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Steaking out Patterns;

A Longitindal Metagenomic Study of Antibiotic Resistance in Argentine Beef Feedlots.

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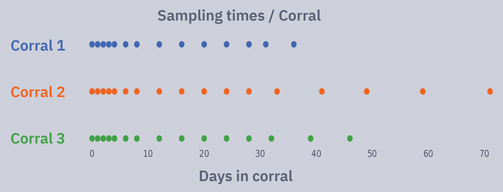
Beef feed-lots, AKA Corrals (Like the one pictured above), are pens that cattle are kept in during beef production. Throughout at different stages in their life cattle are split up and mixed into different corrals, mixing and establishing new microbiome populations as they do so.

There is a well studied connection between AMR(AntiMicrobial Resistance) in agriculture and AMR in human pathogens[1]. It has also been shown AMR and livestock infection have major economic burdens on farmers[2]

As part of larger study investigating AMR in Argentine beef farms, the pipeline explored here is investigating the role different taxonomies may play in establishing the microbiome.

1. The Dataset



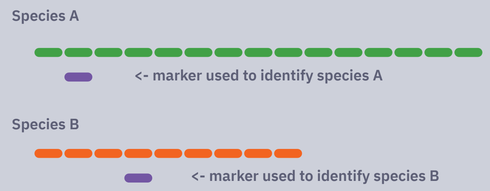
52 datapoints, across 3 corrals taken up to 72 days from arrival in a corral. For each datapoint 1 soil sample was taken from within the corral. The chart above shows which days each corral was sampled.

2. Illumina sequencing

Short read Metagenomic

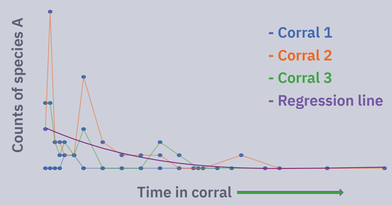
3M-5M reads per sample

3. Profiling using mOTU



mOTU uses small markers to identify a species rather than trying to identify[3].

4. Feature optimisation



Polynomial regression was used to model the data for each species. Corralation analysis is also used to remove species with a duplicate pattern to other

5. Ordering the Species groups

The Sequencer [4], an unsupervised machine learning algorithm is used to reorder the species groups based on their count pattern over time. The heatmap below is the output of normalised species count data fed through The Sequencer. Each row represents a corrolated group of species.

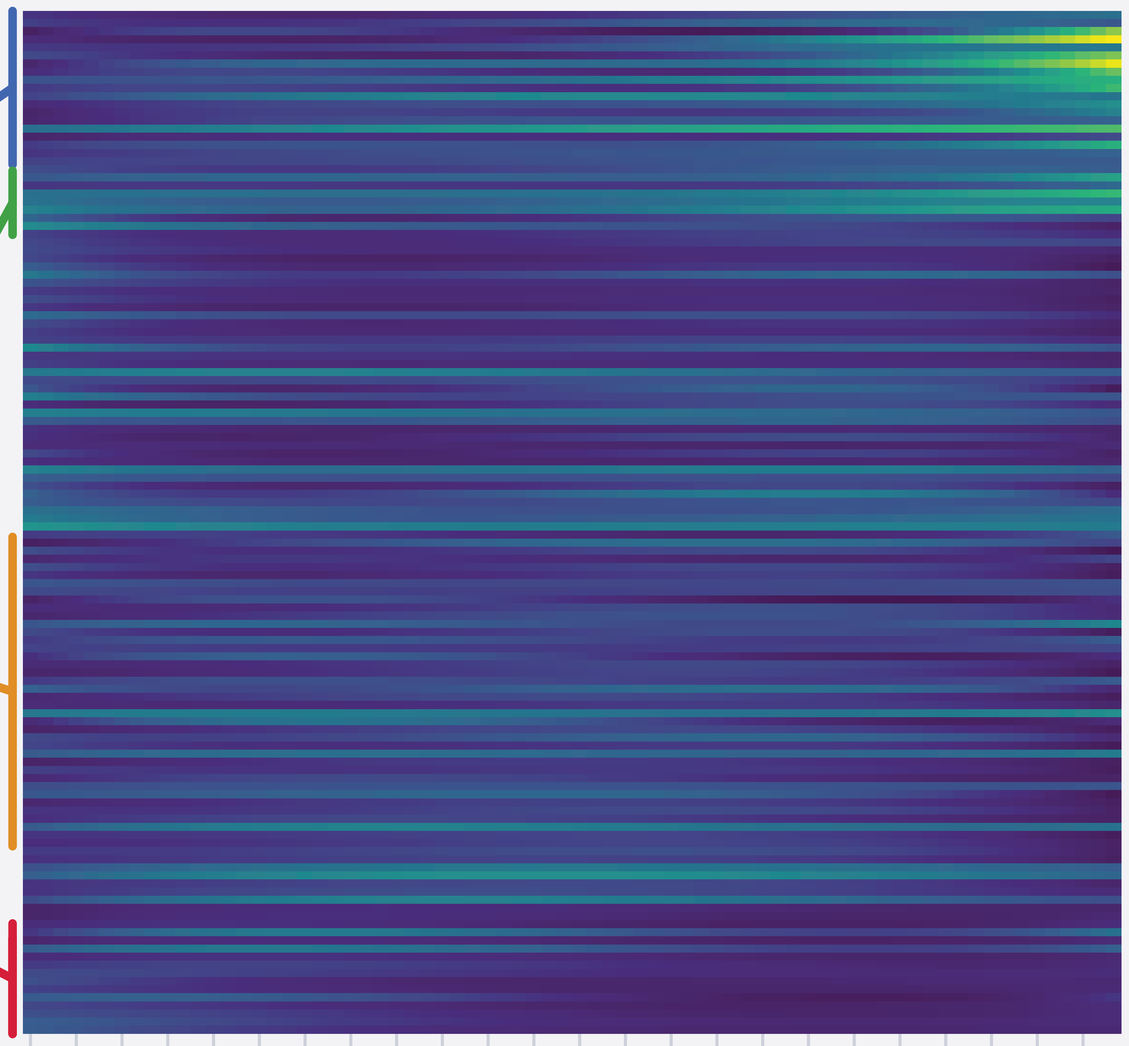
Observable patterns:

Species that start low counts, end on high counts.

Species that start with medium counts, end high.

Species that have peaks in the middle

Species that start with high counts, end with low counts.



What next?

Identify key bacteria for significant infections in cattle. Such as *Fusobacterium necrophorum,* a significant player in liver absesses.

The establishment of these bacteria in the microbiome can be identified with this method. Futher study can identify if there are any changes in the environment.

This can be used to inform lievestock management plans, such as the best time to administer antibiotics.

This analysis can be repeated with different taxonimic profilers, or with different types of features such as AMR or virulence genes. ALl from the same dataset.

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