The present and future cost of antimicrobial resistance (AMR) is enormous and it is projected that by 2050 almost half of deaths may be due to complications from infection with resistant bacteria. Fighting harmful bacteria has long been difficult because the techniques used in traditional microbiology have required cultivating the bacteria in a laboratory. Bacteria live in large communities where they have both friends and enemies, and their composition depends on environmental conditions. Only a small fraction of the members of these communities will grow when transferred to laboratories and placed on "growth media", which gives at most a rough picture of the dynamics studied. Thanks to next-generation sequencing, it is possible to obtain much more accurate data. Here, DNA is taken from all organisms present in the sample and their sequences are read. This makes it possible to obtain very rich information on all organisms present in the sample. This technology enables completely new types of research that will expand our knowledge towards understanding how microbes develop resistance to antimicrobial drugs. In our research, we want to apply this new technology and study the microbial communities present in the hospital environment, on surfaces and in the air, as well as isolated from infections in patients. We plan to collect samples four times of the year, in wards of different type located in hospitals of various referential level and location (big city and provincial ones) for a one year to understand how potentially harmful antibiotic-resistant bacteria move through the hospital environment, and how the bacterial profile changes from season to season. The study will also allow us to build a map of harmful bacteria and predict their future changes. In addition, we intend to compare the results on the spread of resistance genes in the environment with both local and regional antibiotic consumption data to identify the dominant source and cause of drug resistance. By comparing the hospital environment in Poland and China, we will gain additional knowledge about the impact of the conditions in a given country / city on the distribution of antibiotic resistance. We must remember that bacteria are all around us, on us and within us. Only a small part is 'bad', but many of them have a big influence on how we feel. Understanding the surrounding metagenomic world - the human exposome is therefore an important challenge on the way to improving human health by learning about the sources and mechanisms of drug resistance in bacteria that cause infections in patients.