

Resolving Technological and Methodological Gaps in Metagenomics

Call status: Closed

Application deadline: 9 January 2014, 4pm

Summary

We wish to encourage the development of metagenomics as a tool that can be applied across the biosciences to support our strategic aims.

Background

BBSRC recently instigated an **Expert Working Group** to consider metagenomics and its applications across our funded science and its relation to our strategic priorities. The group noted the potential benefits to be accrued from deploying metagenomics techniques, but recognised that the UK had not taken fullest advantage of this tool. The group concluded that one of the factors behind this apparent usage gap was the existing technological and methodological gaps that need to be resolved before metagenomics can match all of its potential utility.

Scientific objectives

Particular areas of focus include (but are not limited to):

Tools applied to analysis of metagenomic data

The advance of sequencing has been driven by tools designed for clonal datasets and shorter reads. Metagenomics analysis will require that tools be available for applications, such as discovery of natural products or identifying operons, that necessitate longer, error-free reads. Tools are required for community genetics and viral genomics, while the majority of tools available have been optimised for a bacterial context. Frequently, the sequence tools available, therefore, are not optimised for the tasks required.

This is also true of algorithms. A number of assembly algorithms have been produced in the last few years, but little consensus has emerged around which are the best and most suitable algorithms for different metagenomics applications. For example, some are intended to generate a consensus genome but this will not be useful for studies examining variation. Major computational challenges exist. As tools must cope with larger and more complex datasets, bioinformatics tools are required that are quicker, and are less memory intensive.

We therefore encourage applications intended to provide:

- Optimised assembly algorithms
- Improved tools and programs for gene predictions
- Improved standard protocols for taxonomic classification of metagenome sequences
- Development of metagenome analysis platforms (including metagenome comparison platforms)
- Improved methods and tools for analysis of diverse complex samples (eg those arising from environmental samples)
- Adaptation or development of tools currently designed for use with prokaryotes to viruses or eukaryotes

Tools intended to improve the tool of metagenomics

A metagenomics application allows the identification of organisms that are difficult to culture allowing discovery in diverse (mixed populations) environments. To successfully implement metagenomics, some of the tools used in conjunction with metagenomics analysis require optimisation, for example those tools used to perform characterisation 'downstream' of the sequencing. This includes improved screening techniques, for example in the areas of functional screening, and assays, and improved cloning strategies that will allow the examination of genes that are otherwise difficult to clone and/or express.

We therefore encourage applications intended to provide:

- Tools to improve metagenomic library construction (including development of broader range of host/vector systems)
- Tools to improve screening techniques, including functional or activity-based screening, and development of alternative screening assays

- Improvement of high throughput cloning strategies for recombinant expression

Development of tools intended for sequence-based approaches related to metagenomics (for example, metatranscriptomics) will also be considered.

Review of next generation sequencing

Metagenomic approaches identify genomic signatures from mixed populations of microorganisms, many of which may be unculturable. These signatures can act as markers (e.g. in environmental monitoring) or be analysed for useful leads (e.g. bioprospecting).

Our **2010 Review of Next Generation Sequencing (NGS)** recognised that improvements in NGS-based metagenomic characterisation technologies would enable a broad range of research areas. Back in 2010, metagenomics was being deployed to analysis the microflora of the human (the Human Microbiome project), the rumen and soil ecosystems, and potential future applications in forensic science and analysing food poisoning outbreaks were envisaged. Metagenomics (and metatranscriptomics) was considered to be an area with great potential but requiring bioinformatics developments to effectively manage and interrogate the data. Indeed the review considered sequencing algorithm development to be highly deficient and severely restricting developments.

From the perspective of our Strategic Plan (see related links), metagenomics maps to the Exploiting New Ways of Working enabling theme with clear application potential in our strategic research priorities addressing Industrial Biotechnology and Bioenergy, and Bioscience Underpinning Health, as well as strong relevance to our Innovation and Skills enabling theme.

Eligibility

For eligibility information please refer to our grants guide (see related links).

Applications must be within our remit.

How to apply

Applications are invited to our next responsive mode deadline, **9 January 2014, 4pm.**

Applicants should complete a standard responsive mode application form in Je-S and select **Metagenomics - Tool Development** from the highlight menu.

Assessment criteria and peer review

Funding for this call is not ring-fenced and successful applications will be funded through responsive mode. Applications selecting the metagenomics highlight will be assessed within the office for their fit to the highlight. Those considered to be outside the criteria for the highlight, but still within our remit will remain in responsive mode but will not be judged against the highlight.

Contact

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