Accessing insoluble phosphorus: mining the metagenome for novel genes

AGRI-FOOD & BIOSCIENCES INSTITUTE

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Background

Phosphorus is essential for all organisms and is the limiting factor of primary terrestrial production. Soluble phosphorus usage exceeds reserves in many countries, resulting in a global shortage affecting global food distribution. Over 30% of soluble phosphorus is used as fertiliser on agricultural lands. Current fertilisers result in nutrient run-off to surface water, accelerating eutrophication, soil compaction, and reducing crop yield[2]. Therefore, alternatives to current phosphorus fertilisation practices need to be examined.
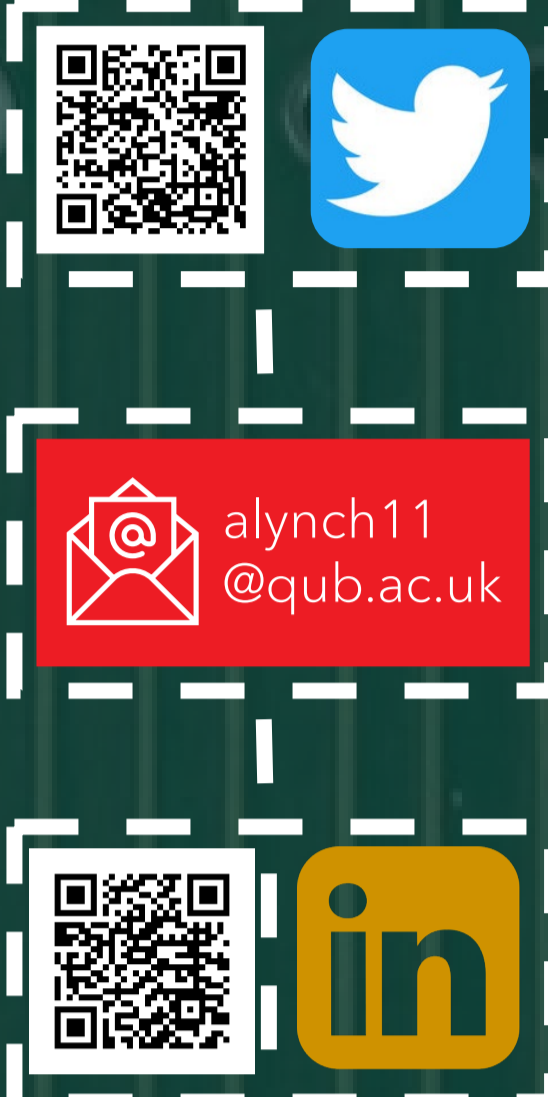
Northern Ireland's agricultural land

Objective: Determine the population and abundance of the microbial communities within Northern Ireland agricultural lands using metagenomic analysis. Compared to physiochemical data of the macronutrients and micronutrients within the soil and the metadata supplied by farmers regarding land usage.

Aim: To determine a correlative relationship between agricultural practices and fertiliser regimes with novel genes and methanotrophic microorganisms which solubilise insoluble phosphate and store carbon.
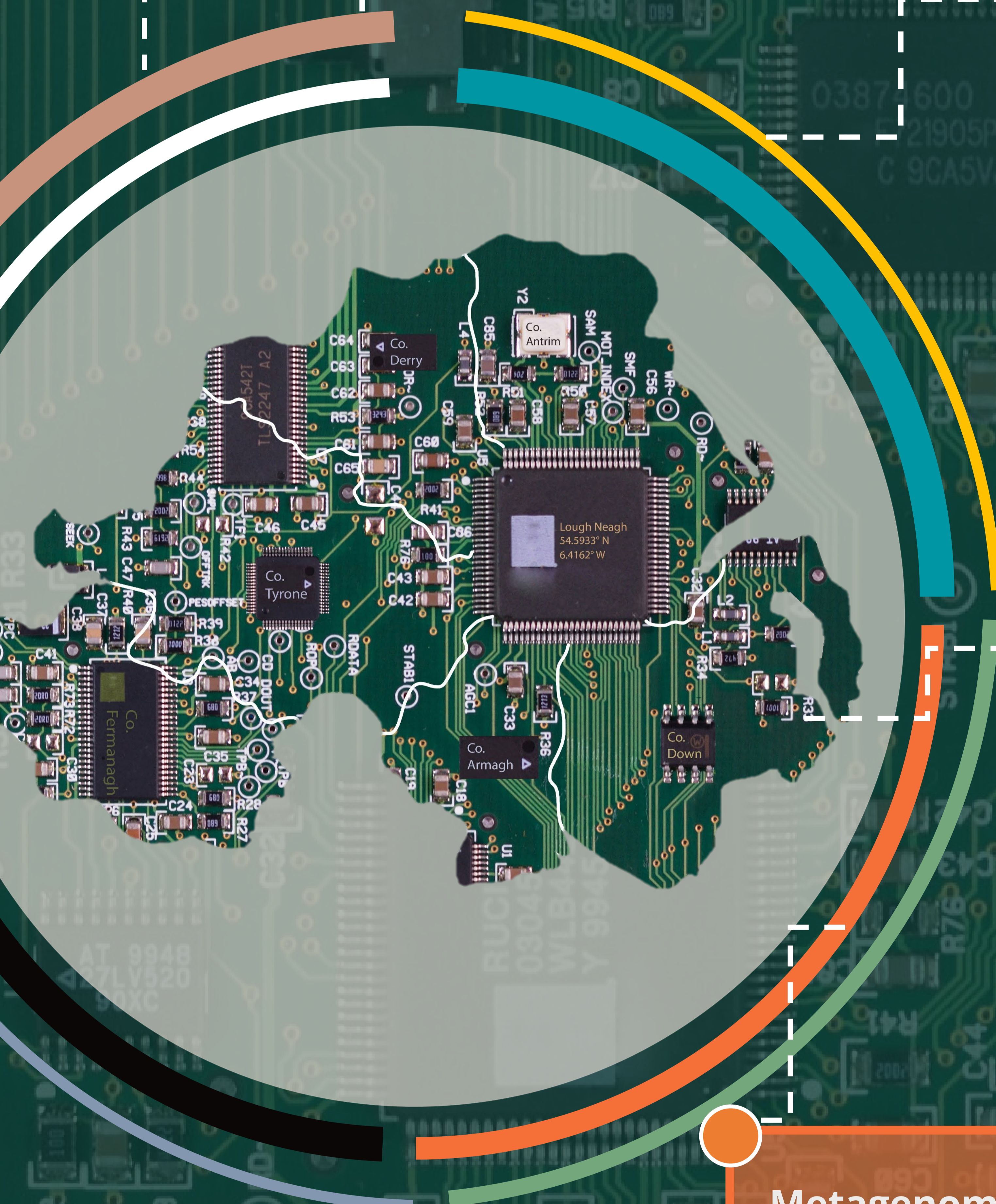
SOIL NUTRIENT HEALTH SCHEME

Experimental agricultural plots

Objective: Determine the population and abundance of the microbial communities of soil sampled from farm plots of known phosphate and nitrogen treatments.

Aim: To determine a correlative relationship between phosphate and nitrogen fertilisation practices and novel genes which aid in carbon storage and reduce solubilised phosphate run off.

SOIL NUTRIENT HEALTH SCHEME

Associated Works:

- Laboratory experiments with phosphate-solubilising microorganisms
- Growth experiments to analyse crop yield with insoluble phosphorous. Determination of carbon storage and nitrogen cycling.
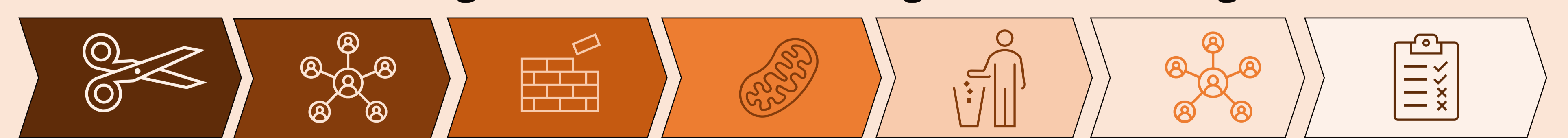- Molecular simulations to predict chemistry.

Metagenomics & Bioinformatics

Sampling → DNA Extraction → Metagenomic Sequencing → Metadata

Metagenome Processing and Binning

Trimming → Evaluation → Taxonomic Classification → Assembly → Protein Coding and Prediction → Binning → Reporting → Visualization