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Population Sequencing

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Review

Sequencing machines are currently designed and sold for the purpose of consensus sequencing, namely, to compile redundant reads to arbitrarily assign acceptance criteria to assert calls across short segments of partial genomes. On account of the massive sequence data, the process to discern sequence artifacts, while under a few well documented situations, e.g., long repetitive sequence content blocks, there remains many artifacts that are unidentified. Custom script algorithms bin the various sequence content, but, on account of consensus sequencing, rule in favor of pre-determined criteria for final sequence content reporting. The research investigations is this Issue has been conducted on genetic populations that have only a few base pair single nucleotide various, however, the raw sequencing data produced by sequencing machines, contains a order of magnitude more variations, not only between analyses of different, albeit, identical samples, but even between multiple re-analyses of the same genetic material, repetitively sequenced.

When errors are treated properly [1], sequence can accurately identify genomes in mixtures that represent major and minor population content in samples. Issue 3 briefly describes research investigations on important topic, where sequencing is making significant contributions, for example, the issue of water quality, microbial resistance identification, and in human clinical health.

For the topic of water quality and measurements of contamination in water supply, research has demonstrated a wide range of antibiotic resistance determinants and phylogenetic variation including overlap with human clinical pathogens [2-4]. Analysis of bacterial populations in drinking water has revealed dynamic relationships of community structure [5]. With ever wide-spread use of sequencing methods, is associated partial genome community identification. The mis-identification of sequence information into the analysis of sample content vs. reference genome database as created the need for post genome quality analysis [6].

Similar to the application of population sequencing on water samples, is analysis of human clinical samples [3]. Population sequencing can be used to focus on detection of very rare mutations or "deep" sequencing, to detect variants associated with clinical relevance. The detection of low abundant genomes is difficult against metagenomics samples, especially against a background of a high number of human host genome [4]. Similar to the research investigations of Issue 3, the community is beginning to adopt the use of multiple algorithms and probabilistic approaches taken from different independent analytical techniques to determine genome identification instead of a "one-size-fits-all" approach.

Issue 3 also ties in the important research topic of microbial resistance. Over-the-horizon and emerging pathogen detection represents a serious capability gap for bio surveillance, bio intelligence and bio reconnaissance. Antimicrobial susceptibility testing and the impact of genetic variation's role in modern clinical microbiology represent critical studies needed to be conducted using population sequencing methods to follow on the heels of PCR-based methods used for human and veterinary pathogens [7]. In light of public health emergency, mapping functional diversity of microbial communities requires population sequence and computational methods [8,9].

In short, while the knowledge (and evidence-based) base requires significant expansion, population sequencing is championing the way forward to infer antimicrobial susceptibility and accurate and probabilistic genome identification. The future of population sequencing will likely characterize all microbes in a sample, enabling the use of all of the genome regions, which are under different evolutionary pressure, to improve identification and traceability to source. It is on account of the variation of major and minor content in mixtures that every sample will have a different genetic content (or available pangenome potential), every sample will be distinguishable from the next.

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