Consiglio Nazionale delle Ricerche

PUBBLICAZIONE, AI SENSI DELL'ART. 19 DEL D.LGS N. 33 DEL 14 MARZO 2013, MODIFICATA DAL D.LGS 25 MAGGIO 2016 N. 97/2016, E INTEGRATA DALL'ART. 1 C. 145 DELLA LEGGE 27 DICEMBRE 2019 N. 160, DELLE TRACCE D'ESAME STABILITE DALLA COMMISSIONE ESAMINATRICE DEL CONCORSO DI SEGUITO INDICATO, NELLA RIUNIONE DEL22 MAGGIO2023.

BANDO N. 367.346 TEC IRIB

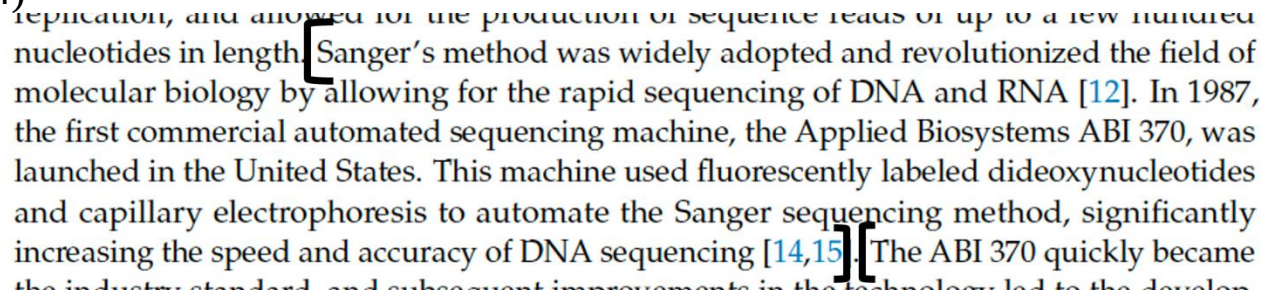
CONCORSO PUBBLICO, PER TITOLI ED ESAMI, PER L'ASSUNZIONE CON CONTRATTO DI LAVORO A TEMPO PIENO E INDETERMINATO DI UNA UNITÀ DI PERSONALE PROFILO TECNOLOGO - III LIVELLO PROFESSIONALE - PRESSO L'ISTITUTO PER LA RICERCA E L'INNOVAZIONE BIOMEDICA (IRIB) DEL CONSIGLIO NAZIONALE DELLE RICERCHE - CATANIA
SETTORE TECNOLOGICO: SUPPORTO ALLA RICERCA

TRACCE DELLA PROVA ORALE

A

SERIE A - ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) Il sequenziamento del genoma umano oggi: il candidato faccia un accenno alle diverse *Next Generation Sequencing* technologies disponibili, oppure, in alternativa, il workflow tecnico-sperimentale di una di esse con cenni della bioinformatica associata.
3) Può dirci la differenza tra RAM, ROM e memoria di massa?
4)


replication, and allowed for the production of sequence reads of up to a few hundred nucleotides in length. Sanger's method was widely adopted and revolutionized the field of molecular biology by allowing for the rapid sequencing of DNA and RNA [12]. In 1987, the first commercial automated sequencing machine, the Applied Biosystems ABI 370, was launched in the United States. This machine used fluorescently labeled dideoxynucleotides and capillary electrophoresis to automate the Sanger sequencing method, significantly increasing the speed and accuracy of DNA sequencing [14,15]. The ABI 370 quickly became

Consiglio Nazionale delle Ricerche

B

SERIE B -NON ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) Può riassumere il workflow tecnico-sperimentale in uno studio a scelta di *epigenomic profiling*, illustrandone le principali fasi realizzative e di analisi bioinformatica?
3) Può elencarci le principali tipologie di reti informatiche?
4)

[and capillary electrophoresis to automate the Sanger sequencing method, significantly increasing the speed and accuracy of DNA sequencing [14,15]. The ABI 370 quickly became the industry standard, and subsequent improvements in the technology led to the development of higher-throughput sequencers capable of producing longer reads [15,16]. While the first-generation technology has been largely superseded by newer, higher-throughput sequencing technologies, it remains an important historical milestone in the development of sequencing techniques. The ability to sequence DNA and RNA has revolutionized many areas of biology and medicine and has led to numerous discoveries and advancements in the understanding of genetics and molecular biology.]

C

SERIE C - ESTRATTA

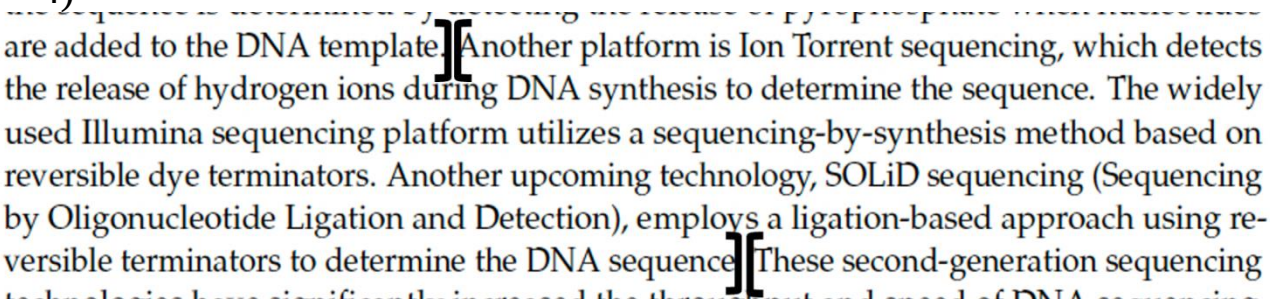
1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) Avendo a disposizione un campione di tumore ed uno di tessuto sano adiacente, il candidato descriva brevemente la strategia e le relative metodiche che utilizzerebbe per identificare le alterazioni genetiche somatiche del tumore.
3) Può dirci cosa è un *browser* ed elencarne alcuni?
4)

Second-generation sequencing methods have revolutionized DNA sequencing by enabling the simultaneous sequencing of thousands to millions of DNA fragments. These methods differ from traditional Sanger sequencing in their ability to perform parallel sequencing. Several widely used second-generation sequencing platforms have emerged, one of which is Roche's 454 sequencing method, which relies on pyrosequencing, where the sequence is determined by detecting the release of pyrophosphate when nucleotides are added to the DNA template. Another platform is Ion Torrent sequencing, which detects

D

SERIE D - ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) La genomica funzionale: il candidato accenni a una o più possibili metodiche legate o non al *Next Generation Sequencing*.
3) Può dirci la differenza tra hardware e software di un computer?
4)



are added to the DNA template. Another platform is Ion Torrent sequencing, which detects the release of hydrogen ions during DNA synthesis to determine the sequence. The widely used Illumina sequencing platform utilizes a sequencing-by-synthesis method based on reversible dye terminators. Another upcoming technology, SOLiD sequencing (Sequencing by Oligonucleotide Ligation and Detection), employs a ligation-based approach using reversible terminators to determine the DNA sequence. These second-generation sequencing

E

SERIE E - ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) Sequenziamento del DNA: metodo di SANGER, ci riassuma il principio e suoi utilizzi passati e moderni.
3) Può elencare i principali sistemi operativi per computer?
4)

versible terminators to determine the DNA sequence. These second-generation sequencing technologies have significantly increased the throughput and speed of DNA sequencing, enabling a wide range of applications in genomics research and clinical diagnostics [17]. These platforms have enabled whole-genome sequencing, transcriptome analysis, and targeted sequencing, leading to breakthroughs in genetic variation, disease research, and personalized medicine. Many developments in the second generation of sequencing methods have been achieved over the years and are represented in Figure 2 and briefly described in Table 1.

F

SERIE F – NON ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) Meccanismi di regolazione epigenetica: il candidato esponga qualche esempio e i principi delle tecniche "*omiche*" per studiarla.
3) Può dirci una procedura veloce per trasformare un file WORD in PDF?

[Third-generation sequencing technologies represent the latest advancements in DNA sequencing, offering new approaches that overcome the limitations of previous generations. These technologies provide long-read sequencing capabilities, enabling the sequencing of much larger DNA fragments compared to earlier methods. Examples include PacBio Sequencing, which uses a single-molecule, real-time (SMRT) approach with fluorescently labeled nucleotides, enabling long-read sequencing of DNA fragments up to tens of kilobases in length][Another technology is Oxford Nanopore sequencing, based on nanopore tech-

G

SERIE G - ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) Può riassumere le principali differenze tra *Next Generation Sequencing* e *Third Generation Sequencing*, vantaggi e svantaggi?
3) Può dirci una procedura veloce per trasformare un file WORD in JPEG, PNG o TIFF?
4)

in length][Another technology is Oxford Nanopore sequencing, based on nanopore technology, where a single-stranded DNA molecule passes through a nanopore, and changes in electrical current are measured to determine the DNA sequence. Oxford Nanopore sequencing provides long-read lengths, portability, and real-time analysis. Third-generation sequencing methods have been summarized in Table 1. Figure 3 describes technologies available on NGS and the type of data generated in each type of NGS assay and their brief application.]

H

SERIE H - ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) In genomica si parla molto delle *Varianti Strutturali* (*SVs*): cosa sono e quali approcci tecnologici sono più indicati ad individuarle?
3) Può dirci cosa è una *Dropbox*?
4) [The basic principle for short-read sequencing involves sequencing by synthesis based on enrichment through hybridization, amplification, or fragmentation. Whereas long-read sequencing works on sequence detection either by synthesis or by electrical voltage change/impedance, generating the current as a single base is passed through the biological membrane pore. Thus, long-read sequencing can generate reads in excess of 10 kb, whereas short reads can generate reads around 600 bp.] Further, the amplification bias is eliminated

SERIE I – NON ESTRATTA

1) Ci parli delle sue esperienze *curricolari*, mettendo in luce quanto attinente al bando concorsuale.
2) Può fornirci i principi di base di una o più tipologie di *microarrays*, applicazioni e limiti?
3) Può elencarci delle "periferiche esterne"?
4)

read sequencing (2)[However, the error rate of long-read sequencing is high as compared to short-read sequencing. One can get high-quality and high-depth data at a lower cost by using short reads. Short-read sequencing is useful for counting the abundance of specific sequences, profiling the expression of transcripts, and identifying the variants, etc., whereas long reads allow researchers to identify complex structural variants such as large insertions, deletions, inversion, duplication, deletions, etc. [5,31].]