

Plain English Summary

Project: Models for transmission of antimicrobial resistance genes in the gut microbiome

Author: Derryk Schieck, 2nd year PhD student

Background:

You can not see them, but they are everywhere. Tiny little living things called bacteria. The gut stores both 'good' and 'bad' bacteria. Good bacteria in the body are known to have a positive impact on health. Bad bacteria can exist in our body at low levels without causing much harm. However, some of these bad bacteria can make you very sick if there are too many inside you.

When you get sick it is possible for a doctor to give you a medicine called an "antibiotic". These are designed to kill the bacteria that are making you sick. There are however two problems.

The first problem:

Some of the bad bacteria have developed a 'shield' against these medicines so that the antibiotics don't work any more. This is a big problem, because the medicine will not make you better. We call this 'shield' AMR, or antimicrobial resistance and it happens when the bacteria change over a period of time.

The second problem:

On top of this first problem there is a second problem. Inside all bacteria there is something called "DNA". This is like a book of instructions that tells the bacteria what it should look like, what it should do and much more. Inside this big book of instructions, there is a lot of information. A very important piece of information tells the bad bacteria how to create the shield against the medicines to stop them working. This is a really big problem, because some bacteria can share a little bit of the DNA with other bacteria that are around it. This means that bacteria can 'teach' each other how to beat the medicine when they share some of their DNA information.

What can we do to find a Solution?:

It is very important to understand exactly how this 'shield' develops and works. In this project we write out mathematical formulas where each term tells us how the shield switches on and off and where the 'shield' is located. We use computer simulations that 'imitate' the exact workings of what is going on between bacteria using the formulas. These formulas are called a model for the real underlying biological system. Doing this helps us understand what is happening in the real world. To make our model perfect we combine the formulas with real data collected from experiments so that we can make the best possible future decisions and predictions.