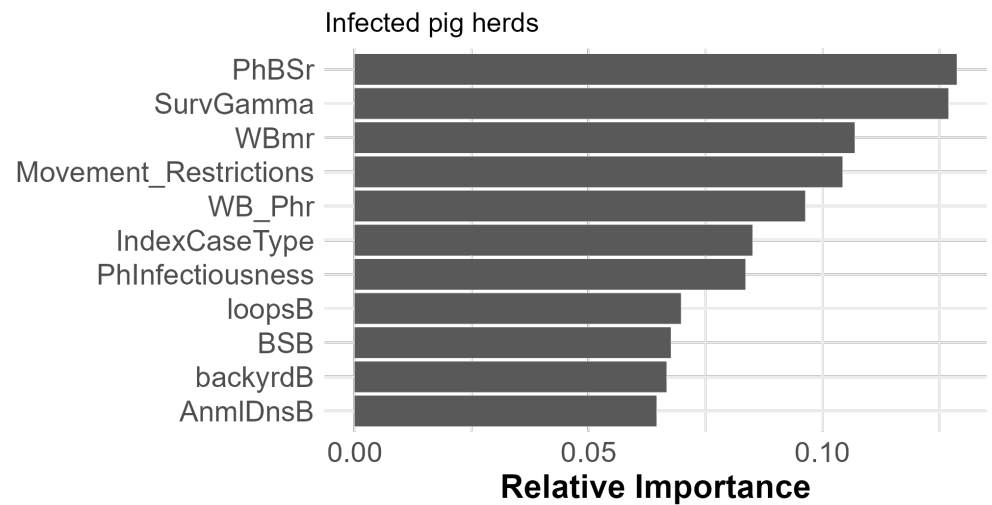
74.17(53.68,94.67)

-24.19(-44.72,-3.66)



Análisis de sensibilidad





Simulated Transmission Networks

n — 100 — 200 authority ● 0.25 ● 0.50 ● 0.75 ● 1.00

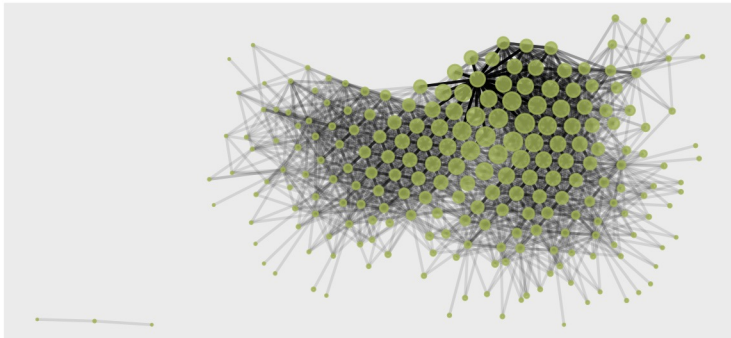
Overall



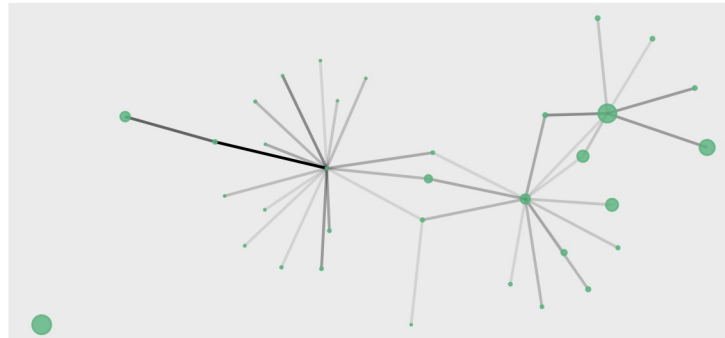
Local spread

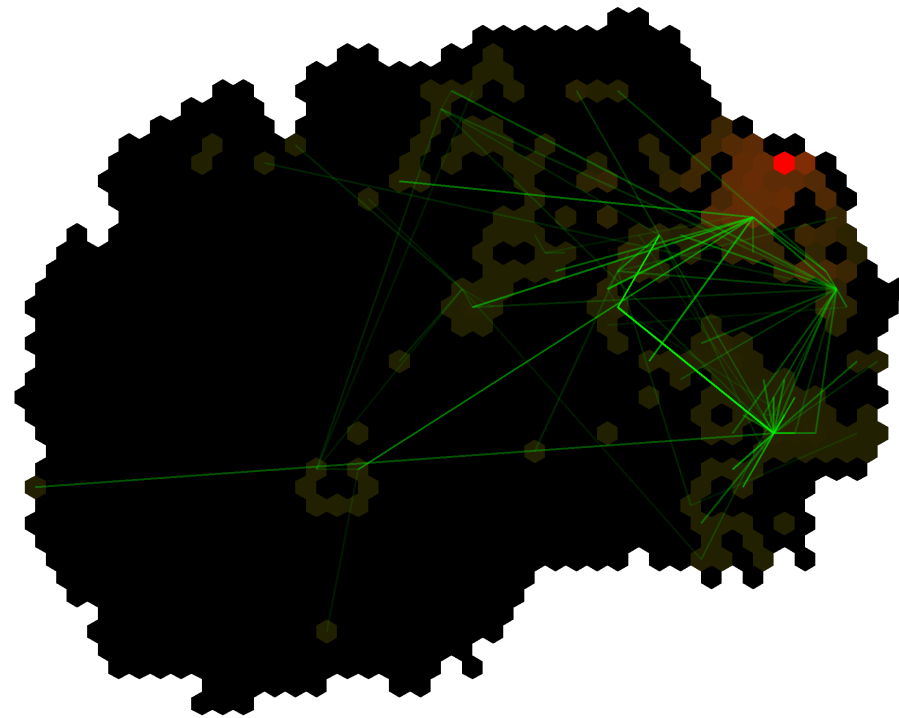


Local wildboar spread

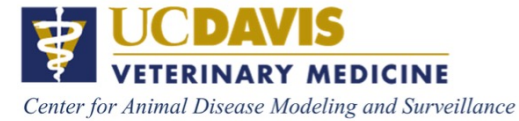


Long distance





Preguntas



<http://www.spablo-temporal.network>

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