



# **Modelling Vector-borne Disease as a Complex Adaptive System: Challenges and Potential Solutions**

---

**Chris Stephens**

C3-Centro de Ciencias de la Complejidad y Instituto de Ciencias Nucleares, UNAM

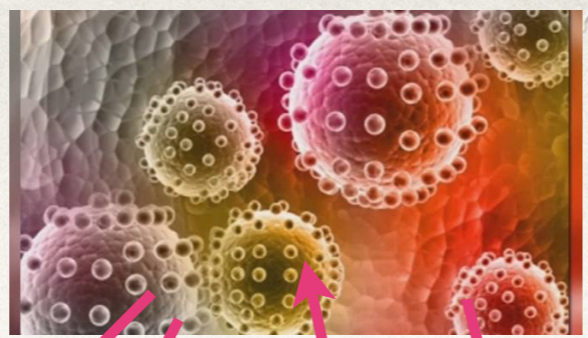
Mexico-US Forum Arbovirus Disease Research: Priorities for Collaboration and Partnership: Nov. 28th-30th 2017



# The Challenges



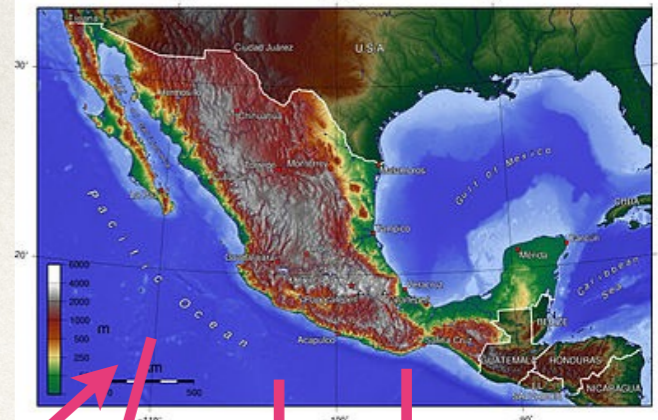
Common breeding site for Aedes Mosquito



Virologists  
Geneticists



Philosophers



Bioinformaticians  
Modellers

Public Health  
Sociologists  
Anthropologists

# Multifactorial Anopheles gambiae Multiplesite interactions



Transporte



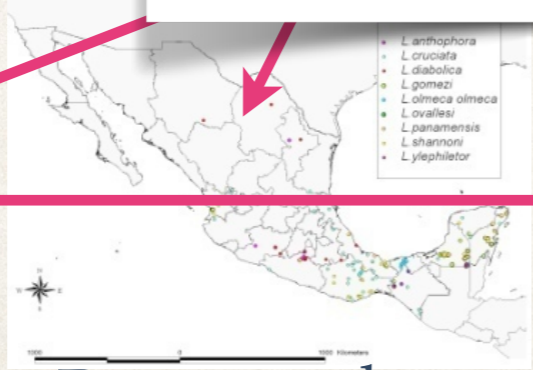
Perinatologists  
Infectologists



Chemist  
Biochemists



Entomologists



Demographers  
Epidemiologists



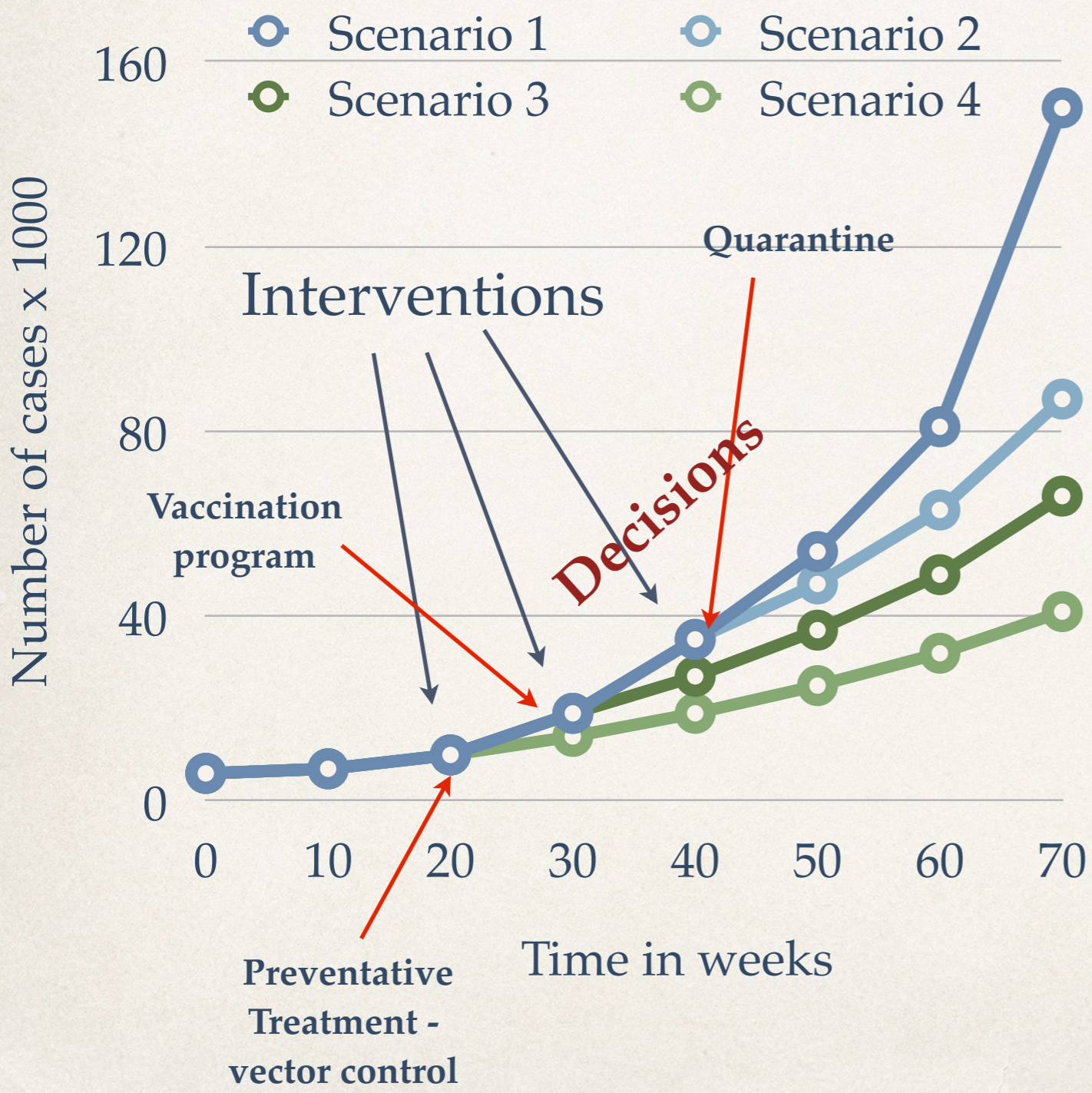
Mammologists  
Ecologists



Politicians  
Civil servants



# They are dynamical and adaptive



We want to predict and understand “histories” but nothing is written in stone. What is the “space” of interventions?

# ARBOVIRUS

Ecology

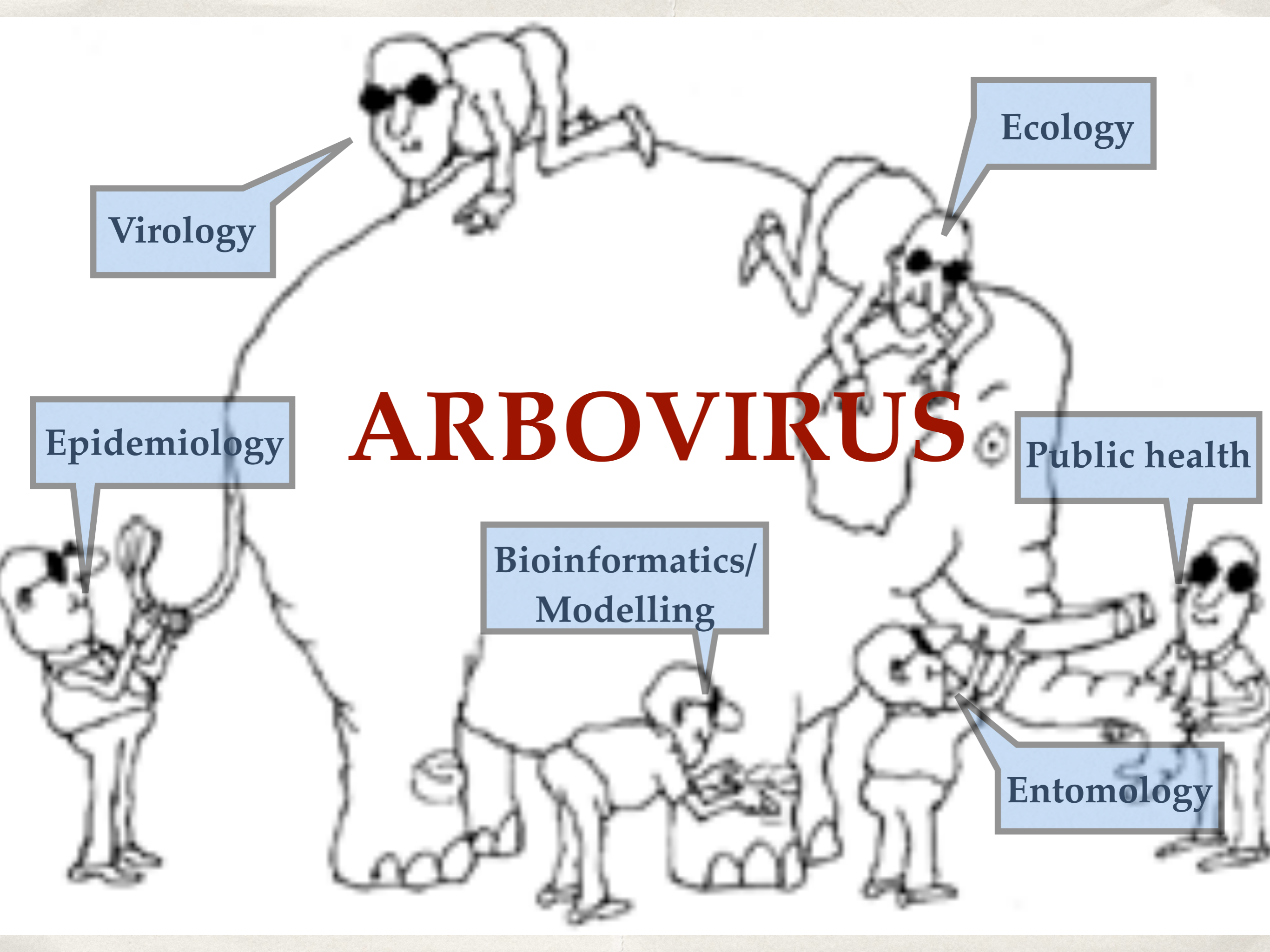
Virology

Public health

Bioinformatics/  
Modelling

Epidemiology

Entomology



# ARBOVIRUS

Clinical data

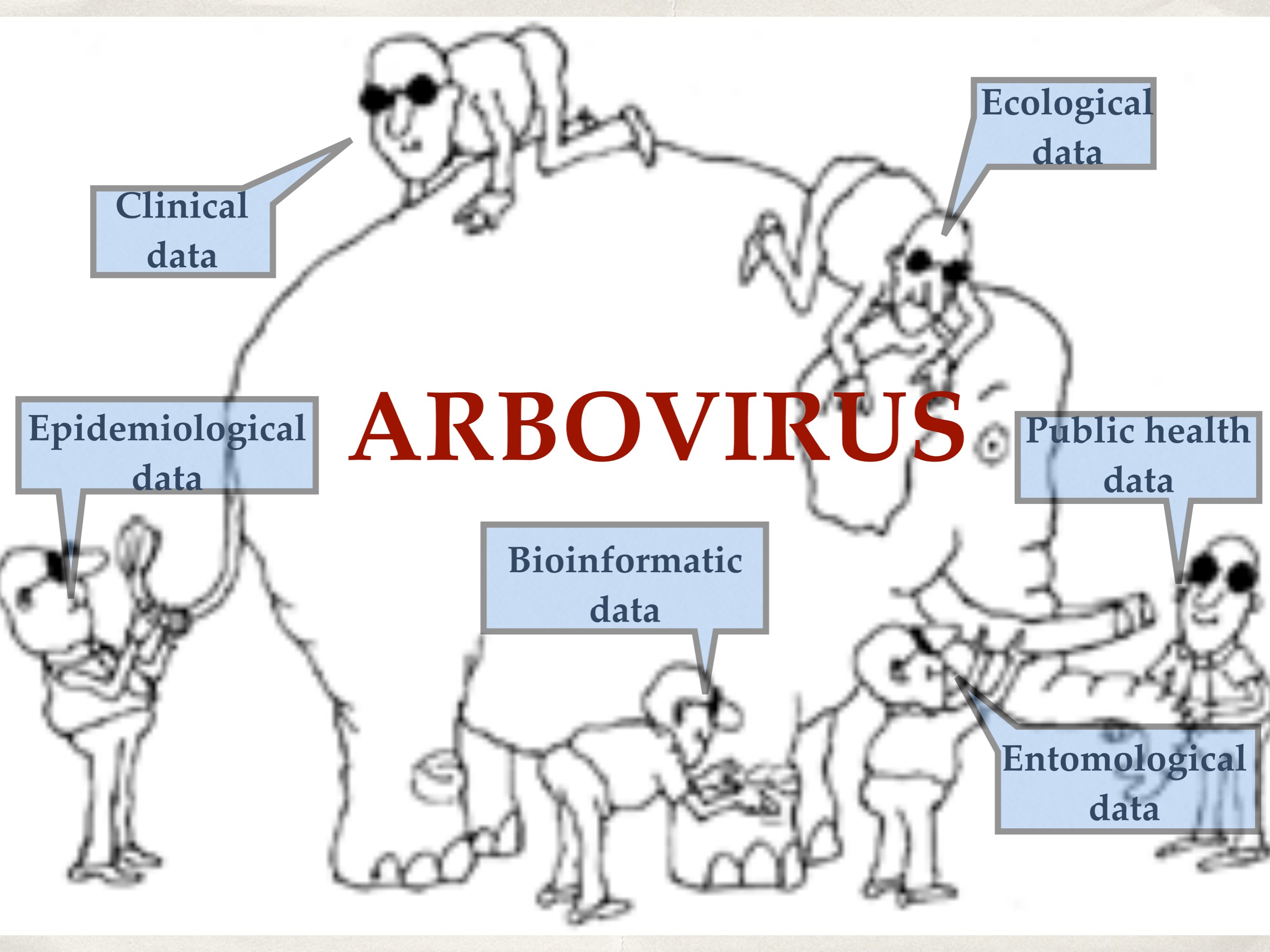
Ecological data

Epidemiological data

Public health data

Bioinformatic data

Entomological data





What do we know...?

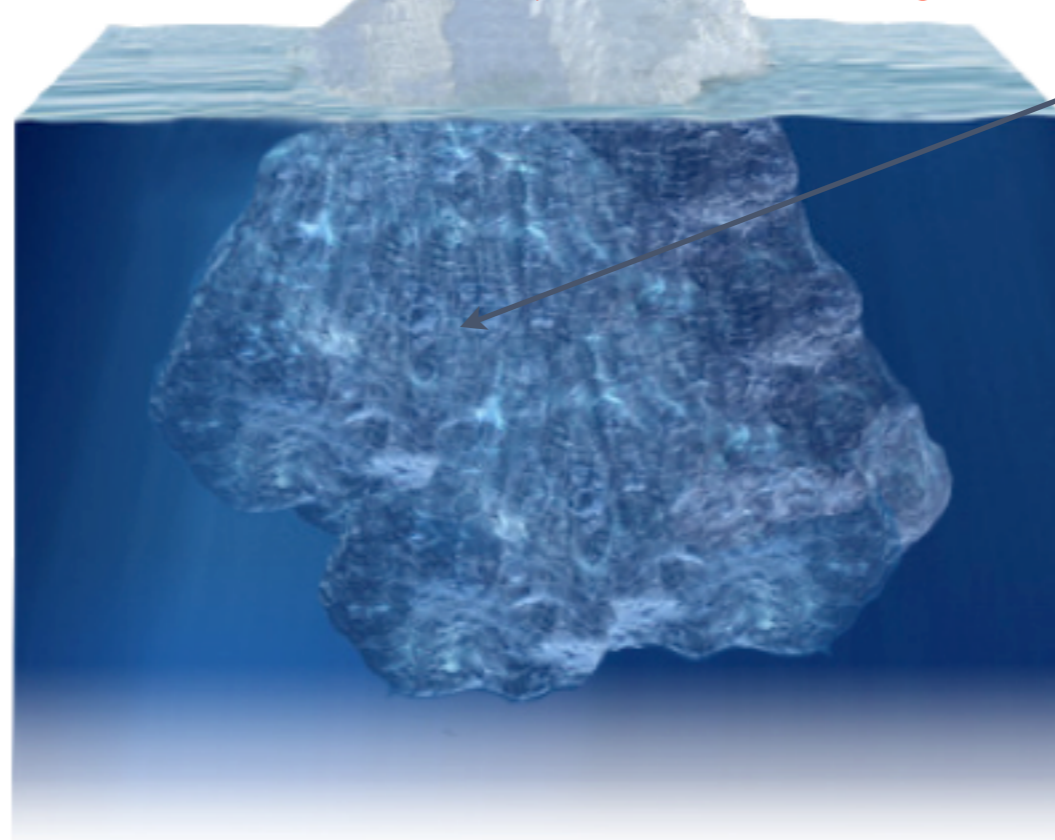
- Known cases
- Known vectors
- Known hosts
- Known risk factors





# How do we infer what's under the water?

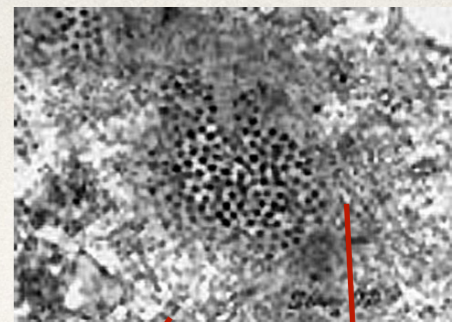
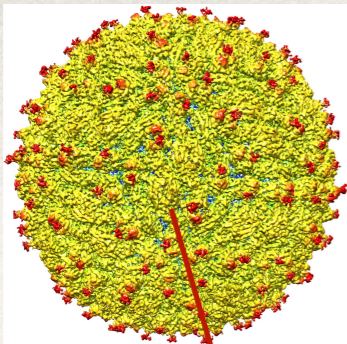
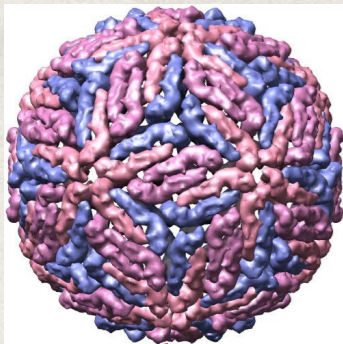
*We need new methods to  
Integrate multiple sources  
model these data...  
and multiple formats  
Adaptive Systems*



What do we know...?  
Known cases  
Known vectors  
Known hosts  
Known risk factors  
**Known interactions**

What don't we know...?  
Unknown cases  
Unknown vectors  
Unknown hosts  
Unknown risk factors  
**Unknown interactions**





Can we infer ecological interactions without direct observation?  
 Just what sort of data is necessary and sufficient?  
 How can we create a system of data applications that can be used to infer ecological interactions without direct observation?



Importancia médica



*T. infestans*



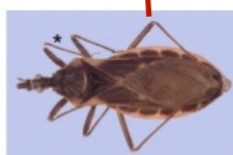
*T. barberi*



*T. pallidipennis*



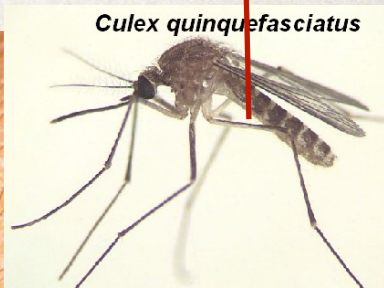
*T. longipennis*



*T. recurva*



*T. neotomac*



*Culex quinquefasciatus*



# What is the niche of an emerging disease?

What do we want to predict?

C - the presence, or abundance, of cases of a disease,...

What affects it?

The "niche"

$$\mathbf{X} = (X_1, X_2, X_3, \dots, X_M)$$

Probability to find disease given the niche factors  $\mathbf{X}$

$$P(C | \mathbf{X}(t))$$

Characterizes niche and "anti-niche"

$$S(C | \mathbf{X})$$

Risk score

A large part of the complexity is in the multi-factoriality of both C and X. Adaptation is inherent in the fact that  $P(C | \mathbf{X})$  can change in time.

$$\mathbf{X} = X(sd) + X(se) + X(n) + X(ev) + X(g) + X(af) + X(hm) + X(i) + X(sp) + \dots$$

Macro-Climactic factors

Micro-Climatic factors

Hydrography

Host species

Human activity

Behavioural characteristics

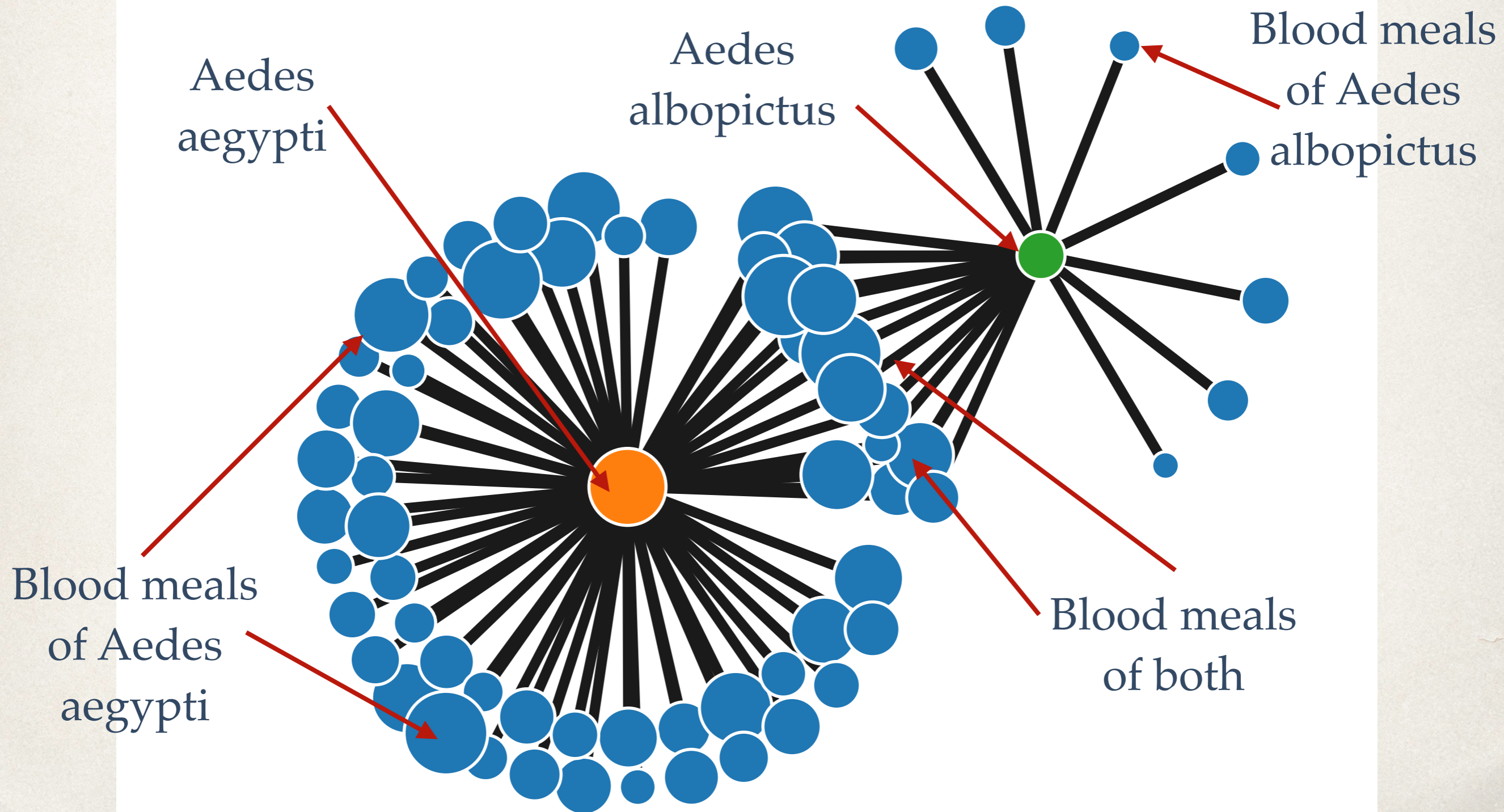
Phenotypic characteristics

Competitor species

Predator species

Problems of co-dependence and causality

# What is a community of emerging diseases?





# The Potential Solutions

# One model = one question

→ one answer

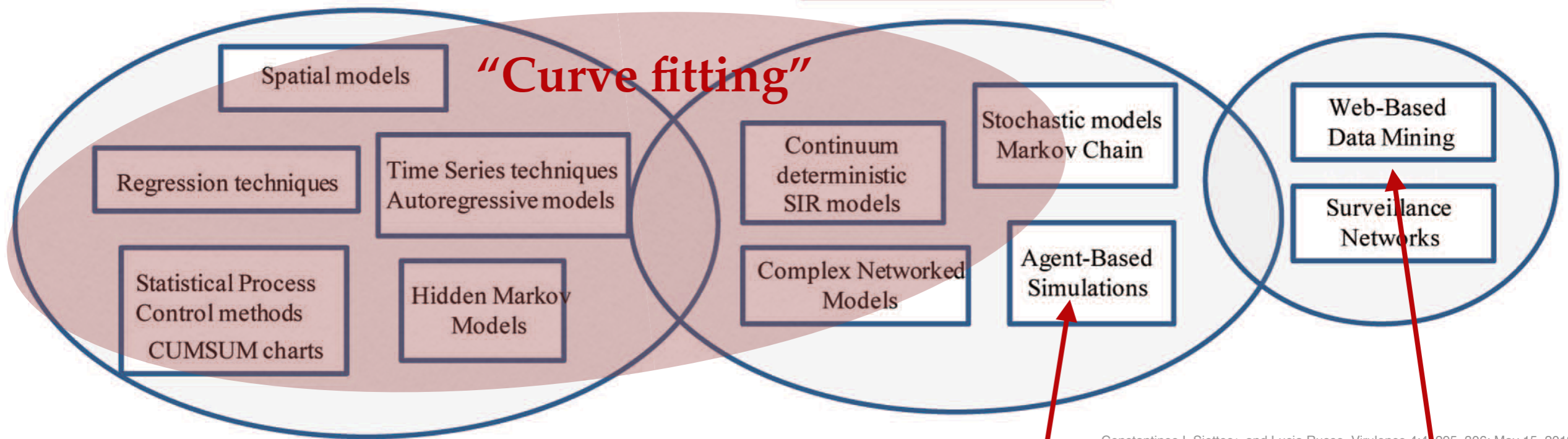


## Mathematical Modeling of Infectious Disease Dynamics

### Statistical-based methods For Epidemic Surveillance

### Mathematical/Mechanistic State-Space Models

### Empirical/ Machine Learning-based Models



Constantinos I. Siettos<sup>1</sup>, and Lucia Russo, *Virulence* 4:4 295–306; May 15, 2013

Where's the Complex Adaptive Systems modelling?

Models heterogeneity,  
but not naturally data based

Google flu,  
REPORTA,  
influenzanet,...



# Standard SIR models



Figure 3: Structure of the SIR model.

Complication of answering just one question - the number of infected, based on a small number of inputs

$$\begin{aligned} \frac{dS}{dt}(t) &= \mu N - \beta S(t)I(t)/N - \mu S(t), \\ \frac{dI}{dt}(t) &= \beta S(t)I(t)/N - \gamma I(t) - \mu I(t), \\ \frac{dR}{dt}(t) &= \gamma I(t) - \mu R(t), \\ \frac{dC_i}{dt} &= p\beta S(t)I(t), \end{aligned}$$

without / with mosquitoes

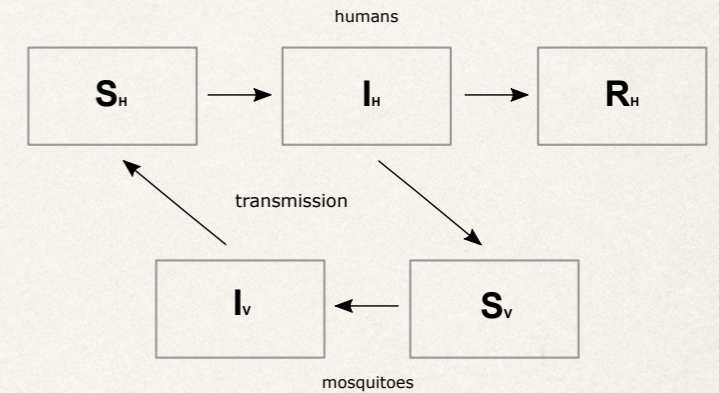


Figure 4: Structure of the SIR/SI model.

$$\begin{aligned} \frac{dS_H}{dt}(t) &= \mu_H N_H - \beta_H S_H(t)I_v(t)/N_v - \mu_H S_H(t), \\ \frac{dI_H}{dt}(t) &= \beta_H S_H(t)I_v(t)/N_v - \gamma_H I_H(t) - \mu_H I_H(t), \\ \frac{dR_H}{dt}(t) &= \gamma_H I_H(t) - \mu_H R_H(t) \\ \frac{dI_v}{dt}(t) &= \beta_v S_v(t)I_H(t)/N_H - \mu_v I_v(t), \\ \frac{dS_v}{dt}(t) &= -\beta_v S_v(t)I_H(t)/N_H + \mu_v I_v(t), \\ \frac{dC_i}{dt} &= p\beta_H S_H(t)I_v(t)/N_v, \end{aligned}$$

but without...

mosquito type, hosts (known / unknown), habitat, socio-economic / socio-demographic factors, climate / weather, previous infection / co-infection (human / vector host), interventions, etc. etc.

**But, for multi-factorial solutions we need multi-factorial data**



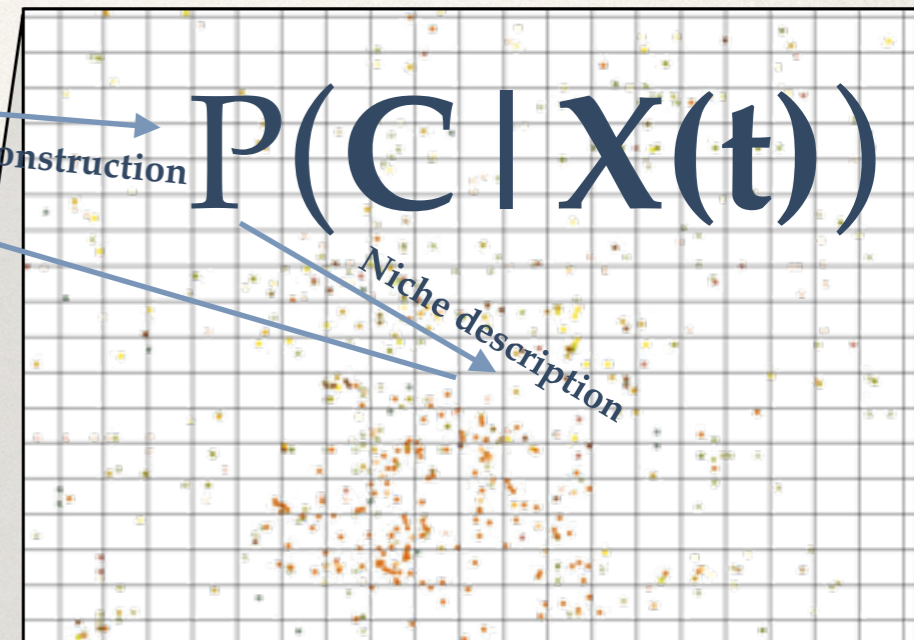
# Ecological modelling from a “Data Science” perspective

The Data Revolution has provided a unique opportunity to construct multi-factorial ecological models for emerging diseases. However, most ecological data is spatio-temporal at multiple scales. Spatial data mining is much less developed than standard data mining.

$$P(C | X(t))$$

Co-occurrence between arbovirus occurrence,  $C$ , and niche variables,  $X(t)$  → ecological interaction

- Collection data
- Ecological niche data
- Ecological niche model data
- Socio-economic data
- Socio-demographic data
- Phenotypic data
- Vegetable and crop cover
- Geographical data
- Medical and public health data...



The data are represented in space and time – spatial data mining

## Problems with data:

### Different sources

Different location, data base, access,...

### Different data types

categorical, metric, continuous, discrete,...

### Different spatial resolution

Explicit – e.g., pixel by pixel in environmental layers

Implicit – 30,000,000 data points versus 30

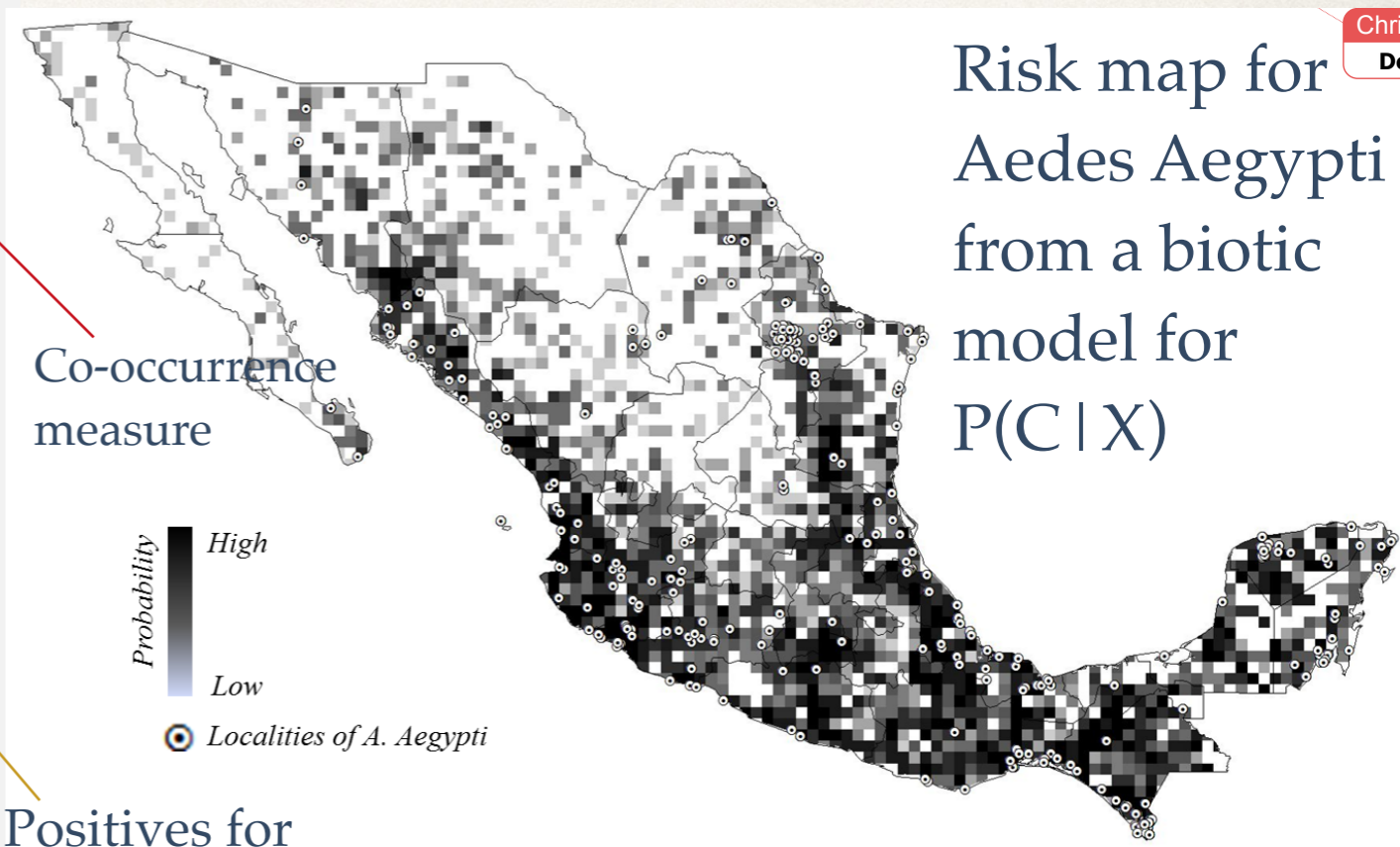
Abiotic versus biotic

# Predictive Model for potential hosts of ZIKV

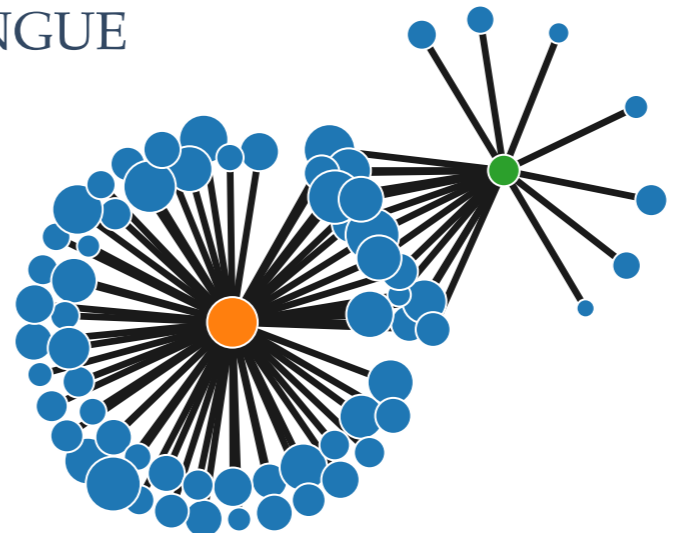


Mammals with most statistically significant geographic overlap with *Aedes Aegypti*

Rank	Mammal	epsilon	Rank	Mammal	epsilon
1	<i>Glossophaga soricina</i>	12.78	38	<i>Dasyopus novemcinctus</i>	7.11
2	<i>Molossus rufus</i>	11.99	39	<i>Sigmodon hispidus</i>	7.02
3	<i>Artibeus jamaicensis</i> *	11.68	40	<i>Uroderma bilobatum</i>	6.82
4	<i>Liomys pictus</i>	11.06	41	<i>Leptonycteris curasoae</i>	6.75
5	<i>Oryzomys couesi</i>	11.04	42	<i>Carollia perspicillata</i>	6.71
6	<i>Carollia subrufa</i>	10.49	43	<i>Centurio senex</i>	6.61
7	<i>Sturnira lilium</i>	10.28	44	<i>Sciurus colliaei</i>	6.59
8	<i>Artibeus lituratus</i> *	9.91	45	<i>Lontra longicaudis</i>	6.49
9	<i>Choeroniscus godmani</i>	9.42	46	<i>Didelphis marsupialis</i>	6.49
10	<i>Liomys salvini</i>	9.33	47	<i>Cratogeomys bulleri</i>	6.35
11	<i>Oligoryzomys fulvescens</i>	9.15	48	<i>Carollia sowelli</i> *	6.27
12	<i>Dermanura phaeotis</i>	9.12	49	<i>Myotis elegans</i>	6.12
13	<i>Rhogeessa tumida</i>	9.06	50	<i>Myotis nigricans</i> *	6.06
14	<i>Pteronotus personatus</i>	9.05	51	<i>Sigmodon arizonae</i>	6.00
15	<i>Baiomys musculus</i>	8.97	52	<i>Rhynchonycteris naso</i>	5.95
16	<i>Glossophaga commissarisi</i>	8.80	53	<i>Tlacuatzin canescens</i>	5.87
17	<i>Didelphis virginiana</i>	8.58	54	<i>Leopardus pardalis</i>	5.84
18	<i>Pteronotus parnellii</i> *	8.58	55	<i>Caluromys derbianus</i>	5.78
19	<i>Orthogeomys hispidus</i>	8.53	56	<i>Molossus molossus</i>	5.76
20	<i>Sciurus aureogaster</i>	8.52	57	<i>Oryzomys rostratus</i>	5.76
21	<i>Molossus sinaloae</i>	8.51	58	<i>Osgoodomys banderanus</i>	5.76
22	<i>Desmodus rotundus</i>	8.23	59	<i>Myotis carteri</i>	5.66
23	<i>Saccopteryx bilineata</i>	8.22	60	<i>Micronycteris microtis</i>	5.52
24	<i>Lasiurus intermedius</i>	8.15	61	<i>Sylvilagus brasiliensis</i>	5.47
25	<i>Phyllostomus discolor</i>	8.12	62	<i>Sylvilagus floridanus</i>	5.37
26	<i>Philander opossum</i>	8.10	63	<i>Spermophilus annulatus</i>	5.36
27	<i>Peromyscus gymnotis</i>	7.90	64	<i>Peromyscus leucopus</i>	5.30
28	<i>Balantiopteryx plicata</i>	7.81	65	<i>Conepatus leuconotus</i>	5.30
29	<i>Eptesicus furinalis</i>	7.69	66	<i>Chaetodipus pernix</i>	5.27
30	<i>Pteronotus davyi</i>	7.55	67	<i>Sciurus yucatanensis</i>	5.23
31	<i>Dermanura tolteca</i>	7.48	68	<i>Sigmodon mascotensis</i>	5.13
32	<i>Sciurus variegatoides</i>	7.48	69	<i>Eira barbara</i>	5.12
33	<i>Mormoops megalophylla</i>	7.45	70	<i>Ateles geoffroyi</i>	5.11
34	<i>Oryzomys melanotis</i>	7.42	71	<i>Neotoma phenax</i>	5.07
35	<i>Artibeus intermedius</i>	7.40	72	<i>Noctilio leporinus</i>	5.06
36	<i>Chaetodipus artus</i>	7.20	73	<i>Reithrodontomys fulvescens</i>	4.95
37	<i>Nasua narica</i>	7.18			



Positives for DENGUE

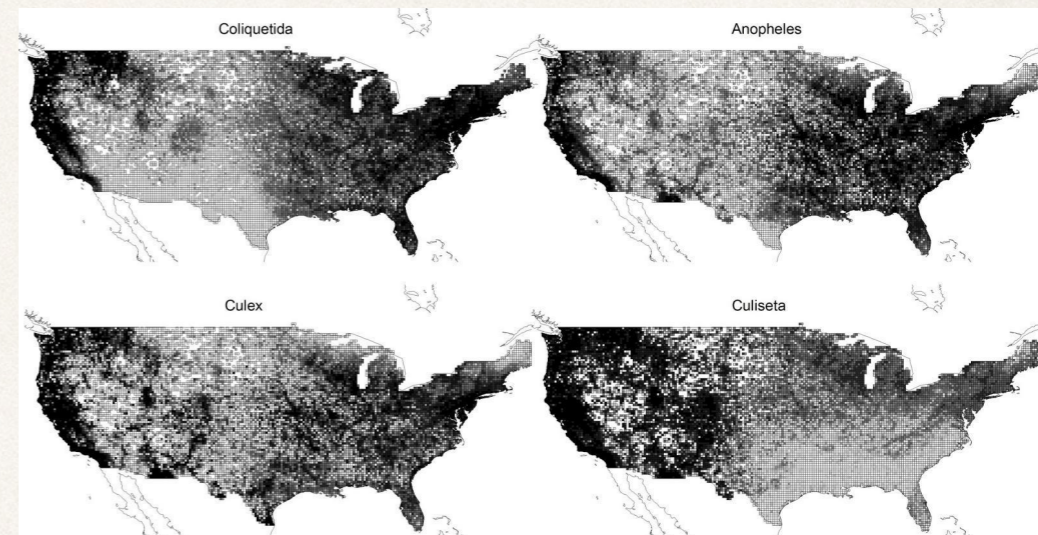
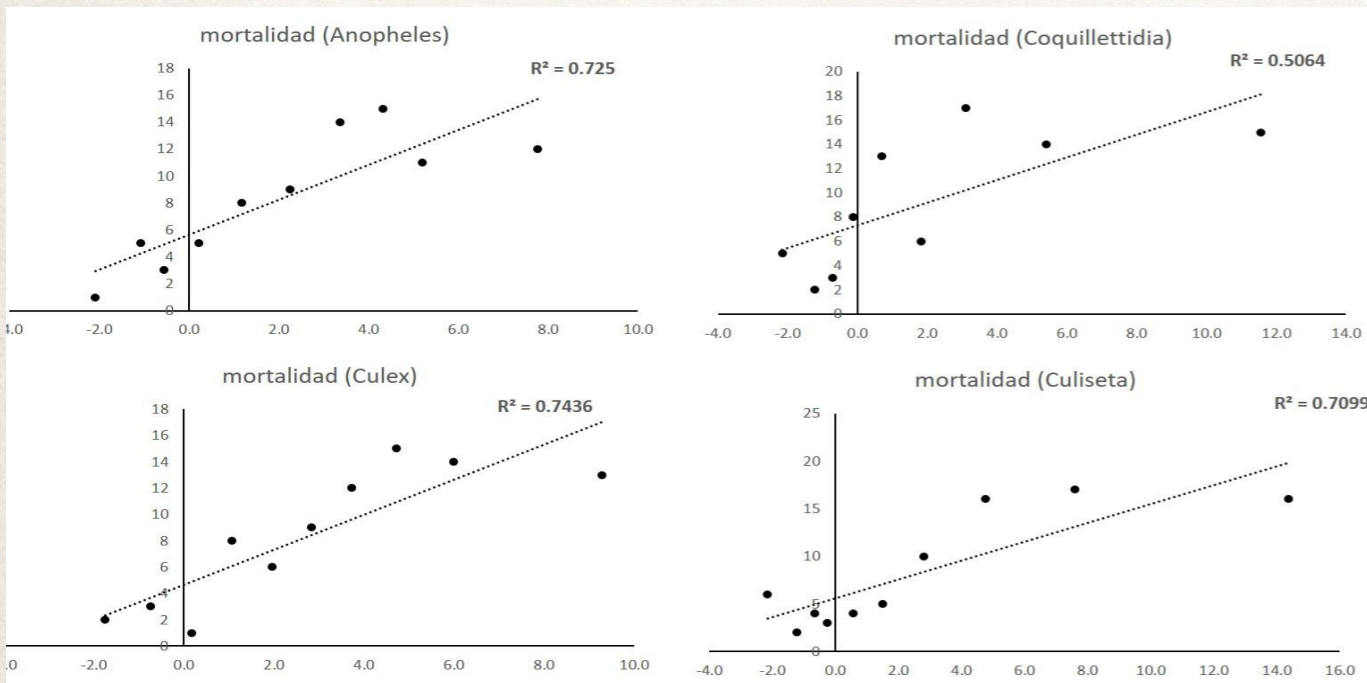


Complex Inference Network for *Aedes aegypti* and *Aedes albopictus*

Chris Del

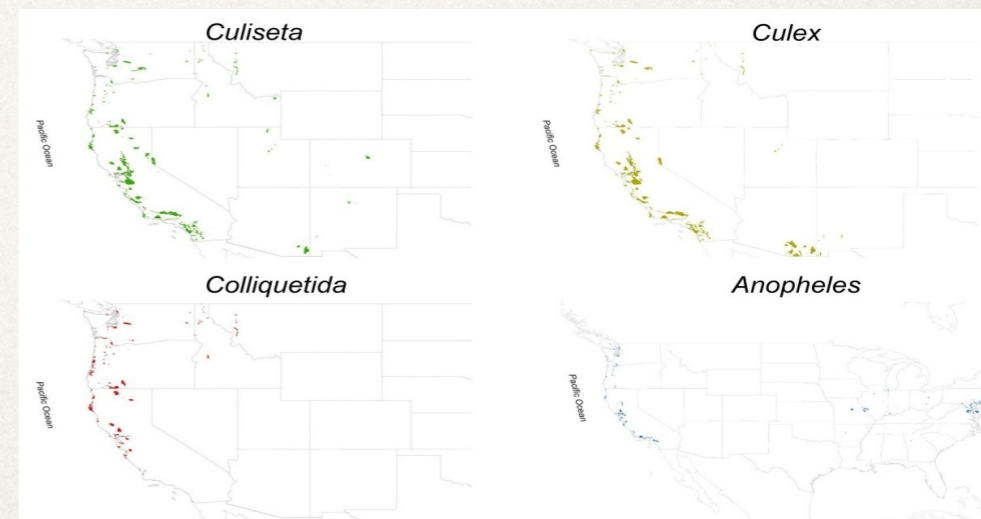


# Predictive Model for bird mortality from WNV



Risk map for presence of pathogenic strains of WNV

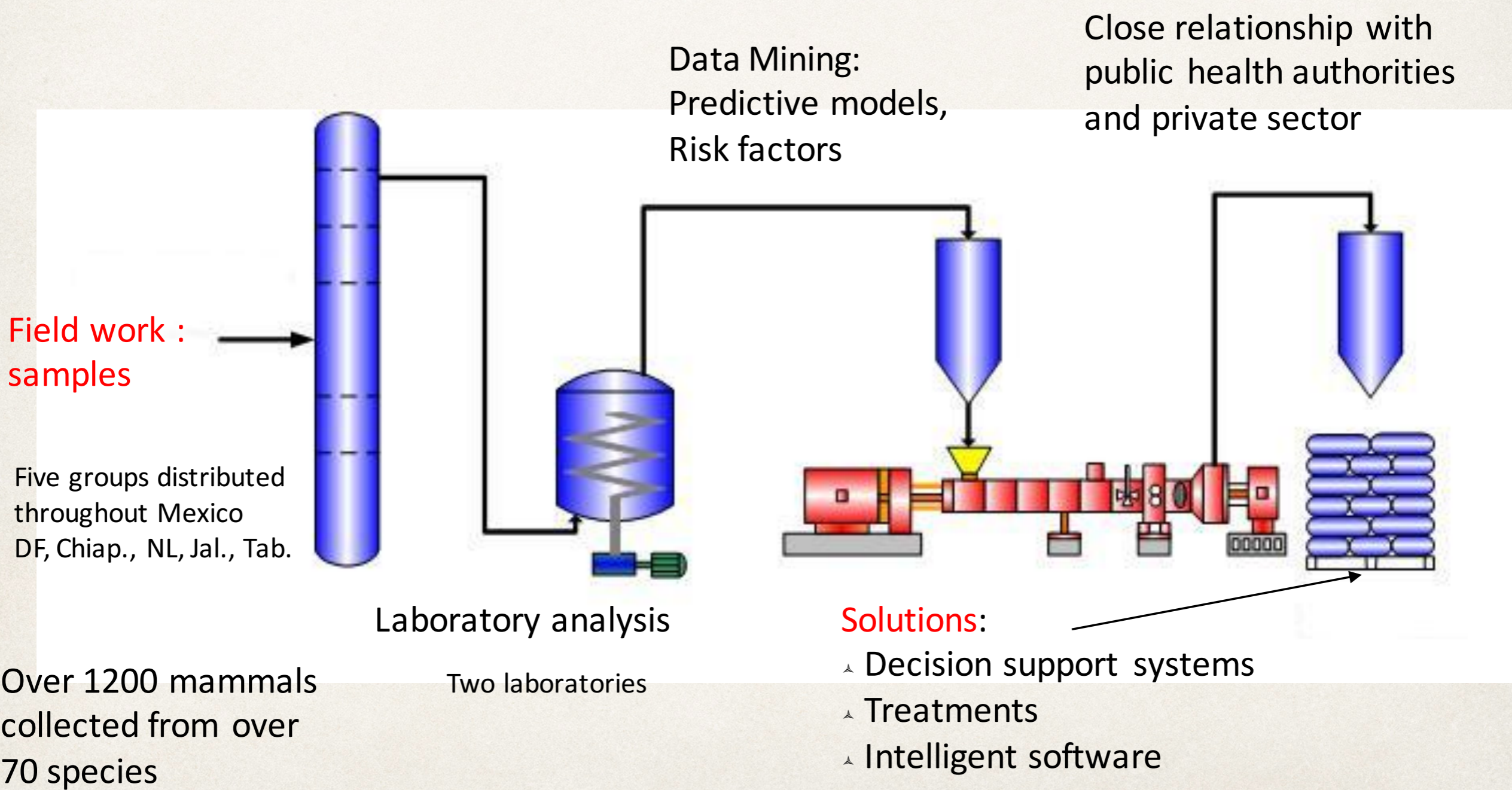
Relation between bird mortality and mosquito genera by geographic co-occurrence between them



Risk map for presence of pathogenic strains of WNV in bird conservation areas

# To Link Data-Predictions-Experiment

## The Emerging Disease (Arbovirus) “production line”



Over 1200 mammals collected from over 70 species

# Data-Predictions



Bienvenido a la Plataforma de exploración de datos ecológicos del C3 y la CONABIO.

¿Que deseas modelar?

Nicho ecológico

Comunidad ecológica

<http://species.conabio.gob.mx/>

Lynx rufus





# Predictions-Experiment

## Test zoonosis - Leishmaniasis

Species	ε	Negative	Positive	Total	% positive	Confidence (95%)
<i>Carollia sowelli</i>	8.83	43	2	45	4.4	-1 - 14
<i>Heteromys gaumeri*</i>	8.8	5	0	5	0	-15 - 29
<i>Peromyscus mexicanus</i>	8.79	115	6	121	5	2 - 11
<i>Heteromys desmarestianus*</i>	8.72	30	0	30	0	-2 - 16
<i>Molossus rufus</i>	8.63	1	0	1	0	-42 - 56
<i>Glossophaga soricina</i>	8.57	19	7	26	26.9	-3 - 16
<i>Carollia perspicillata</i>	8.5	8	0	8	0	-11 - 24
<i>Pteronotus parnellii</i>	8.16	4	0	4	0	-18 - 31
<i>Desmodus rotundus</i>	8.15	13	1	14	7.1	-6 - 20
<i>Sturnira lilium</i>	8.03	56	7	63	11.1	1 - 13
<i>Artibeus phaeotis</i>	8.01	35	1	36	2.8	-1 - 15
<i>Oryzomys couesi</i>	7.73	2	0	2	0	-28 - 41
<i>Ototylomys phyllotis*</i>	7.56	9	1	10	10	-9 - 22
<i>Sigmodon hispidus*</i>	7.28	36	4	40	10	-1 - 14
<i>Peromyscus yucatanicus*</i>	7.25	3	0	3	0	-22 - 35
<i>Didelphis virginiana</i>	7.12	3	0	3	0	-22 - 30
<i>Didelphis marsupialis</i>	6.44	11	0	11	0	-8 - 21
<i>Philander opossum</i>	6.25	6	1	7	14.3	-12 - 25
<i>Centurio senex</i>	6.01	1	0	1	0	-42 - 56
<i>Artibeus jamaicensis</i>	5.98	81	5	86	5.8	1 - 12
<i>Artibeus lituratus</i>	5.84	38	3	41	7.3	-1 - 14
<i>Myotis keaysi</i>	5.61	2	0	2	0	-28 - 41
<i>Chiroderma villosum</i>	5.56	5	0	5	0	-15 - 29
<i>Saccopteryx bilineata</i>	5.3	1	0	1	0	-42 - 56
<i>Sciurus aureogaster</i>	5.23	71	8	79	7.3	1 - 12
<i>Baiomys musculus</i>	5.21	2	0	2	0	-28 - 41
<i>Artibeus watsoni</i>	5.13	2	0	2	0	-28 - 41
<i>Choeroniscus godmani</i>	5.05	10	3	13	23.1	-7 - 20
<i>Pteronotus personatus</i>	5.03	3	1	4	25	-18 - 31
<i>Reithrodontomys mexicanus</i>	4.91	1	0	1	0	-42 - 56
<i>Oryzomys rostratus</i>	4.87	22	1	23	4.3	-4 - 17
<i>Micronycteris microtis</i>	4.23	1	0	1	0	-42 - 56
<i>Oligoryzomys fulvescens</i>	4.2	6	0	6	0	-13 - 27
<i>Peromyscus leucopus</i>	3.8	22	4	26	15.4	-3 - 16
<i>Sturnira ludovici</i>	3.79	24	1	25	4	-3 - 17
<i>Vampyroides caraccioli</i>	3.69	1	0	1	0	-42 - 56
<i>Liomys pictus</i>	3.61	47	1	48	2.1	0 - 14
<i>Glossophaga commissarisi</i>	3.49	2	6	8	75	-11 - 24
<i>Lonchorhina aurita</i>	3.48	1	0	1	0	-42 - 56
<i>Phyllostomus discolor</i>	3.48	0	1	1	100	-42 - 56
<i>Platyrrhinus helleri</i>	3.36	5	0	5	0	-22 - 35
<i>Uroderma bilobatum</i>	3.34	4	0	4	0	-18 - 31
<i>Urocyon cinereoargenteus</i>	2.97	1	0	1	0	-42 - 56
<i>Procyon lotor</i>	2.95	1	0	1	0	-42 - 56
<i>Myotis velifer</i>	2.58	3	0	3	0	-18 - 31
<i>Microtus mexicanus</i>	2.53	16	0	16	0	-6 - 19
<i>Myotis nigricans</i>	2.47	2	0	2	0	-28 - 41
<i>Leptonycteris yerbabuena</i>	2.43	1	1	2	50	-28 - 41
<i>Reithrodontomys fulvescens</i>	2.08	20	0	20	0	-4 - 18
<i>Neotoma mexicana</i>	1.99	5	0	5	0	-15 - 29
<i>Eptesicus fuscus</i>	1.82	1	0	1	0	-42 - 56
<i>Peromyscus levipes</i>	1.34	1	0	1	0	-42 - 56
<i>Sorex saussurei</i>	1.29	3	0	3	0	-22 - 35
<i>Osgoodomys banderanus</i>	1.21	9	0	9	0	-10 - 23
<i>Liomys irroratus</i>	1.16	8	0	8	0	-11 - 24
<i>Myotis auricularis</i>	0.22	2	0	2	0	-28 - 41
<i>Tadarida brasiliensis</i>	-0.09	1	0	1	0	-42 - 56
<i>Peromyscus hylocetes</i>	-0.28	2	0	2	0	-28 - 41
<i>Antrozous pallidus</i>	-0.34	1	0	1	0	-42 - 56
<i>Peromyscus zarhynchus</i>	-0.46	2	0	2	0	-28 - 41
<i>Chaetodipus hispidus</i>	-0.71	4	0	4	0	-18 - 31
<i>Peromyscus pectoralis</i>	-0.73	2	0	2	0	-28 - 41
<i>Neotomodon alstoni</i>	-0.9	17	0	17	0	-5 - 19
<i>Baiomys taylori</i>	-1.16	10	3	13	23.1	-7 - 20
<i>Chaetodipus nelsoni</i>	-1.24	3	0	3	0	-22 - 35
<i>Neotoma micropus</i>	-1.27	16	0	16	0	-6 - 19
<i>Peromyscus maniculatus</i>	-1.37	58	2	60	3.3	0 - 13
<i>Peromyscus eremicus</i>	-1.41	0	1	1	100	-42 - 56
<i>Perognathus flavus</i>	-1.52	1	0	1	0	-42 - 56
<i>Dipodomys merriami</i>	-2.01	1	0	1	0	-42 - 56

- Only about 50 (2.5%) of mammals on the American continent have been identified as hosts of Leishmania
- In Mexico only 8 out of 419 (2.1%) had been identified as hosts
- We collected 922 individuals from 70 species
- Predicted and confirmed 21 new species of mammal as carriers of Leishmania in Mexico
- 13 of them are bats, identified for the first time in Mexico
- Squirrels identified as carriers
- 33% of collected species were confirmed as hosts
- Overall infection rate was 6.7%
- No species could be rejected as a host at this infection rate at the 95% confidence level
- Changes the picture for control of Leishmania totally;
- Leishmania and Lutzomyias are eclectic in their host source.
- Linnean classification is NOT ecologically relevant

# Data-Predictions-Experiment

## Test zoonosis - Leishmaniasis



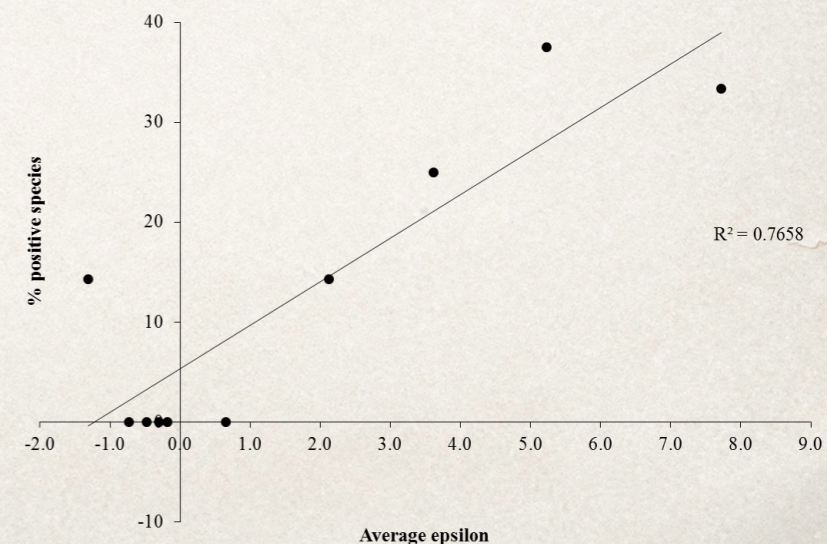
	Mammals	Epsilon	Conf.
1	Eira barbara	10.1683	
2	Rhogeessa aeneus	9.3649	
3	Artibeus intermedius	9.1628	Yes
4	Reithrodontomys gracilis	8.8921	Yes
5	Carollia sowelli	8.8303	Yes
6	Heteromys gaumeri	8.8000	Yes
7	Peromyscus mexicanus	8.7859	Yes
8	Heteromys desmarestianus	8.7164	Yes
9	Molossus rufus	8.6277	
10	Glossophaga soricina	8.5713	Yes
11	Carollia perspicillata	8.5030	Yes
12	Orthogeomys hispidus	8.3468	
13	Pteronotus parnellii	8.1632	Yes
14	Desmodus rotundus	8.1519	Yes
15	Dasyprocta mexicana	8.1128	
16	Sturnira lilium	8.0290	Yes
17	Dermanura phaeotis	8.0055	Yes
18	Dasyprocta punctata	7.9678	
19	Oryzomys couesi	7.7253	
20	Potos flavus	7.7246	
21	Conepatus semistriatus	7.6879	
22	Ototylomys phyllotis	7.5587	Yes
23	Ateles geoffroyi	7.4787	
24	Cryptotis magna	7.4207	
25	Cuniculus paca	7.3220	
26	Lamproncyteris brachyotis	7.2852	
27	Sigmodon hispidus	7.2805	Yes
28	Peromyscus yucatanicus	7.2486	Yes
29	Oryzomys chapmani	7.1242	
30	Didelphis virginiana	7.1150	
31	Peromyscus melanocarpus	7.0260	
32	Microtus umbrosus	6.9630	
33	Thyroptera tricolor	6.9630	
34	Nasua narica	6.8953	
35	Megadontomys cryophilus	6.6830	
36	Oryzomys alfaroi	6.6816	
37	Sorex veraepacis	6.6797	
38	Carollia subrufa	6.6316	
39	Peromyscus aztecus	6.6173	
40	Didelphis marsupialis	6.4390	Yes
41	Sciurus yucatanensis	6.3865	
42	Philander opossum	6.2546	Yes
43	Habromys ixtlani	6.1120	
44	Microtus waterhousii	6.1120	
45	Pteronotus rubiginosus	6.1120	
46	Reithrodontomys microdon	6.0967	
47	Coendou mexicanus	6.0268	
48	Centurio senex	6.0076	
49	Artibeus jamaicensis	5.9786	Yes
50	Glossophaga morenoi	5.8847	

	Mammals	Epsilon	Conf.
51	Molossus sinaloae	5.8518	
52	Artibeus lituratus	5.8422	Yes
53	Mormoops megalophylla	5.8374	
54	Habromys lepturus	5.7848	
55	Myotis keaysi	5.6148	
56	Chiroderma villosum	5.5562	
57	Tamandua mexicana	5.4845	
58	Tylomys nudicaudus	5.4510	
59	Saccopteryx bilineata	5.2984	
60	Macrotus mexicanus	5.2472	
61	Sciurus aureogaster	5.2267	Yes
62	Baiomys musculus	5.2092	
63	Rhogeessa tumida	5.1950	
64	Sciurus deppei	5.1414	
65	Dermanura watsoni	5.1338	
66	Otonyctomys hatti	5.1338	
67	Orthogeomys grandis	5.0556	
68	Alouatta palliata	5.0457	Yes
69	Choeroniscus godmani	5.0457	
70	Peropteryx macrotis	5.0457	
71	Pteronotus personatus	5.0266	
72	Lontra longicaudis	4.9330	
73	Reithrodontomys mexicanus	4.9120	
74	Oryzomys rostratus	4.8681	Yes
75	Mimon cozumelae	4.8327	
76	Pteronotus davyi	4.7943	
77	Herpailurus yagouaroundi	4.7100	
78	Glossophaga leachii	4.6849	
79	Rhogeessa gracilis	4.6317	
80	Sylvilagus brasiliensis	4.6317	
81	Hodomys alleni	4.5155	
82	Leopardus wiedii	4.4420	
83	Peromyscus simulatus	4.4195	
84	Sigmodon alleni	4.3707	
85	Bassariscus sumichrasti	4.3110	
86	Oryzomys fulvescens	4.3110	
87	Diphylla ecaudata	4.3013	
88	Oryzomys melanotis	4.2907	Yes
89	Micronycteris microtis	4.2338	
90	Mazama americana	4.2274	
91	Microtus oaxacensis	4.2061	
92	Rheomys thomasi	4.2061	
93	Oryzomys saturator	4.2061	
94	Myotis elegans	4.2024	
95	Oligoryzomys fulvescens	4.1984	
96	Natalus stramineus	4.0626	
97	Balantiopteryx io	4.0522	
98	Nyctinomops laticaudatus	4.0522	
99	Tlacuatzin canescens	4.0119	
100	Odocoileus virginianus	3.9265	

	Mammals	Epsilon	Conf.
101	Balantiopteryx plicata	3.8590	
102	Peromyscus leucopus	3.7994	
103	Sturnina ludovici	3.7888	Yes
104	Enchisthenes hartii	3.6929	
105	Vampyroides caraccioli	3.6929	
106	Eptesicus furinalis	3.6453	
107	Liomys pictus	3.6107	
108	Glossophaga commissaris	3.4861	Yes
109	Lonchorhina aurita	3.4781	
110	Phyllostomus discolor	3.4781	Yes
111	Peromyscus gymnotis	3.4516	
112	Anoura geoffroyi	3.4201	
113	Platyrrhinus helleri	3.3586	
114	Eumops bonariensis	3.3398	
115	Sciurus variegatoides	3.3398	
116	Uroderma bilobatum	3.3373	
117	Lasiurus intermedius	3.2197	
118	Lasiurus ega	3.1739	
119	Peromyscus megalops	3.1410	
120	Eumops glaucinus	3.0564	
121	Urocyon cinereoargenteus	2.9697	
122	Procyon lotor	2.9502	
123	Hylonycteris underwoodi	2.9343	
124	Rhynchonycteris naso	2.8580	
125	Eptesicus brasiliensis	2.8106	
126	Myotis albescens	2.8106	
127	Lophostoma evotis	2.8106	
128	Tapirus bairdii	2.8106	
129	Vampyrum spectrum	2.8106	
130	Marmosa mexicana	2.7731	Yes
131	Peromyscus furvus	2.7731	
132	Myotis velifera	2.5757	
133	Spilogale putorius	2.5411	
134	Microtus mexicanus	2.5268	
135	Dasyplus novemcinctus	2.4725	
136	Myotis nigricans	2.4704	
137	Lophostoma brasiliense	2.4407	
138	Didelphis albiventris	2.4407	
139	Sciurus niger	2.4407	
140	Leptonycteris curasoae	2.4268	
141	Nyctomys sumichrasti	2.4026	
142	Sigmodon mascotensis	2.3815	
143	Alouatta pigra	2.3374	
144	Peromyscus melanophrys	2.2204	
145	Dermanura tolteca	2.1920	
146	Trachops cirrhosus	2.1663	
147	Bauerus dubiaquercus	2.1612	
148	Spilogale pygmaea	2.1612	
149	Leptonycteris nivalis	2.1402	
150	Sylvilagus floridanus	2.1002	



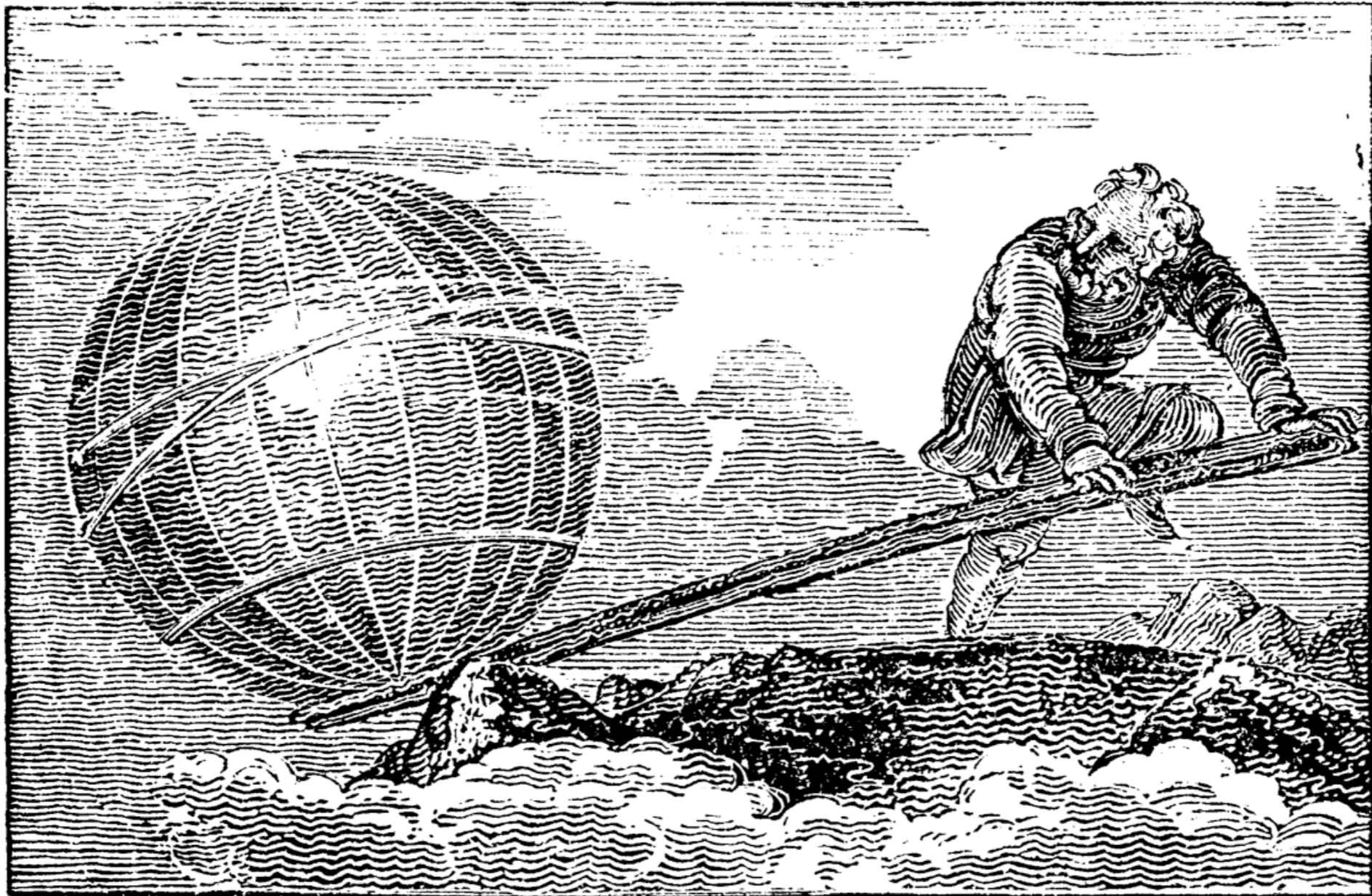
Biotic facilitation seems to be the norm. Species are not distributed randomly



# Conclusions



- 
- \* Prediction of arbovirus disease risk factors and interventions is of huge public health importance
  - \* Arbovirus diseases are Complex Adaptive Systems
    - \* Multi-factorial, multi-scale, multi-discipline → multi-interaction
    - \* Many arbovirus are multi-host, multi-vector
    - \* There are too many interactions to observe directly
    - \* Standard mathematical techniques model only a few factors
  - \* The Data Revolution has made available large amounts of data with which their complex, adaptive nature may be better modelled
    - \* Spatio-temporal data about organisms, relative to each other (biotic) and relative to the environment (abiotic), can be used to deduce the nature of their interactions
    - \* This can be done at the niche level (one to many) and at the community level (many to many)
    - \* Obtaining and integrating data is a huge challenge - political and technical
  - \* The optimal use of this data requires innovation in modelling using multiple techniques - from SIR-type models to agent-based modelling and the use of advanced machine learning and AI techniques.
  - \* Our work on various zoonosis show the utility of innovative approaches that use data of arbitrary spatial resolution and format, such as predicting host range.
    - \* Importance of a Data-Predictions-Experiment production line approach to emerging diseases
    - \* Importance of a multi-pathogen, multi-vector, multi-host approach



δῶς μοι πᾶ στῶ καὶ τὰν γᾶν κινάσω

Give me a place to stand on and I'll move the earth

**Give me enough data and I'll predict anything**

**The Data Revolution will revolutionise our  
ability to model and understand ecology**