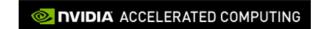
Generating Better Macroecological Data From Literature OR Gold in the Garbage Dump

Noam Ross (@noamross), Allison M. White, Cale Basaraba, Brooke Watson, Erica Johnson, Karissa Whiting, Melanie Kirshenbaum, Jacob Kotcher, Ayomide Sokale, Mushtaq Dualeh, Zach Matson, Nchedo Ezekoli, Carlos Zambrana-Torrelio, Peter Daszak







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Origins at #ESA2017

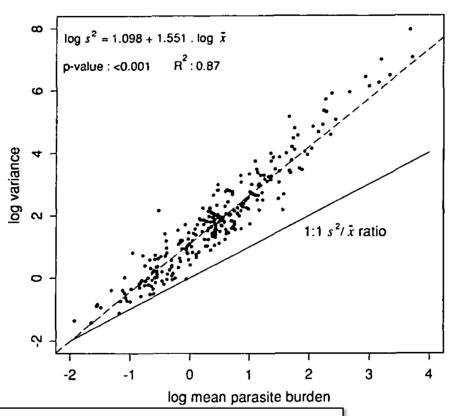
Noam: "We're kind of scraping the barrel with these host-pathogen-interactions-from-the-literature papers."

John Drake: "No, we keep finding new things."

Noam: "We're kind of scraping the barrel with these host-pathogen-interactions-from-the-literature papers"

John Drake: "No, we keep finding new things"

Carl Boettiger: "The problem is that we're still combing through these papers by hand."



Patterns of macroparasite abundance and aggregation in wildlife populations: a quantitative review

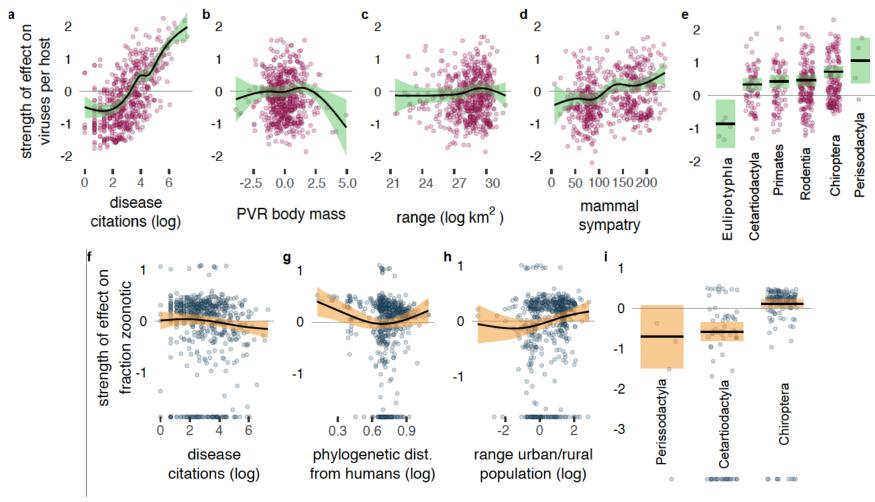
D. J. SHAW1 and A. P. DOBSON2

SUMMARY

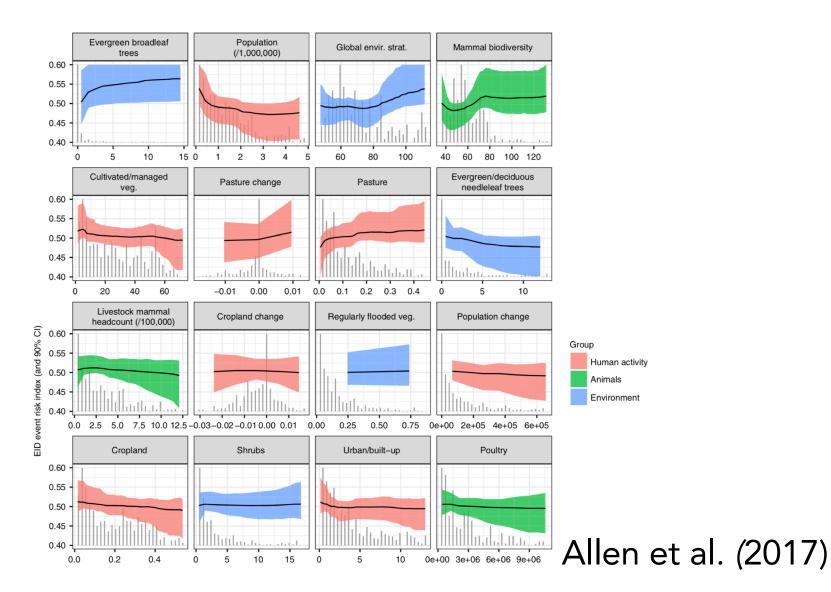
Dobson and Shaw (1995)

¹Department of Zoology, University of Cambridge, Downing Street, Cambridge, CB2 3EJ, UK

² Department of Ecology and Evolutionary Biology, Eno Hall, Princeton University, Princeton, New Jersey, USA



Olival et al. (2017)



Dobson and Shaw (1995)

263 Host-Parasite Associations

Allen et al. (2017)

747 literature sources

Olival et al. (2017)

1317 literature sources





ute data pics blog who we are

Welcome to the Interaction Web Database. This is a nonprofit, cooperative database containing published data on species interaction networks. It is hosted by the National Center for Ecological Analysis and Synthesis, at the University of California, Santa Barbara, U.S.A.

You must read our Privacy Policy before using the Interaction WebDatabase website







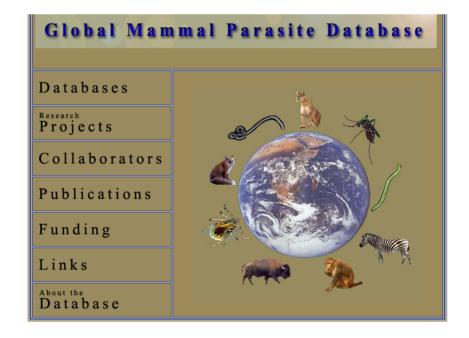




Global Biotic Interactions (GloBI) provides open access to species interaction data (e.g., predator-prey, pollinator-plant, pathogenhost, parasite-host) by combining existing open datasets using open source software.



Welcome to the <u>ENHanCEd</u> Infectious Diseases (EID2) database. This evidence-based database annotates and integrates existing data on vectors, hosts and their pathogens. The database enables users to obtain:









A good idea defeated by high soil processing costs?

US and European experiences.

(A real slide from someone's very different conference)

Bitcoin?!?!

A new landfill mining project: Macroecology of Antibiotic Resistance Emergence

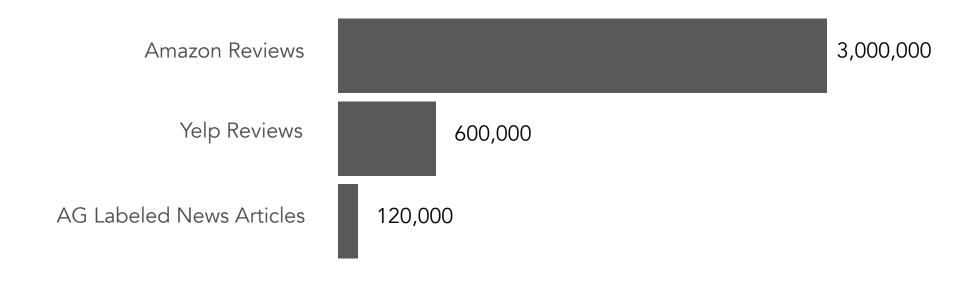
Identify global correlates of emergence of new AMR mutations

Use machine learning and text classification to identify relevant events from the literature

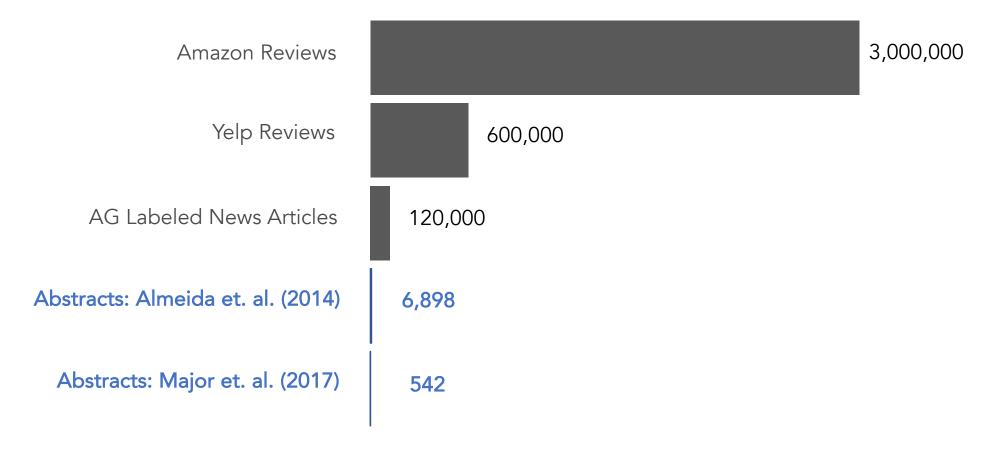
A Wicked Text-Classification Task

Does an article or report describe at least one clinical case of infectious disease in a human patient caused by a novel resistance to a particular antimicrobial combination in bacteria?

Data Set Sizes in Neural-Net Text Classification Research



Data Set Sizes in Neural-Net Text Classification Research



24,000 articles found via search for AMR keywords

Each abstract classified by 2 readers

1000+ hours of screening effort

~25+ person-weeks

Very Deep Convolutional Networks for Text Classification

Alexis Conneau

Facebook AI Research aconneau@fb.com

Holger Schwenk

Facebook AI Research schwenk@fb.com

Yann Le Cun

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Loïc Barrault

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GloVe: Global Vectors for Word Representation

Jeffrey Pennington, Richard Socher, Christopher D. Manning Computer Science Department, Stanford University, Stanford, CA 94305 jpennin@stanford.edu, richard@socher.org, manning@stanford.edu

Character-level Convolutional Networks for Text Classification*

Xiang Zhang Junbo Zhao Yann LeCun

Courant Institute of Mathematical Sciences, New York University 719 Broadway, 12th Floor, New York, NY 10003 {xiang, junbo.zhao, yann}@cs.nyu.edu

Enriching Word Vectors with Subword Information

Piotr Bojanowski* and Edouard Grave* and Armand Joulin and Tomas Mikolov Facebook AI Research

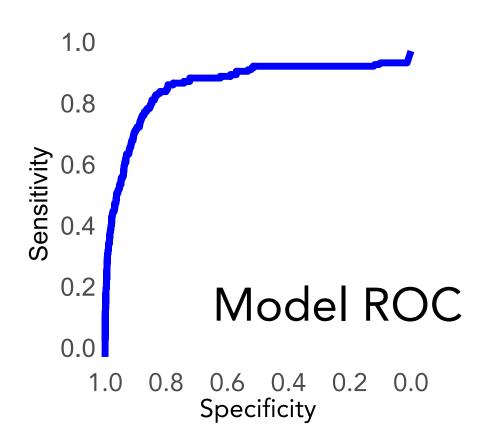
{bojanowski, egrave, a joulin, tmikolov}@fb.com





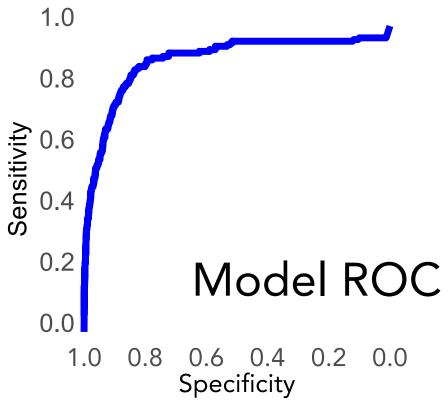
7% of articles were true cases

85% balanced accuracy





85% balanced accuracy



We can get 95% of Specificity events automating 65% of screening

Next: Automated Semantic Extraction

We present the first known case of osteomyelitis associated to an CTX-M-15-producing A. hydrophila isolate carrying also the $bla_{\text{TEM-1}}$ gene, as well as genes conferring resistance to aminoglycosides, aac(3)-IIa, and to aminoglycosides and ciprofloxacin, aac(6')-Ib-cr.

A 37-year-old woman was hospitalised in May of 2009 for an open fracture grade III of the right tibial pilon. External fixators were placed and empiric treatment with ciprofloxacin plus vancomycin was established. Seven

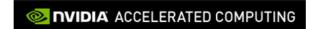
The patient was treated with meropenem (1g tid) plus amikacin (750 mg bid) for a course of 30 days, and treatment with meropenem alone was continued for 15 days more. The patient's progress was monitored by acute phase reactants, serial imaging studies and clinical evolution.

Machine learning may not help us infer mechanisms but it can help find data!

Publish **negative** data from your literature review!

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