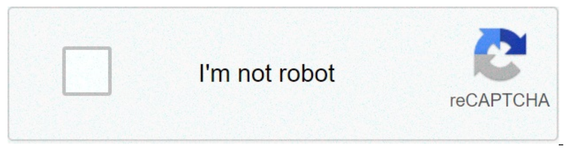

Continue

Sop for stool analysis pdf

Sop for stool analysis pdf.

PDF Split View Article Summary Figures and Tables Video Additional Data Audio Video Sequencing of the next generation (NGS) Combined with bioinformatics has been successfully used in a wide range of analysis for the search for infectious diseases for the relevance of public health. For example, NGS and Bioinformatics approaches have been used to identify epidemic origins, transmissions trace, investigate epidemic dynamics, determine the etiological agents of a disease and discover new human pathogenic agents. However, the implementation of NGS and bioinformatics of high quality research and public health laboratories can be challenging. These challenges mainly include the choice of the sequencing platform and the sequencing approach, the choice of bioinformatics methodologies, access to the adequate of the calculation and information infrastructure and the recruitment and the personnel of consideration with the competences and specialized experiences in this field. In this review, we summarize the most common NGS and bioinformatics workflows in the context of the infectious disease of genomic surveillance and the discovery of pathogens, and highlights the main challenges and considerations for the creation of a public health laboratory of the infectious disease of the NGS and of bioinformatics. We describe the most commonly used sequencing platforms and review their strengths and weaknesses. We examine sequencing approaches that have been used for various pathogens and study questions, as well as the most common difficulties associated with these approaches that should be considered when they implement in public health or research. Furthermore, we provide a review of some common bioinformatic tools and procedures used for the discovery of pathogens and the assembly of the genome, together with the most common challenges and solutions. Finally, we summarize the bioinformatics of the characterization of viral pathogens, bacterial and advanced parasite, including the types of study questions that can be answered while using NGS and BioInformatics. The next-generation sequencing technology (NGS), or high throughput sequencing, combined with bioinformatics has become a powerful tool for detecting, identifying and analyzing human pathogens. Its advantages compared to conventional methods are many, since the sequences produced can be used for more accurate detection and characterization of pathogens, screening for the presence of mutations / resistance genes, vaccine escape variants, recombination or reabsortment and Virulence and Pathogenity factors [1 - 10]. The Assembly and Analysis of Pathogenic Genomes can shed light on the spread of pathogens, contact the track, the dynamics of epidemics and even possible sources, times and geographical pathogenous geographical origins [11 "17]. This, coupled with rates improvements of sequencing error and simpler laboratory approaches and the decreasing costs of NGS and computational requirements, have carried out NGS and BioInformatics a more achievable and increasingly desirable feature of research laboratories and public health worldwide. However, NGS is It is powerful but complex and fume, which requires significant experience and skills for the production of accurate and informational results. Furthermore, the implementation of NGS and BioInformatics methods as routine surveillance and detection tools require specialized IT technologies (IT) and Quality management systems that can satisfy the goals of health laboratories P Ubbi. There are permanent challenges in creating a NGS laboratory and high quality bioinformatics capacity, such as choosing the correct sequencing platform, the method of The wet laboratory, bioinformatics analyzes tools, personnel with the right kind of skills and experience and computational and computer infrastructure to support the analysis of large amounts of data produced by NGS and BioInformatics. While some standards and guidelines have been developed, these may not be widely applicable to all infectious diseases and public health laboratories [18]. Therefore, the small nuances in the extraction of nucleic acid and e Approaches, combined with the different functionalities of the sequencing platform, become important factors in the capacity sector. There are many sequencing and wet laboratory approaches, and it is important to recognize their benefits and weaknesses. Moreover, with the myriad of bioinformatic tools available today, and with rapid growth and constant change in this field, it becomes difficult to standardize the analyzes through laboratories and teams. Therefore, the choice of the tools and analysis of bioinformatics becomes important to consider in NGS and development of bioinformatics laboratory capacity. Furthermore, bioinformatics will require adequate computational infrastructure, including networks and storage systems, as well as staff with specialized knowledge and experiences with pipelines, wet laboratory methods, characteristics of the sequencing platform and ideally familiar with pathogens of interest. All these become important to consider during the NGS and the bioinformatic capacity of the construction capacity in a research or public health. In this review we summarize factors and important considerations for the creation of a high quality NGS and the search for focused infectious diseases and public health laboratory, in the settings with both limited resources, as well as substantial. We focus on the most common methods in sequence and bioinformatics, and we describe some challenges commonly addressed during this development of capacity. We provide recommendations that could allow a simplified process of NGS and Bioinformatics Laboratory implementation. NGS technologies and platforms from the introduction of NGS technology in 2005, the number of high-speed sequencing platforms with different costs, chemical, capacity and applications have increased dramatically. Illuminates alone offers many platforms, from the enthusiastic sizes of small laboratories / classrooms and clinical laboratories, to large high-speed sequencing centers. In addition to its most versatile platform until today, the Miseq, illuminates launched the GAIX, MISEQDX (the first diagnostic diagnostic test platform regulated by food and drugs), NEXTSEQ, NOVASEQ, MINIEQ and ISEQ, to accommodate a different level And needs of capacity. Meanwhile, the Ion Torrent / Ion S5 platform (acquired by the technologies of life), despite having higher rates of error than the systems illuminates, has continued to be used due to its accessibility and its ease of use. Furthermore, 2 companies have pioneer the single molecule sequencing market with platforms offering ultralung readings. Pacific Biosciences (Pacchio) was the first with the Pacbiors / Rsii, and the most recent platform, the sequel, which can get average reading length of 10 KB. PACBIO platforms have high-throughputs but also a high monolayer sequential error rate of 14%, which can be reduced by conversion to the circular consent sequence of 2% [19, 20]. Oxford Nanopore has released its first sequencer of individual flash moleculars, the minion, in 2014. Marketing of this product inspired a large user following, since the company has allowed the scientific community to dictate what was to be developed for The unit in terms of hardware and software. Software developments focused on correction for higher error rates (eg 13% Ã ¢ â,¬ "20%) of this platform [20" 22]. Oxford Nanopore has also released the High-Throughput Promethion and Gridion Platforms, which allowed for the parallelization of sequencing by stacking multiple cells.Selection flow of a platform depends heavily on a laboratory ¢ s search objectives (Table 1). In general, the sequencing of the entire genome of bacteria or viruses Successful on smaller targeted platforms, such as Miseeq, Nextseq or Ionian torrent [11, 13, 14, 23]. Some genome sequencing applications, such as highly repetitive bacterial genoma structures or bacteria with modular plasmid structures, have more robust necessary platforms and can provide a longer readings (pacchio) or A sequence Reading length and greater depth (Hiseq, Novassq) [24]. The minor variant and individual polymorphisms of nucleotide (SNP) of detection detection studies involving larger genomes and highly different organisms were better served by higher throughput platforms (Hiseq, Novassq) [16]. In addition to research objectives, the choice of the platform depends on the experience of personnel and ability levels. Ion Torrent is easy to use and simple in the laboratory, but the challenges of data analysis require staff with the appropriate bioinformatic fund. In comparison, the miseq requires more workout, but offers data storage and the support of the bioinformatics of the platform with a user-friendly graphic interface. A key attribute that must be considered is the connectivity of the sequencing platform and the training and availability skills, which is a factor in many countries in Africa, South America, Central America and Asia. These laboratories should not consider availability of qualified laboratory and biinformatic personnel, but also reagent availability, installation, stroke and maintenance of a sequencing platform, including configuration of IT infrastructure, data storage and backups Power A supports the instrument [25, 26]. It is important to underline that the IT infrastructure and computational requirements must be considered at the total cost of these systems for all laboratories, but more in the development of nations where availability is considerably poor. 1.Examples table of sequencing platforms currently supported and their advantages / disadvantages Sequencing / year platform released. Applications. Fast outer observer applications,%. Dreadtime. - Compossive resources. - Sanger Abi 3730XL / 2002 AÃ, ~ 0.18 20 min-â,¬ "48 HÃ ¢ None of high quality, Long readings, low-cost for small studies) low throughput, high costs, replacement errors, sequenced material must Be pure to produce good quality sequence data, Pacbio Rsii / 2010., M, E, HE, RT, CP, EPÃ ¢ ~ 13 A pass;