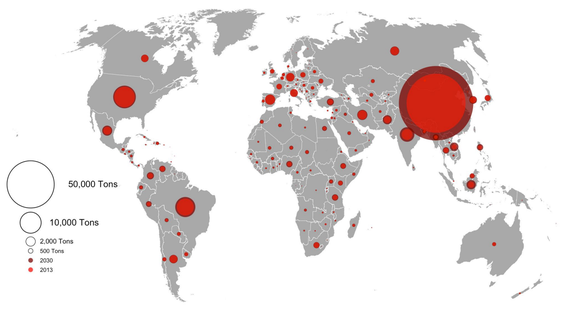
ETH zürich

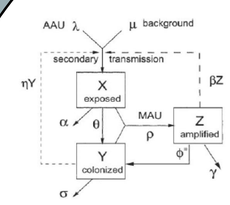
Health Geography and Policy Group

Thomas Van Boeckel



I lead the activities of the Health Geography and Policy Group. Collectively, our goal is to generate evidence to guide policy on antimicrobial resistance (AMR) – the ability of microbes to wishtand the effect of tratment. AMR is a threat to humans, but also to animals. Collectively, animals raised for food consume 73% of antimciorbials on earth. We generate maps to monitor antimicorbial use, and resistance, with a focus on low- and middle-income countries. Our maps are accessible through the platform resistancebank.org. In the future, my personal interest is to expand those efforts to i) projections of antimicorbial use under different socio-economic development pathways, ii) produce a first global map of veterinarians who play a key role in administering antimicrobials, iii) team up with field veterinarians to encourage the adoption of resistancebank.org as the main portal for reporting and sharing data on antimicrobial resistance in food production.

Giulia Brunelli



$$\dot{X} = (\mu + \lambda + \eta Y + \beta Z)W - (\theta + \alpha + \rho)X$$

$$\dot{Y} = \theta X + \phi Z - (\rho + \sigma)Y$$

$$\dot{Z} = \rho(X + Y) - (\gamma + \phi)Z$$

$$N_i^+ \sim Binomial(p_i, N_i)$$

$$logit(p_i) = \alpha + \boldsymbol{X_i\beta} + \epsilon_{GP_i}$$

$$\epsilon_{GP} \sim GP(0, \boldsymbol{K}_{space} \otimes \boldsymbol{K}_{time})$$

$$\boldsymbol{K}_{space} = \left(\tau 2^{\nu-1}\Gamma(\nu)\right)^{-1}(\kappa \boldsymbol{D})^{\nu} K_{\nu}(\kappa \boldsymbol{D})$$

$$\boldsymbol{K}_{time_{k,l}} = \rho^{|t_k - t_l|}$$

The goal of my project is to improve and fit models to produce maps of AMR and its trasmission in Europe. I will use Bayesian approaches and SIR models. I would like to test some methods for extending forecasts of the spread of AMR where large amounts of data are not available.

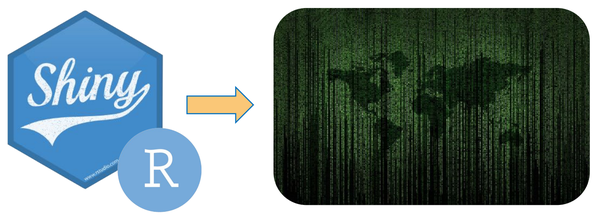
Cheng Zhao

My project is aimed at identifying priority regions where future surveillance effort of AMR in animals in China. I use geospatial models to produce a map of AMR in China, and a map of uncertainty levels associated with the predictions. In particular my work aim to identify where the next 50 surveys to be carried out in China should be conducted in the future, such that the overall uncertainty in the geographical trends in AMR in China is minimized.

Katie Tiseo

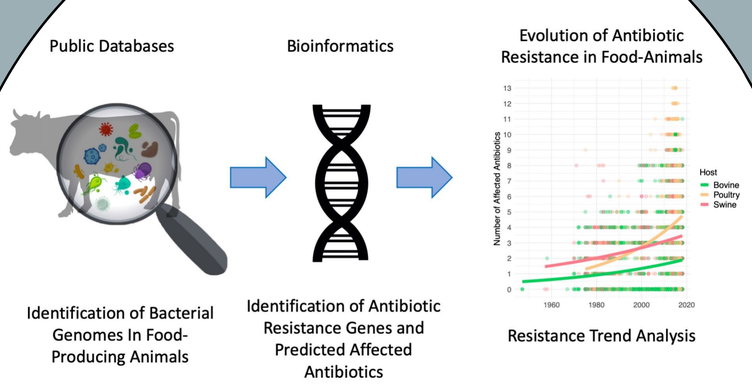
I am conducting systematic reviews for point prevalence surveys on antimicrobial resistance in food-producing animals in Europe. These studies will be used to produce maps of antimicrobial resistance to be disseminated via resistancebank.org.

Nicola Criscuolo



I use reactive programming languages (R, HTML and Java) to develop, maintain and update resistancebank.org, an open-access online Shiny platform that collects and distrubutes data on antimicrobial resistance in animals. The goal of this platform is to provide a focal point to the community of researchers and veterinarians working on AMR. Generally, my work aims to develop the field of digital epidemiology to improve the way in which online surveillance systems can inform better policies for antimicrobial use in animals raised for food.

Joao Pires



Antibiotic resistance genes provide bacteria with the ability to evade the effect of antibiotics. These genes can be transferred among bacterial populations, further spreading resistance. My project aims to assess the global distribution of antibiotic resistance genes in *Escherichia coli* recovered from food-producing animals. Our goal is to identify high-priority areas for intervention. Additionally, observed differences in the antibiotic resistance genes among the animal hosts will be used to inform treatment strategies and antibiotic use policy.

Laura Huber

Distribution of Antimicrobial (ATB) resistance in samples collected from pigs in farms in Khon Kaen - Thailand

This project focuses on determining a dose-response relationship between the use of antimicrobials and resistance in swine production in Thailand. In addition, we aim to determine the geographic distribution of the risk of human infection with resistant organisms originating from pigs. Along with the simulation of future trends under different intervention scenarios, the results of this work will provide valuable information on the impact of reducing antimicrobial use in pig farming.

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