

MultiSeq: A novel computational method for multiplexing Next-Generation Sequencing

Description

The recent advances in Next-Generation Sequencing (NGS) of nucleic acids (i.e. DNA or RNA) have transformed biology and medicine. Today, NGS is one of the main pillars of research in various biological disciplines and it has already pervaded numerous fields of applications ranging from the clinics to the biotechnological industry. Given its versatility and high demand, the global market for NGS is rapidly expanding, with the number of sequenced samples doubling every two years.

However, while major advances in NGS were mainly related to a rapid increase in sequencing throughput per machine, the preparation of sequencing libraries - the other integral step of NGS, has largely remained unchanged. Currently, this step is the major financial and operational bottleneck for sequencing projects, limiting the widespread adoption and utility of NGS. Current state-of-the-art solutions for overcoming these problems either require high upfront costs and/or are laborious. Here, we propose a bioinformatics solution to these problems which minimises the cost and time of library preparation.

Our solution, called MultiSeq, allows designing a multiplexing strategy for samples with sufficiently different genetic material and sequencing them as a single library followed by computational demultiplexing. Hence, MultiSeq makes sequencing more affordable, shortens its turn-around time and reduces laboratory waste. We have already implemented the initial software prototype, performed a successful pilot experimental proof of concept, and made initial market analysis for our approach. In this project, we will perform the major steps towards the valorization of our technology, including but not limited to business plan development, IPR protection, a thorough market analysis and initial customer attraction, and ultimately transferring of MultiSeq to a spin-off company.

MultiSeq can be highly efficient, requiring minimal investments and expertise compared to other solutions, which altogether can facilitate its rapid scale-up. Overall, our solution will further democratise the field of NGS making it cheaper, faster and more sustainable, benefiting both society, enterprise and scientific community.

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