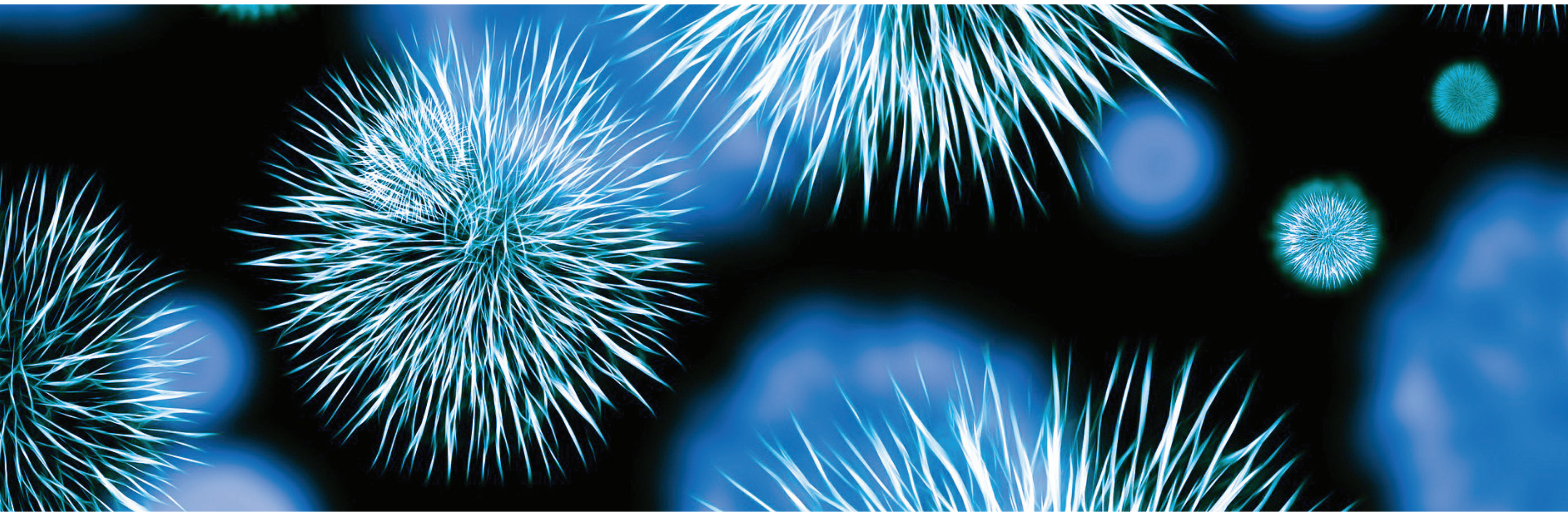
MICROBIOME & METAGENOMICS



Microbiome

AGRF's Diversity Profiling service is a method of identifying the relative proportion of organisms present in a mixed community.

To do this, AGRF will take your sample (either raw sample, or extracted gDNA) and PCR amplify a region of interest from your mixed community.

We will then pool and sequence the bar coded amplicon(s) on the MiSeq platform utilising Illumina®'s Paired End Chemistry.

We use validated fusion primers that can directly amplify many of the popular regions including:

- 16S: 27F-519R
- 16S: 341F - 806R
- ITS1 - ITS2

Once sequencing is complete, you will be provided with your sequences and an overview report. This report includes an Operational Taxonomic Units (OTUs) table for each sample, taxonomy summary files (at different levels from kingdom down to family) and taxonomy summary plots.

Metagenomics

Whole genome shotgun metagenomic approaches can provide robust estimates of microbial community composition and diversity without the biases inherent to the PCR amplification of a single gene.

Metagenomic sequencing captures all of the kingdoms of life, not just bacteria, and facilitates the *de novo* assembly of novel species. Metagenomic data can also be used to determine the gene content of a sample, and possible functional roles based on gene presence.

We can supply a range of library preparation methods and sequencing options to accommodate projects depending on the diversity of the samples being profiled and the depth of sequencing required.

Our highly experienced Bioinformatics team can provide you with a tailored Metagnomics Whole Genome Sequencing Pipeline application to your sample type and application.

Our funding partners

AGRF is a not-for-profit organisation supported by the Commonwealth Government infrastructure schemes administered through Bioplatforms Australia.

These schemes include NCRIS, EIF, Super Science Initiative CRIS and NCRIS 2.

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