Hunting Zika Virus using Machine Learning

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#Data4Good

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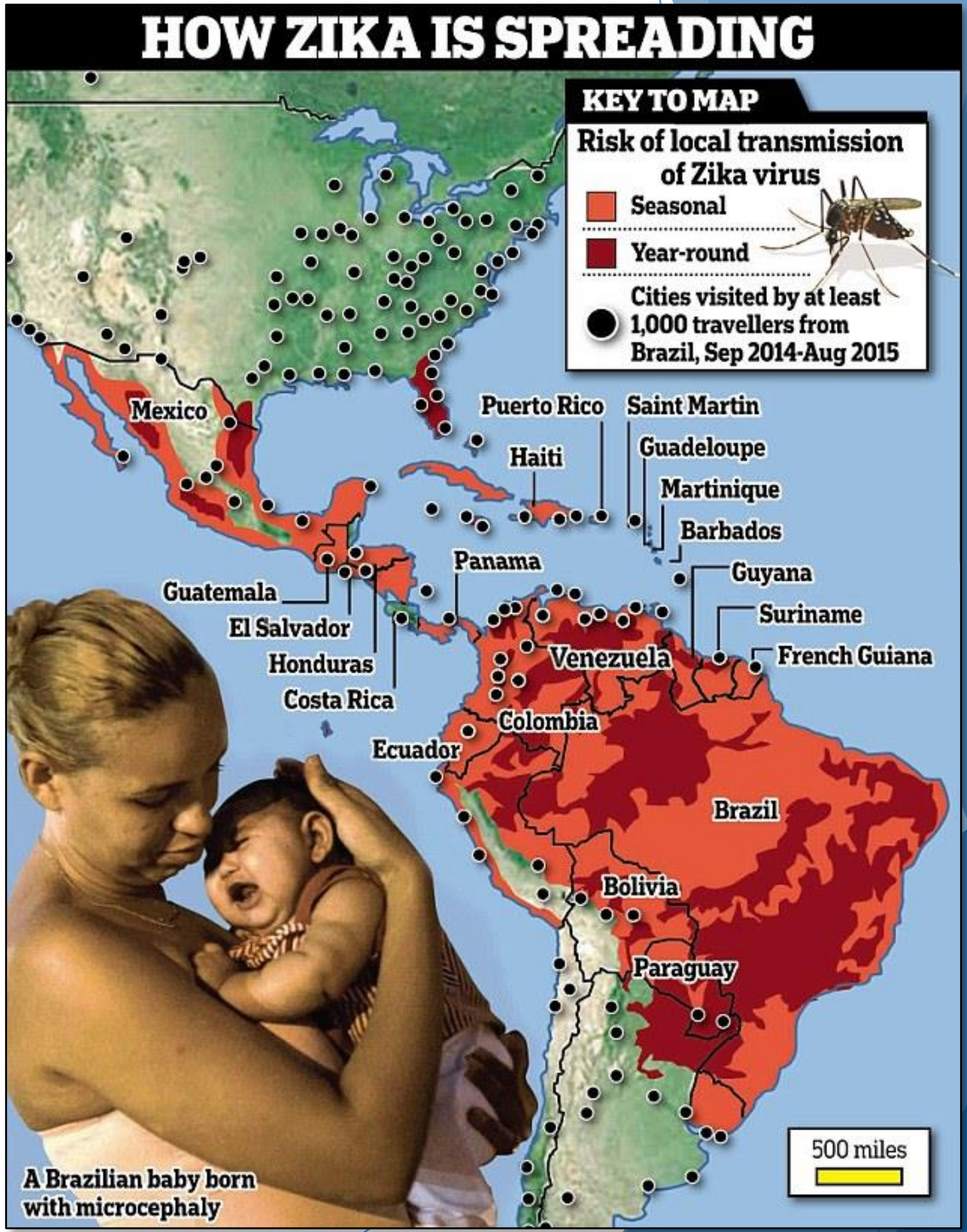
The Zika problem

Recently there is a Zika outbreak in Brazil and it is spreading fast.

Symptoms include rash, fever, muscle and joint pain, headache;

Zika is non-lethal but causes Microcephaly (= small head size) and eye problems in babies of infected mothers.



How Zika spreads

- The virus naturally resides in the blood of host animals;
- The animals don't get infected because they have antibodies, or have subclinical infections;
- Virus survives by passing from generation to generation of animals.

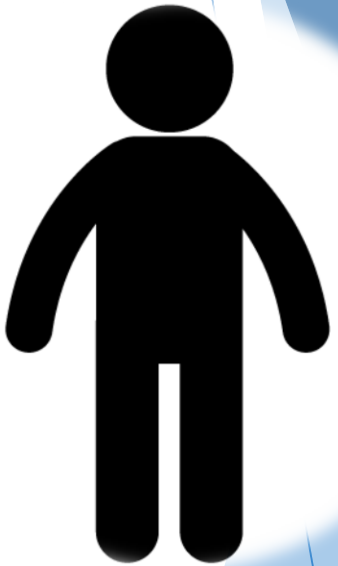



Known primate hosts of Zika

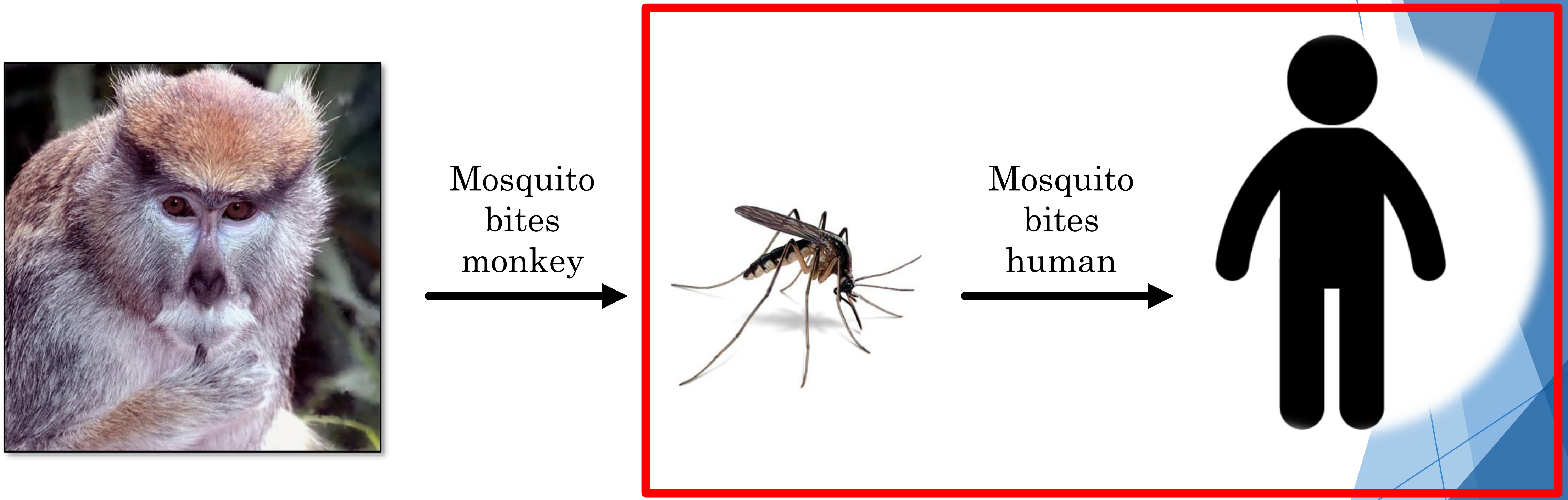
How Zika spreads

Mosquito
bites
monkey

Mosquito
bites
human



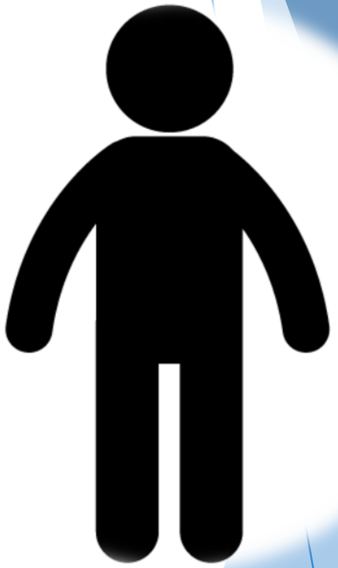
Present: REACTIVE approach to contain outbreak



Present: REACTIVE approach to contain outbreak

Mosquito bites monkey

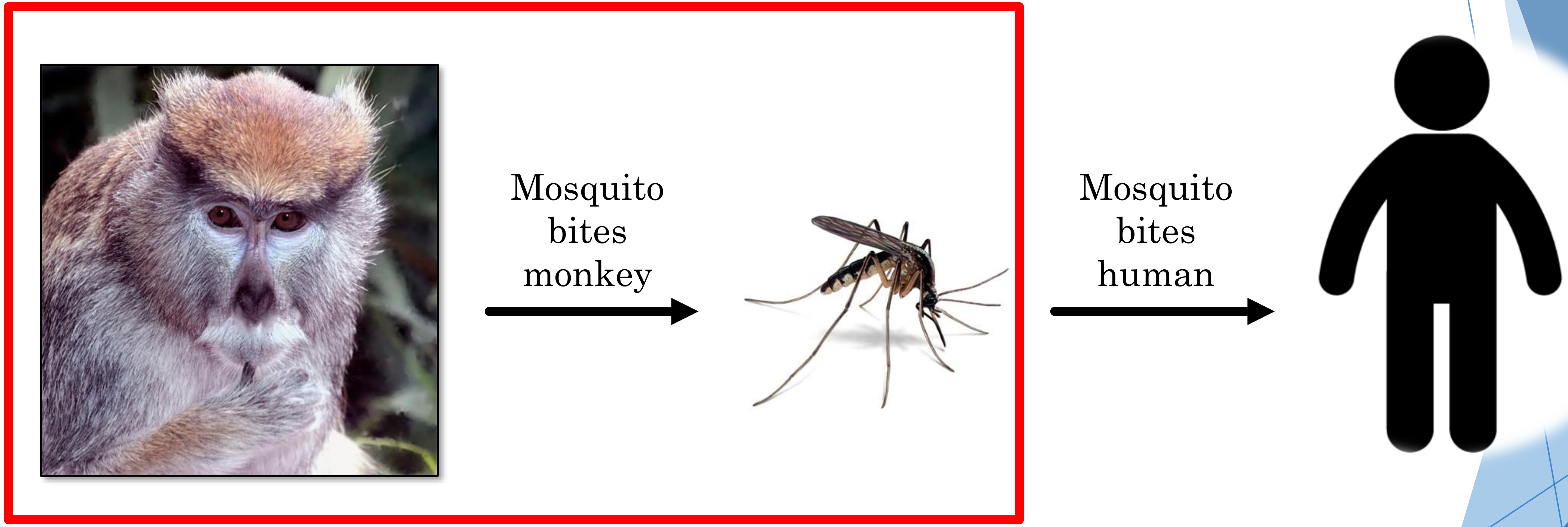
Mosquito bites human



Eradicate mosquitos in spillover areas

Not Good!

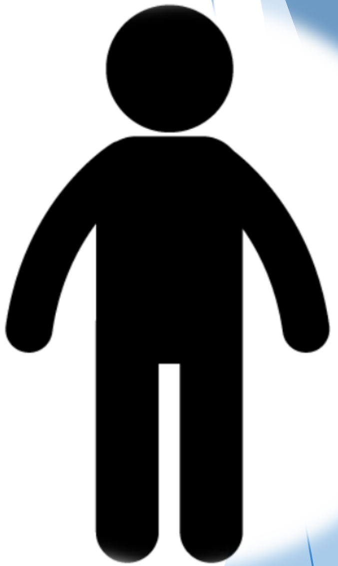
Objective : PROACTIVE approach to stop outbreak



Objective : PROACTIVE approach to stop outbreak

Mosquito bites monkey →

Mosquito bites human →



Find out the source animals to prioritize mosquito eradication efforts

Kills the problem at source

Data

Dataset 1: Reservoir status

Animal	Carries Zika?	Carries Dengue?	Carries Yellow fever?	…
Monkey 1	No	Yes	No	…
Monkey 2	Yes	No	No	…
Monkey 3	No	Yes	No	…
Monkey 4	No	No	No	…
Monkey 5	Yes	No	Yes	…
Monkey 6	No	Yes	No	…
…	…	…	…	…

376 monkeys, 8 diseases

Dataset 2: Animal characteristics

Animal	Body mass	Litter size	Maximum longevity	…
Monkey 1				…
Monkey 2				…
Monkey 3				…
Monkey 4				…
Monkey 5				…
Monkey 6				…
…	…	…	…	…

50 characteristics

Challenges

Dataset 1: Reservoir status

Animal	Carries Zika?	Carries Dengue?	Carries Yellow fever?	…
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…	…	…	…	…

376 monkeys, 8 diseases

- Reservoirs are extremely rare;
- Only 4 known reservoirs for Zika;
- There are only 26 positive entries in this matrix;
- Need specialized methods to deal with the situation.

Challenges

- Data on animal characteristics are not complete: lot of entries are missing in many animals;
- Some characteristics are almost completely missing for all animals;
- Some animals have almost all variables missing;

Dataset 2: Animal characteristics

Animal	Body mass	Litter size	Maximum longevity	…
Monkey 1				…
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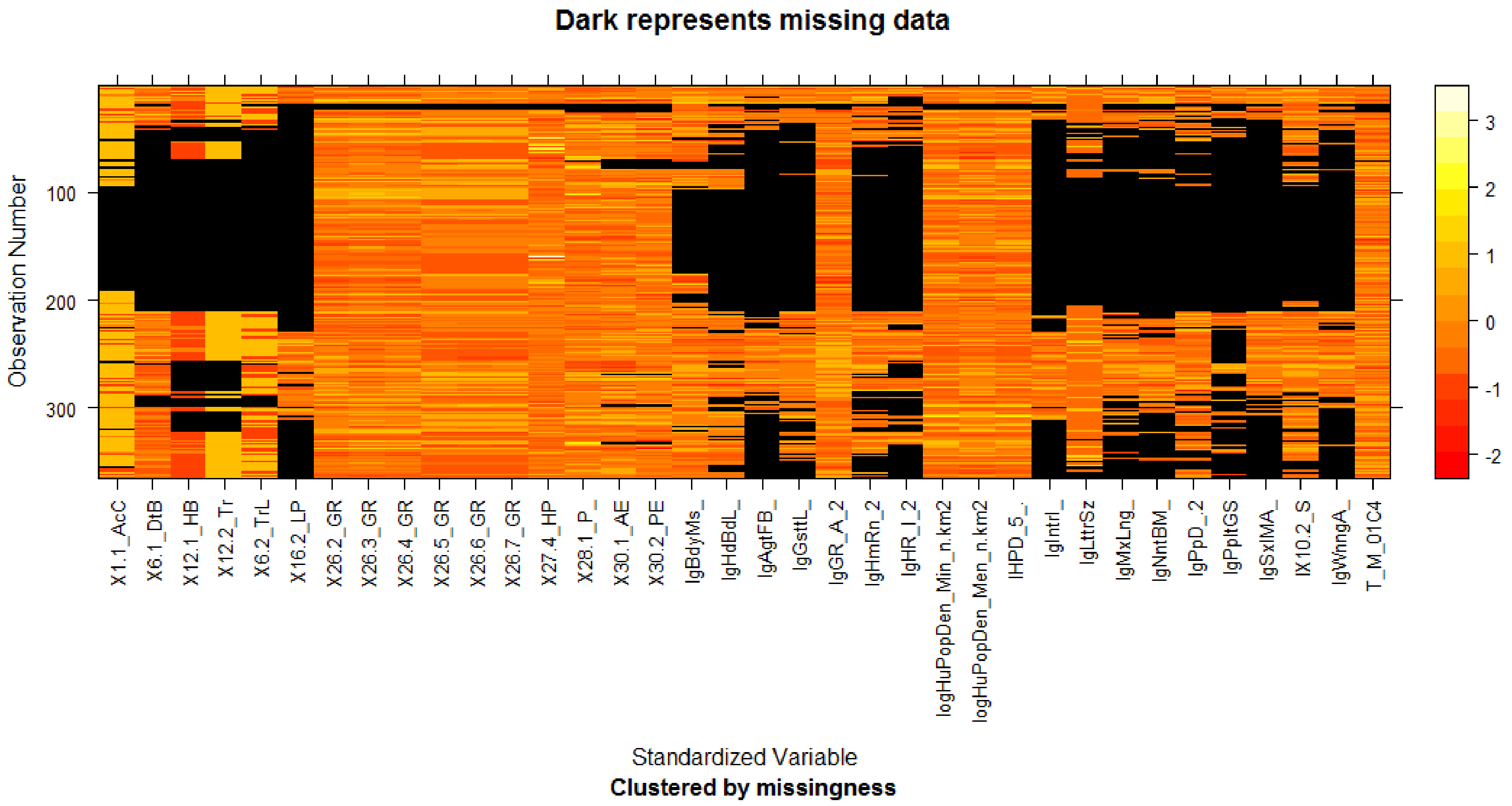
…	…	…	…	…

The missing data problem



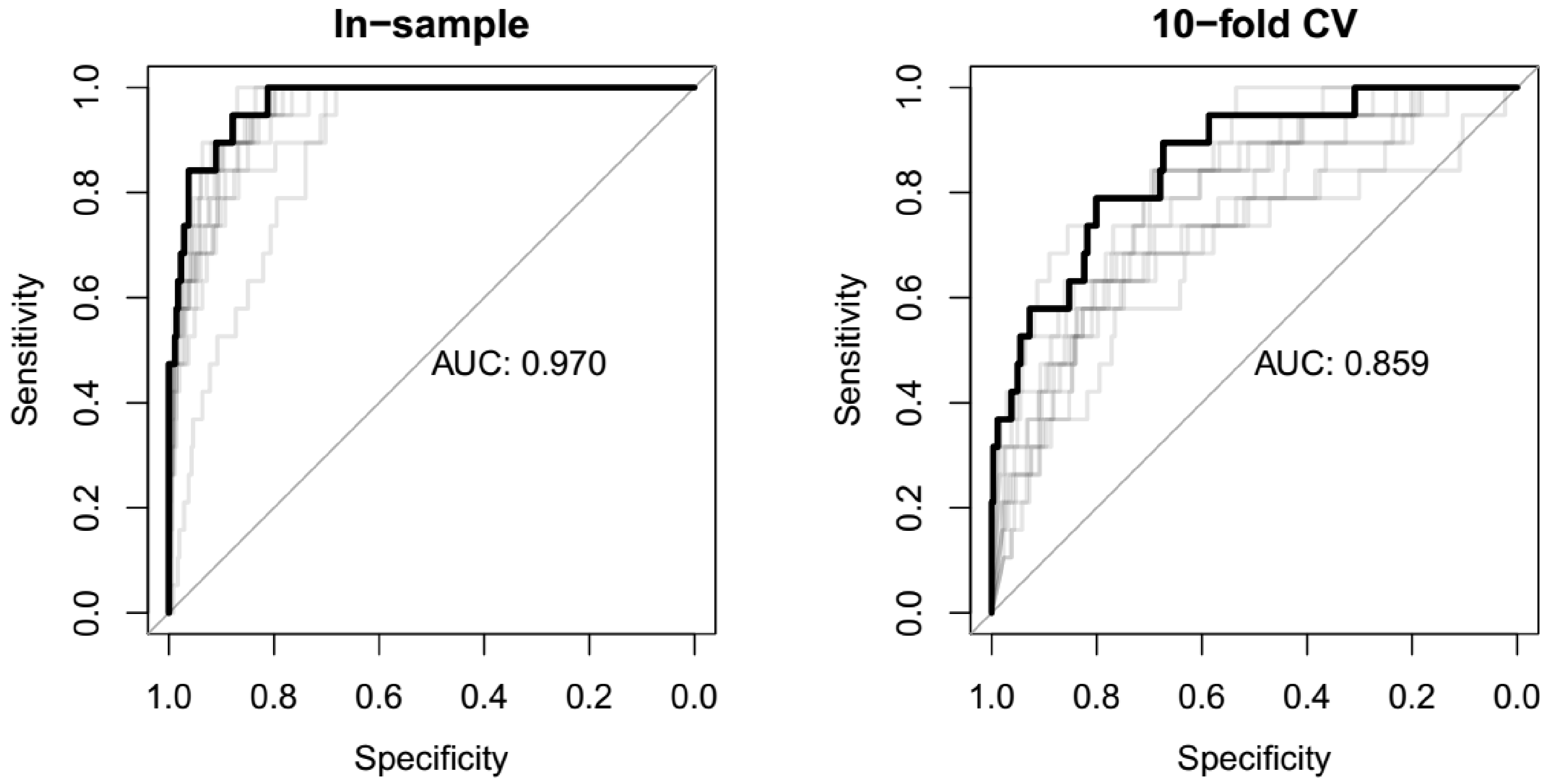
Modelling approach

1. **Missing data imputation:**
   use a multiple imputation procedure called Multiply Imputed Chained Equation (MICE: Raghunathan *et al*, 2001)

2. **Predictive model:**
   - Model reservoir status for all Zika-like simultaneously;
   - Use a Bayesian model that assumes the response variable is generated through a hierarchical process, taking into account covariate information in a nonlinear fashion (Rai *et al*, 2015)

Validation

Stratified 10-fold CV: make folds for positive and negative classes separately and group together. Needed because positive class is rare.

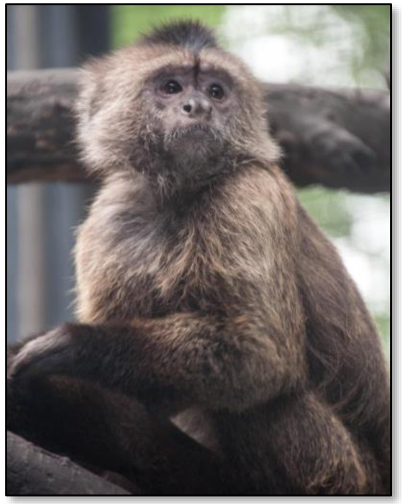


Results

- We are interested in high-risk animals in South America that haven't been detected yet.
- Top 3 high-risk species:

White-fronted Capuchin monkey (*Cebus albifrons*)

Common squirrel monkey (*Saimiri sciureus*)



Weeper Capuchin monkey (*Cebus olivaceus*)

Trait profiles of high-risk animals

	Importance	mean.low	mean.hi
logHuPopDen_Min_n.km2	0.61	2.12	1.09
logGR_Area_km2	0.5	9.59	13.21
X26.2_GR_MaxLat_dd	0.48	-6.95	11.09
logAgeatFirstBirth_d	0.47	6.71	7.12
logHuPopDen_5p_n.km2	0.47	2.19	1.61
logNeonateBodyMass_g	0.47	3.84	5.34
logHomeRange_Indiv_km2	0.4	-2.68	-0.48
paleotropical	0.38	0.72	0.75
logHomeRange_km2	0.36	-3.06	-0.89

- Larger animals that have high body mass, longer gestation periods and larger social groups seem to be more likely reservoirs

What to do with the outputs?

- Work with disease ecology researchers to collect blood samples from these monkeys and test for presence of Zika virus;
- If a new reservoir is detected, focus on mosquito eradication efforts around the animal's habitat;
- Provide a much needed empirical baseline for future similar studies regarding a proactive approach towards infectious disease management.

Future work

- Integrate with the Prospector tool (Krause, Perer and Ng, 2016) to understand how risk scores are affected by different levels of a covariate, i.e. partial dependence plots;
- Modify outcomes for unknown reservoirs based on their geographic range overlap with known reservoirs, as well as incorporate primate-mosquito interactions;
- Extend the underlying model to incorporate covariate information on the different viruses;
- Build a unified framework for simultaneously imputing missing data and modelling the outcomes.

References

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THANK YOU!