SAFE
Case Study

Creme Global

About the Project

The Sequencing Alliance for Food Environments (SAFE) Innovation Partnership Programme was a three-year project partnership between UCD Centre for Food Safety, Creme Global and six leading food and nutrition companies.

Aim of SAFE was to enhance food quality and safety approaches using environmental intelligence data. Current methods used to control bacteria in food manufaturing and processing facilities are not sufficiently quick or specific. The SAFE programme aimed at mitigating against the risk of bacterial contamination in the food supply chain in a smarter, faster and more specific way while also improving sustainability.

By tracking the environments in a number of food manufacturing plants in Ireland during a two-year period and mapping the microbiomes across the seasons the consortium has developed databases which leverage gene sequencing technology and statistical analysis to define bacterial characteristics at the DNA level. These databases are then used to develop a predictive software tool to enable quicker and more accurate quality control analysis of the bacteria present in food facilities.

Data and Sample Analysis

Over the duration of SAFE project the following amount of data has been collected and analyzed:

6 Sampling Rounds
98 Sampling Points

515 Samples Analyzed
2085 Distinct genera detected

16s Sequencing Output

With a huge amount of data available from just a single sample, the approach was typically to look just at several bacteria of interest.

The output from the sequencing is a count on the number of reads per bacteria (OTUs). The counts will vary based on sample quality so we focus on relative abundance rather than absolute counts. Sample can be viewed at multiple levels of the taxonomic hierarchy, from phylum down to genus.

Comparing Samples

When comparing the microbiome between a pair of samples we looked at abundances for all bacteria. Some samples could be very similar in terms of their microbiome composition and while they could be grouped by hand if the volume of samples was low - with over 500 samples this becomes impossible. This is where clustering techniques are applied to gather similar samples together automatically.

These clusters indicate a 'fingerprint' for each company - on average their microbiomes will be unique, as such microbiome based analysis opens up an avenue for bespoke insights and recommendations. On a company by company basis this kind of clustering also allows for a different kind of monitoring - by looking at outliers we can identify shifts in the microbiome which could be indicative of an issue or a change in the environment - even if there are no spoilers/pathogens present.

We can also compare product samples with environmental samples to identify where controls in place could be insufficient, leading to the environment impacting the product. This allows for action to be taken upfront and facilitate a move away from reactive control. Regardless of which bacteria appears in a sample, the diversity of the microbiome can give us a clear indication of quality controls within the environment.

Project Insights and Next steps

Abundance and Seasonality Effects

Looking at all samples combined, the most abundant bacteria can be determined. We can also track seasonality effects in the bacteria abundances - for example we identified certain bacteria that peak in spring, persist through the summer before dropping off in winter. Other bacteria then increase in abundance during the winter to fill this gap.
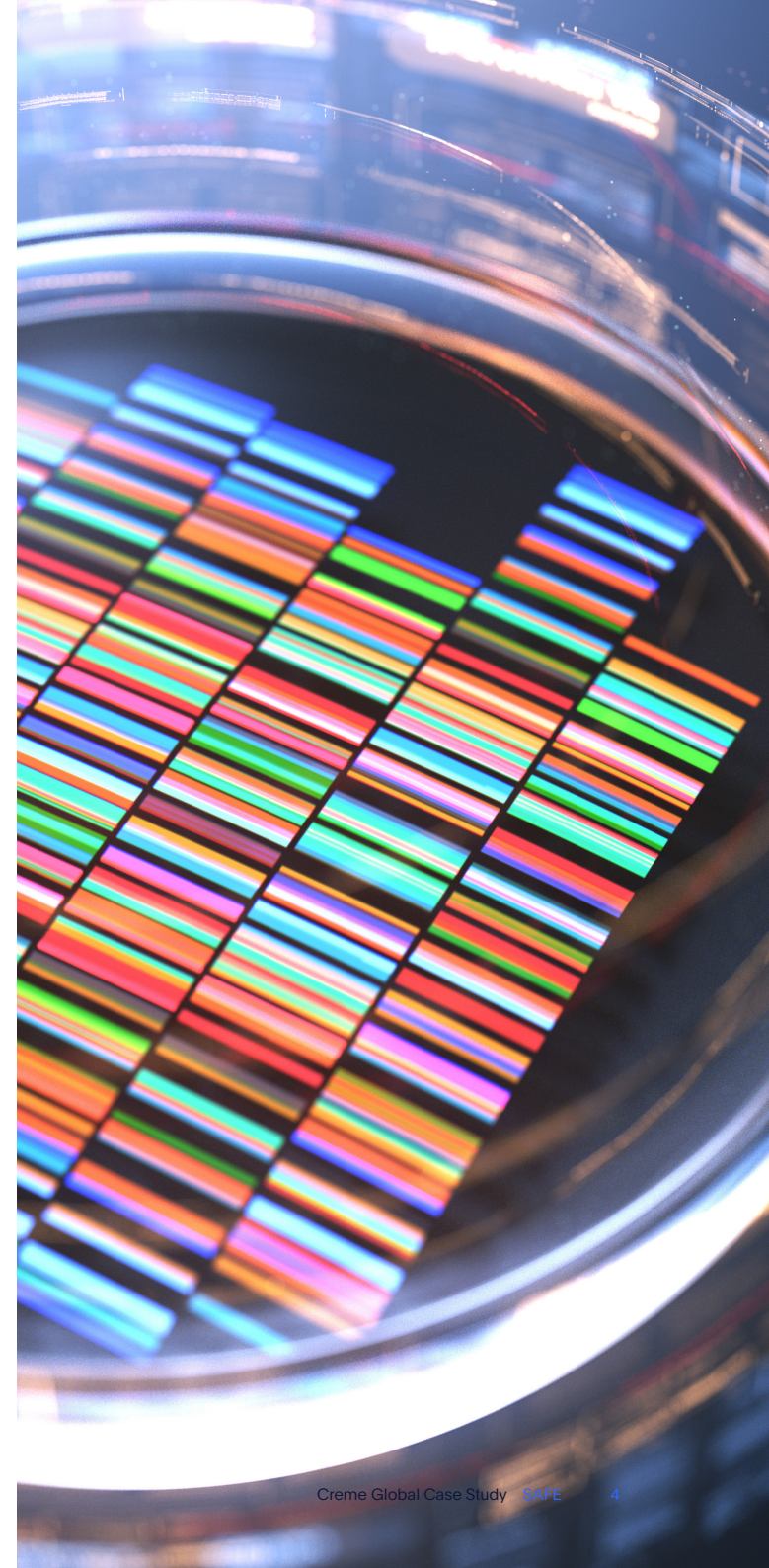
For example we noticed a clear increase on presence of a certain bacteria where over a third of the sampling locations (37/98) had their highest relative abundance in summer 2018. This coincided with higher than average warm summer conditions in Ireland during that time.

Predictive Modelling and Machine Learning

Next Generation Sequencing (NGS) techniques can facilitate the monitoring and detection of both culturable and non-culturable bacteria. This overcomes the challenge of traditional techniques which focus on a single bacteria per test.

NGS generates a rich amount of data which can be leveraged through by using a machine learning pipeline to identify what the key predictors of a particular bacteria are and then train a model to predict the occurence.

The old one-size-fits-all approach to microbial safety is no longer really sufficient and using the power of sequencing, big data and data science, every plant should be able to tailor its approach to address the characteristics unique to it.

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