

RESEARCH ARTICLE

# Socioeconomic drivers of the human sewage microbiome in global cities

Minglei Shi<sup>1,2</sup>, Shaojun Dai<sup>3</sup>, and Jun Wang<sup>1\*</sup>

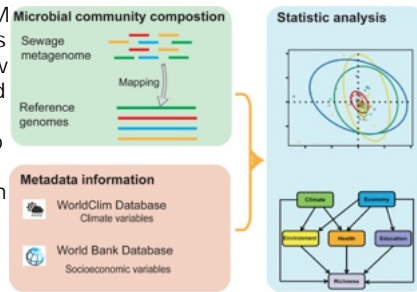
<sup>1</sup>Key Laboratory of Lake and Watershed Science for Water Security, Chinese Academy of Sciences, Nanjing 210008, China

<sup>2</sup>State Key Laboratory of Lake Science and Environment, Nanjing Institute of Environmental Sciences, Chinese Academy of Sciences, Nanjing 210008, China

<sup>3</sup>Nanjing Institute of Environmental Sciences, Ministry of Ecology and Environment, Nanjing 210008, China

## HIGHLIGHTS GRAPHIC ABSTRACT

We built a pipeline framework to profile human microbes from sewages (HSM). There were 195,000 microbial species successfully recaptured from sewage. The HSM composition showed a decay pattern at a global scale. The HSM communities from developed and developing regions were separated from developing regions. Economy was the key socioeconomic driver of the HSM diversity.



## ARTICLE INFO

Article history:  
Received 18 February 2024  
Revised 25 March 2024  
Accepted 26 March 2024  
Available online 1 August 2024

Keywords:  
Human sewage microbiome  
Biogeography  
Socioeconomic factors  
Climate factors

## ABSTRACT

The human microbiome leaves a legacy in sewage microbiomes (HSM), and could cause potential risks to the associated communities remain understudied. microbial diversity, community composition and read mapping framework to estimate HSM abundance across seven continents. Our human microbiome identified from global sewage, demonstrating that human-associated microbes while bypassing the line. Significant biogeographic patterns for the HSM at high latitudes and temperate zones, with Asia and America being separated from Asia and Africa. The HSM communities were mainly clustered by climate and socioeconomic variables, such as country export in goods and services composition and other socioeconomic factors. This study provides the global biogeography of human-associated communities.

©Higher Education Press

## 1 Introduction

Corresponding author  
E-mail: wang@niglas.ac.cn

# These authors contributed equally to this work. <sup>†</sup>Special-Topic Editor: Milos Stoeckl, Institute of Microbiology, Occurrence and Control (Responsible Editor: Yunho Lee)

Anthropogenic activities in the biological world, such as the release of toxic substances into the environment, have led to the emergence of sewage ecosystems (Shen et al., 2010).



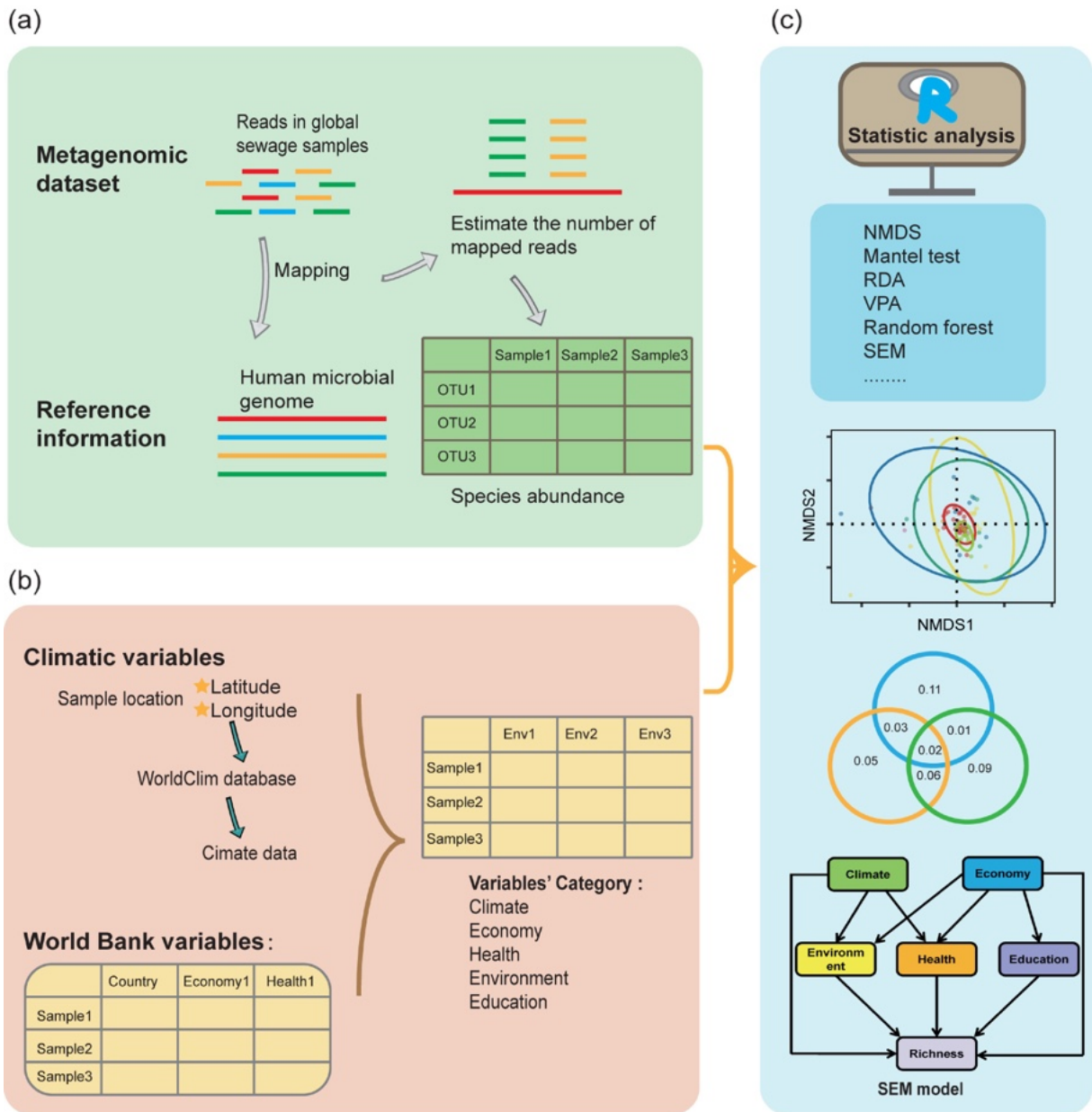


Fig. The overview of the framework for exploring HSM. The framework consists of three main steps: (a) Taxonomic identification of the human microbiome (HSM), (b) Integration of environmental and socio-economic data from the curated databases, (c) Statistical analyses.

genomes spanned six different body sites, including the nose, mouth, stool, oral cavity, skin, and vagina. The diversity of the human microbiome is highly variable and is influenced by a variety of factors, including geography, diet, and lifestyle. Therefore, these genomes represent a valuable resource for understanding the diversity of the human microbiome and for identifying potential pathogens. Second, we estimated the abundance of each OTU in the human reference genomes and compared it to the abundance of each OTU in the recruitment approach. Three potential factors were checked using the Mantel test, indicating no significant correlation between sequencing reads and environmental variables. The results showed that the average Phred quality of the sequencing reads was 25, which is consistent with the

be used to target the sequences of the microbial community. The abundance of the microbial community was determined by the total number of reads of the sequence. Finally, the abundance of each reference genome in the sample was determined by the relative abundance of the sequence. The abundance of each reference genome in the sample was determined by the relative abundance of the sequence. The abundance of each reference genome in the sample was determined by the relative abundance of the sequence.

2. Screening socioeconomic factors

We collected two types of socioeconomic and climate data to investigate the influence on the diversity of the microbial community. The data were collected from the World Bank database and published in the literature. The data were collected from the World Bank database and published in the literature. The data were collected from the World Bank database and published in the literature. The data were collected from the World Bank database and published in the literature.

2. Statistical analyses

The taxonomic alpha diversity indices, including richness, Shannon index, and Simpson index, were calculated using the function from the R package. Nonmetric multidimensional scaling (NMDS) was performed to evaluate the relationship between the microbial community and socioeconomic factors. The distance matrix was calculated using the

variables were used to account for the effect of the five categories of factors. We first considered a reasonable path, then a regression equation, and paths until the final model (P < 0.05). The final optimal Akaike information criterion was selected after comparing the AIC values. The HSM analysis was conducted using the R package v0.6.16. The analyses described above

### 3 Results and discussion

#### 3.1 Global patterns of the HSM

The map-based framework was applied to the 468 human-associated species in sewage, accounting for 95% of the species richness (Fig. 1). The results showed that the framework to recapture associated species from sewage (HSM) was significantly different from the microbiome species % derived from stool (Fig. 1). The HSM dominated by human stool-based results are consistent with the human gut microbiome. The influent sewage bacteria throughput (16S rRNA) are dominated by Proteobacteria (50%), Bacteroidetes (30%), and Firmicutes (15%). As expected, the dominant phyla are among the most abundant taxa in human gut, highlighting the close relationship between human gut microbes and wastewater. The results are explained by the fact that nearly half of the bacterial biomass is released to the environment, untreated (Fig. 2). A large volume of sewage effluent assemblages from multiple sources, from human domestic waste such as feces, urine, washing bath water, etc. The HSM cases from global sewage was not surprising, highlighting its ubiquity and the fact that it is a common feature of the ecosystem. Recent studies have shown that the metagenomics sequencing data is a good indicator of the SARs during the period (n = 5). Climate variables, in

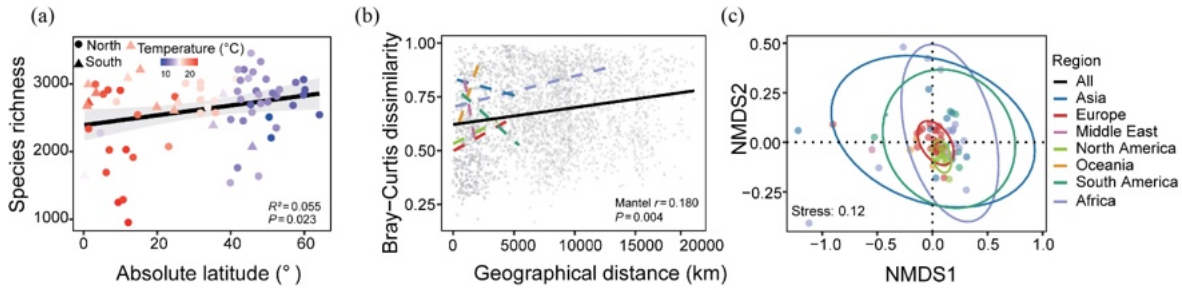
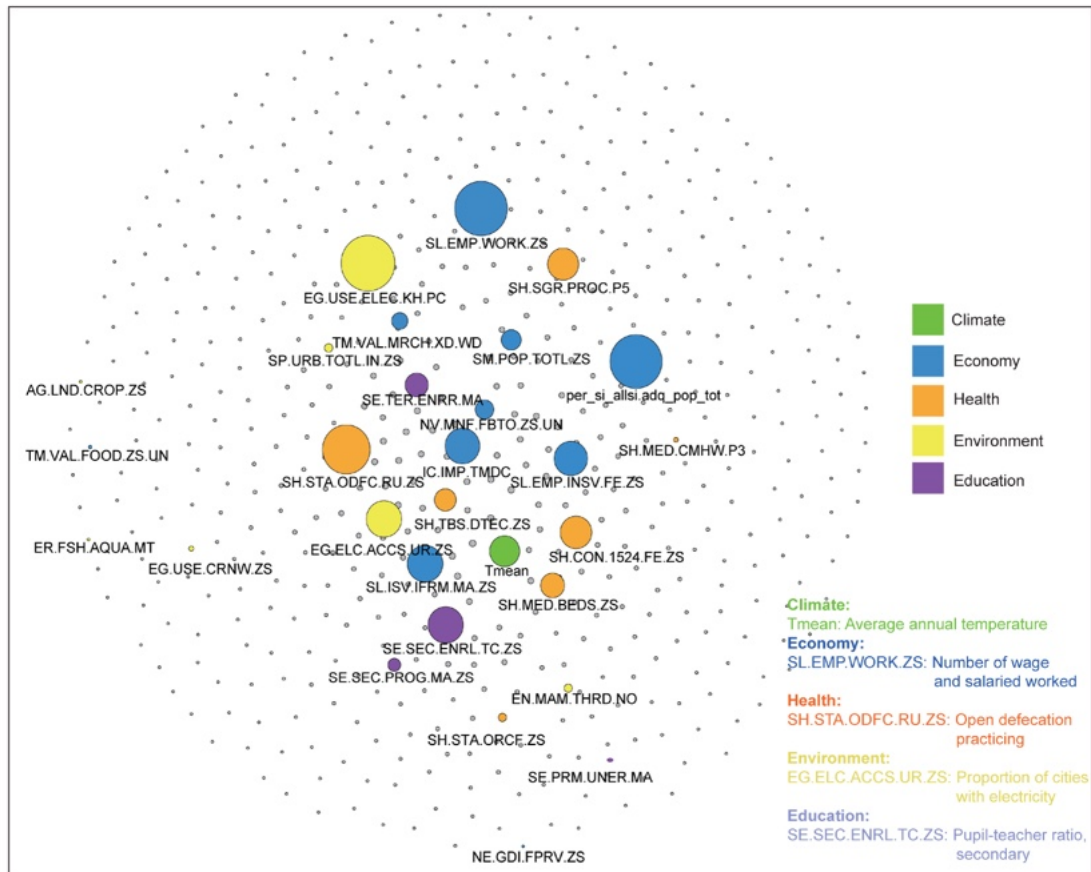


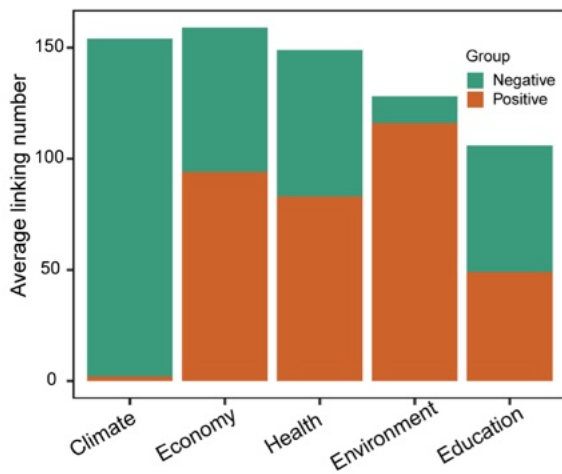
Fig. 1 Global distribution and diversity of the HMS. (a) Latitude of HMS species richness vs. (b) Distance between sites in the HMS, showing the distribution patterns of HMS communities across glo

temperature and precipitation from the WorldClim database based on each site (Fig. 1). The relationships between two types of variables network analysis represent the relative abundance of HMS species for socioeconomic variables. (Fig. 1). The network shows that the adequacy of (economy), the number of (economy), electric power category (environment), (health) were significant HSM species with the greatest health showed distinct links to the HSM richness of the HSM was with most of these variables regression analysis, including temperature, import and export sanitation, siting, and Moreoever, the healthy therapy coverage for transmission (PMTCT), and the tuberculosis case correlated with HSM (Fig. S4). In selected by the community 28% of the total variance RDA2, respectively. variables such as the significant effect of HSM finding is consistent with antiretroviral combination

(a)



(b)



(c)

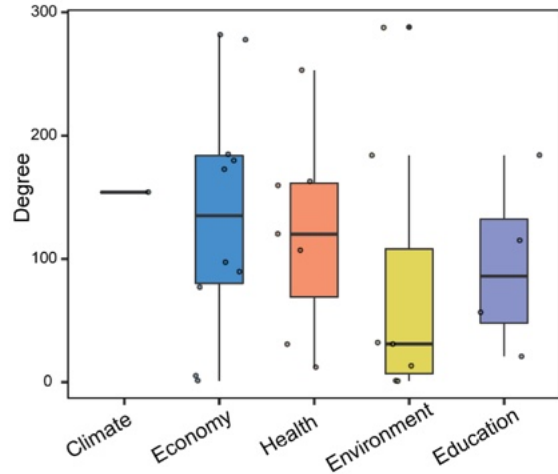


Fig. The correlation network of the HMS and variables. The network shows both two types of variables (a). The distributions of average linking number are shown in panels (b, c).

2019 For example, there are positive correlations between the human gut microbial diversity and socioeconomic parameters in the UK (Mackay et al., 2015). The human demographic characteristics are also related to the human gut microbial diversity (Mackay et al., 2015).

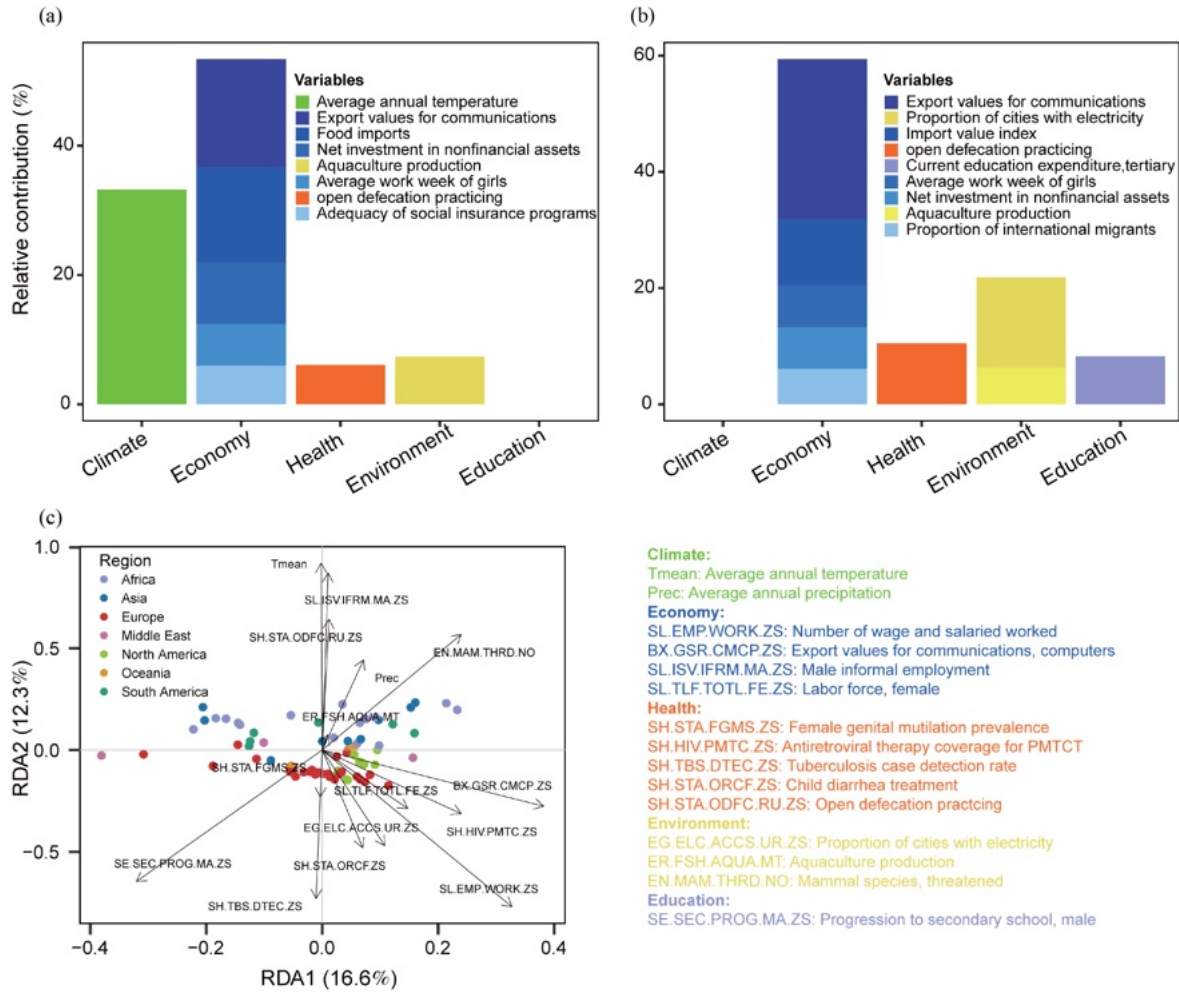


Fig. 4 The relative importance of the variables to HMS diversity, richness and community composition based on the random forest model. The variables and their relative importance to HMS were shown based on redundancy analysis (c).

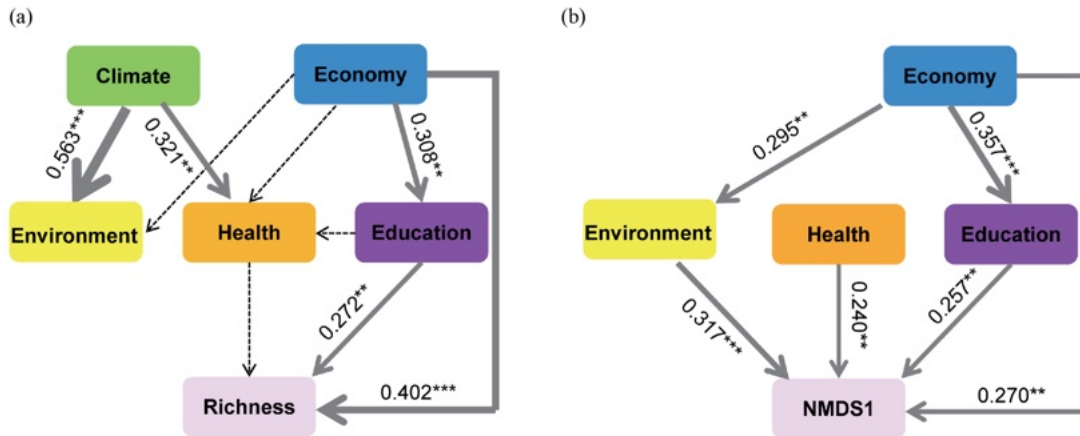


Fig. 5 The drivers of the HMS diversity revealed through SEMs. The standardized path coefficients from the independent variables to the dependent variables (a, b). The width of the arrows denotes the strength of the relationship. The numbers denote the standardized path coefficients.

higher rates of biodiversity loss, environmental factors and land use changes (Ahrnabi et al., 2021). Together, these characteristics of the human environment are likely to drive the



Hendriksen R S, Munk P, Njage M, Svogni M, Shwabe B, McNeil S, et al. (2015) Microbiome diversity in a rural community in Kenya. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Lukjancenko O, Röder T, Nieuwenhuis M, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Kjeldgaard M, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Avershina E, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Hijmans, R J, Cameron S E (2006) *terra*: R software for environmental science. *PLoS One* 1(1):e16. doi: 10.1371/journal.pone.00016

Very high resolution interpolation techniques for irregularly spaced data. *Int. J. Geographical Information Science* 20(8):930-949. doi: 10.1080/10899990600571709

Hu, A, Wang J, Sun H, Niu B, Si F, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Zhou J, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

functions: interplay between genes and environment. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

ment. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Ji M, Liu Z, Sun (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

pollution control: a case study in China. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

mental. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Jones E R, van Vliet M T (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Countdown to 2015: progress and challenges. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

collection, and analysis. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

LaMartina E L, Mohaima (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

wastewater bacterial community structure. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

stability. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Langmead B, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Bowt. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Li B, Ju F, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

pathogens in sewage treatment plants. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

metagenomic. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, et al. (2009) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Abecasis (2009) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

and SAMtools. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Li M, Song G, Li (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

control of pathogenic microorganisms in municipal sewage treatment. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Frontiers in Environmental Science. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Martínez I, Stegeman J, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Greenhill (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

New Guineans: composition, diversity, and function. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

proc. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Mat-Sagasta-Salazar, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

and sludge production, treatment, and reuse. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Wichelns D, eds. *Wastewater: Design, Construction, and Operation*. CRC Press, 2015. doi: 10.1080/10899990600571709

Matus M, Duvallet C, Soule M K, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Brito I, Ratti C, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

omics analysis of residential human microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

informs public health. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Miller G E, Engen P A, Gillevet P M, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

C B, Mutlu E, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

socioeconomic status associated with the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

colonic microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Nadimpalli M L, Marks S J, Monte (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

J, Saito M, Tsukayama P, Njeng (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

(2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

resistance and the need for a global action plan. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Microb. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819

Newton R J, McLellan S, Dilla D, et al. (2015) The impact of antibiotic resistance on the human gut microbiome. *PLoS One* 10:e0141819. doi: 10.1371/journal.pone.0141819