



Specialty vocabulary

Familiarity with bioinformatics and its widely used words and expressions

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Abstract

Bioinformatics is an interdisciplinary science that uses a combination of statistics, mathematics, and computer science to collecting, editing, recovery, data mining, and analyze biological macromolecules, including nucleic acids and proteins. Bioinformatics has four main general parts, which are Genomics, Transcriptomics, Proteomics, and Metabolomics. Genomics involves the study of the genome of individuals; That is, all studies, whether structural or functional, combine the two directly on DNA. Structural studies mean the detection of mutations or measurements of chromosome length and studies such as those of the DNA molecule itself. But in functional studies, the goal is to study the physiological function of the gene. In the transcriptomics section, the transcriptome or DNA-transcribed product, in other words, all the DNA-generated RNAs are studied. But because RNA has a very short half-life, it first converts it into a more stable molecule called cDNA (cDNA library) and then studies it. In this section, the main purpose of the study is to measure gene expression, but other actions such as identifying mutations as well as identifying new genes that were previously unknown can be performed with regard to recent advances in the bioinformatics basin. In the proteomics section, the proteome is the case for all the proteins produced by the expression of DNA genes, and in the metabolomics section for all the physiological functions that result from the expression of DNA genes, like all chemical reactions that take place in the body. The study is included.

Keyword(s): Genomics, Transcriptomics, Data Mining, Editing, Macromolecules

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Access Gene Number	شماره دسترسی ژن
Adaptor	سازگارگر (آدپتور یک قطعه کوتاه از DNA شناخته شده است که به DNA ژنومی متصل می‌شود)
Alignment	هم‌ردیف کردن
Assemble	سوار کردن (تهیه یک توالی reference یا جامع)
Basic Local Alignment Search Tool (BLAST)	ابزار جستجوی هم‌ردیفی پایه‌ای موضعی
Bipolar Cohesion	چسبندگی دوقطبی
Coding	کدشونده
Complementary DNA (cDNA)	DNA مکمل (فقط شامل نواحی اگزون و UTR)
Data Set	مجموعه داده‌ها
Gene	ژن
Genetic Diversity	تنوع ژنتیکی
Genome	ژنوم (مجموعه ژن‌ها)
High Throughput	پُربرون داد
House Keeping Gene	ژن خانه‌دار (به ژن‌های ساختاری گفته می‌شود)
Linkage Disequilibrium (LD)	عدم تعادل لینکاژ
Marker	نشانگر
Microarray	ریزآرایه
Multiple Nucleotide Polymorphism(MNP)	چندشکلی چندنوکلئوتیدی
Mutant	جهش
Non Coding	غیر کدشونده
Open Reading	قابل خوانش
Paired End	رشته خوانده شده از هر دو طرف
Phylogenic Tree	درخت فیلوژنی یا تبارزایی
Primer	آغازگر
Proteome	پروتئوم (مجموعه پروتئین‌ها)
Raw Data	داده خام
Read	خوانش (رشته‌ی توالی‌یابی شده)
Real Time PCR	PCR در زمان واقعی
Restriction Site	سایت برشی
Run	فرآیند انجام خوانش
Sequence	توالی (رشته‌ی توالی‌یابی و ویرایش شده)
Single End	رشته خوانده شده فقط از یک طرف
Single Nucleotide Polymorphism(SNP)	چندشکلی تک‌نوکلئوتیدی
Single Polar Cohesion	چسبندگی تک‌قطبی
Splicing	پیرایش
Transcriptome	ترنسکریپتوم (مجموعه ترنسکریپت‌ها یا RNAها)
Whole Genome Sequencing	توالی‌یابی کل ژنوم

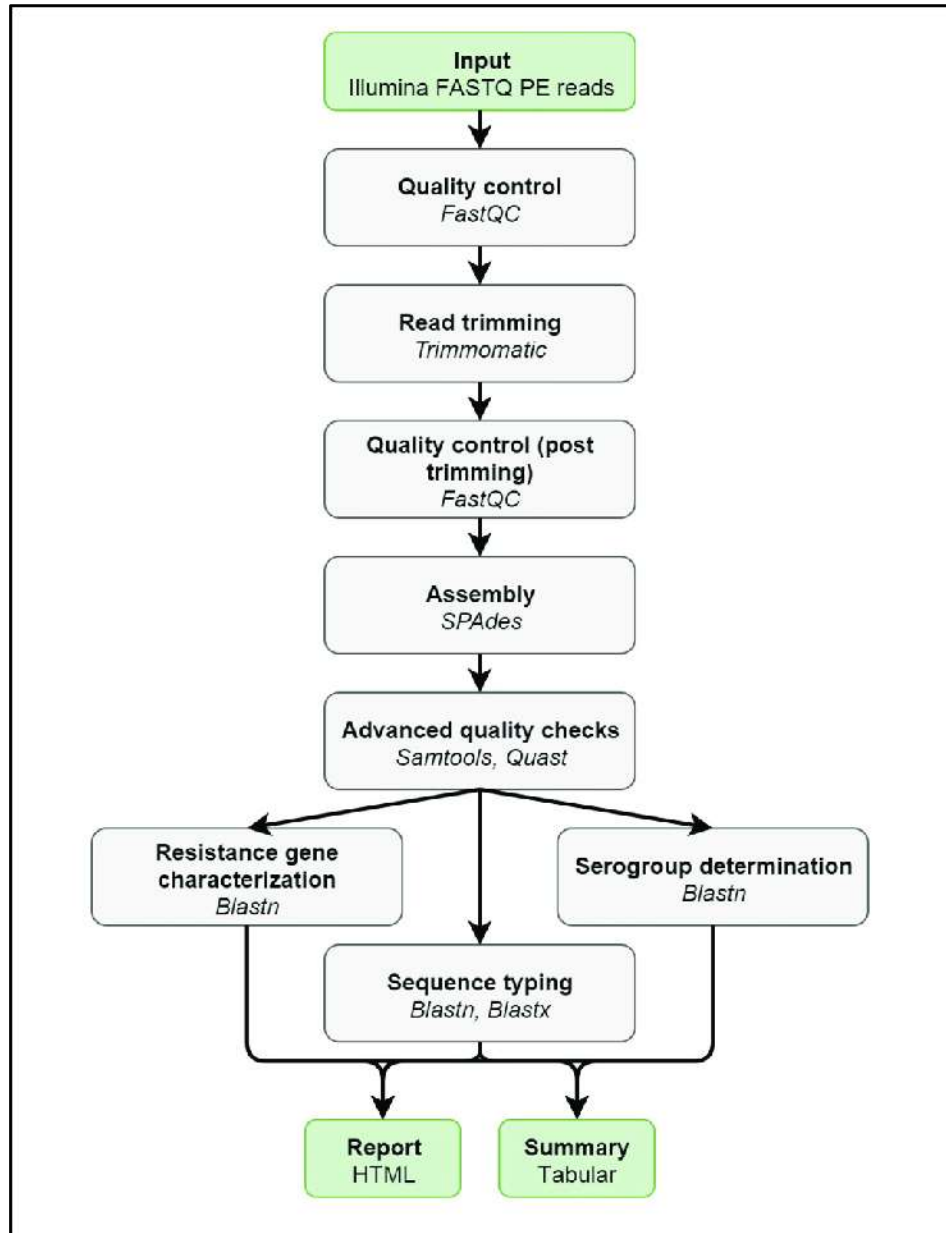


Figure 1. Overview of the bioinformatics workflow. Each box represents a component corresponding to a series of tasks that provide a certain well-defined functionality (indicated in bold). Major Bioinformatics utilities employed in each module are also mentioned (indicated in italics). Abbreviations: Paired-End (PE).