



Category: Bioinformatics

An automated sample allocation system for multiplexed Next-Generation Sequencing

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Abstract

The Illumina Next-Generation Sequencing (NGS) technology enables us to sequence several samples together. This is made possible by adding unique barcode to each sample sequenced. The multiplexing of the samples should be done in such a way that there is not barcode clash and samples loaded into the flowcell should provide high sequencing throughput. In addition, when there is a pool of libraries, the samples with higher priority should be given preference for selection. Currently, there is no program available that can prepare an optimal run plan for the Illumina sequencing runs. The sequencing team spends several manual hours to generate a run plan. Some of the complicated run plans can take up to 24 hours to prepare. Despite spending several hours to prepare run plan it can still have errors and be non-optimal. In this study, we present an automated system to generate run plan for a given sequencing run. Our system utilizes constraint optimization framework to make optimal run plan. We use MiniZinc software to develop the constraint optimization framework. Our method takes input library barcode sequence, data amount needed, priority and sample identifier to generate the optimal run plan. The method is programmed to maximize the inclusion of samples per lane and give priority to sample with high priority. The model provides with an optimal plan for 80 libraries within 18 seconds. In addition to several advantages we observed that this method provides better utilization of flow-cell to provide maximum throughput. This system was widely validated on previous runs. The system is available as web-based tool and we are in process to integrate it with our Laboratory Information Management System (LIMS).

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