**Understanding the role of global food trade on the transmission dynamics of antibiotic-resistant foodborne bacteria**

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**ABSTRACT**

**INTRODUCTION**

1. Resistance is a big issue – specifically the resistance that might occur from livestock.
2. This is part of this one health issue – with studies often exploring the impact of transmission from livestock
3. However transmission from livestock is a multifaceted issue – transmission can come in the form of direct contact with domestic livestock, food products from domestic sources, but also from imported sources
4. Note some studies which have done this – the Ludden et al study as an example – which sampled food products from local supermarkets which obviously have food products from imported sources
5. But also mentioned that this often is not done – there needs to be more of an emphasis to explore the heterogeneity in terms of AMR transmission from livestock populations – to stratify the livestock population into both imported and domestic
6. This is important considering the implications of having heterogeneity in terms of transmission pressure – for example – give examples of other mathematical models showing that heterogeneity in terms of transmission pressure
7. This is therefore also the case in terms of AMR in a one health context – many reviews have stated that to understand AMR mechanistically from a modelling POV – we need to understand how the different sources of AMR might also contribute to AMR transmission
8. One such example is understanding how import of AMR on food products from different sources may also impact AMR transmission to humans – especially from livestock
9. This is an important aspect to consider considering a slow increase in food products over the next few years – the increase in the population requiring food to be imported
10. A likely reliance on imported food – and Brexit signing deals with countries with less than stellar food safety records
11. Means it makes sense to explore the impact of imported food products on the overall dynamics
12. We seek to explore the effect of heterogeneity in transmission pressure from livestock populations through the use of a compartmental metapopulation type model where we try to understand the impact of stratifying livestock antibiotic usage
13. We try to understand the impact on the impact of interventions such as the effect of curtailing livestock antibiotic usage when there is an import fraction.

**METHODS**

1. Model Structures (two plots one for simple and one for the complex model)
   1. Model description (parameters)
2. Model outcome measures - (we have 3) – but with a focus on the efficacy of curtailment on resistance
3. Data
   1. Separate the data into three chunks
      1. General fitting dataset – to fit the relationship between usage and resistance
         1. What data we used from the ECDC to fit the model – specifically talk about how we tweaked the antibiotic usage data and how we only chose countries with >10 data points and how we used the data (multiple years) the way we did
      2. Import Dataset – used to specifically parameterise the import fraction
         1. We use this data to determine the share of the UKs food from UK and imported food supplies and to parameterise resistance and contamination from each of these countries
            1. (if we actually end up using the three case studies – this point we can use a table to show the import fractions).
         2. Need to explain how the import fractions were tweaked from the original one on the government website using other data (and also why we only took import data for 2018 – because historical data from previous years are not available).
         3. Need to explain what data we used to parameterise the importing countries – specifically the type of contamination data (carcasses) and the type of resistance data – specifically chosen to match each other
            1. With the contamination data there is a lot of nuance – converting from FBOp to competent authorities – using scaling calculations etc.
            2. How we only chose countries with 400cm^2 swabs – to keep it fairly uniform.
      3. UK dataset
         1. Need to describe that we need to parameterise quite a bit of UK data, livestock contamination, livestock resistance, human FBD, human resistance – as we are using a UK datasource
         2. Need to describe how we selected the data we did for the UK dataset
         3. Specifically the removal of certain datapoints because they were unrealistic (where it was just 45/45 resistant), the fact that we used 3 years worth of data (2015, 2016, 2017, 2018) – although one of these intermediate years aren’t available
         4. The eta parameter and how we use that one study ([Abattoir-based study of Salmonella prevalence in pigs at slaughter in Great Britain | Epidemiology & Infection | Cambridge Core](https://www.cambridge.org/core/journals/epidemiology-and-infection/article/abattoirbased-study-of-salmonella-prevalence-in-pigs-at-slaughter-in-great-britain/3FDEA88F8CF084908FC34C7A6A57052E)) – to model a static reduction from prevalence in the caecum of pigs to level of contamination found on swabs
4. Bayesian model fitting – how all this ties into the data
   1. What parameters we are fitting
   2. What distance measures are we hoping to use
   3. Choice of priors
   4. Specific details of ABC-SMC you can probably just leave to the referencing the Toni et al, paper
   5. How many generations we are running for, threshold values and distance measures etc
5. How and what senstivity analyses did we conduct
   1. Essentially mentioned the details of the LHS-PRCC and the need for monotonicity plots
   2. Mention that we conducted an eFAST analysis etc.

**RESULTS**

**Section 1**

**Result 1 - Basic Model Output of the effect of withdrawing antibiotic usage on levels of attributable resistance and the model fit**

* Have two models the pig one and the general one
* But put the pig one in the supplementary material

Chart, bar chart

Description automatically generated

* MENTION - General sensitivity analysis plots – mention here – also mention that we do monotonicity plots – mention that we do an LHS PRCC and a eFAST analysis with the general model fit.

**Result 3 – effect of altering the ratio of FBD and resistance on the results**

* We have two heatmaps the change in the main outcome measure – but also the change in the other outcome measure – the change in the amount of foodborne disease
* We then have some supplementary material showing the fbd and resistance for the pig case study/

Chart, radar chart

Description automatically generated

Result 4 – sensitivity analyses LHS-PRCC and eFAST – general case study only

* Supplementary material monotonicity plots

Chart

Description automatically generated

**Section 2**

Result 5 - Show model fit

Result 6 - Basic Model Output of the effect of withdrawing antibiotic usage on levels of attributable resistance

* Pick a single model to work with – chose baseline since it’s more rounded parameter set
* Supplementary analysis – the effect

Result X – Uncertainty analysis with this plot

* Pick a single model to work with – chose baseline since it’s more rounded parameter set

Result 7 – The complex changing of usage plot

* Pick a single model to work with – chose baseline since it’s more rounded parameter set

Result 8

* What happens if key parameters change
* We can do a domestic change – keep the fitted parameters – but just alter certain parameters (such as the reduction in contamination)
* Also a side analysis with the import parameters – draw from distribution etc
* What parameters drive this relationship into the red zone
* Could integrate this into the final figure

**DISCUSSION**