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Introduction To Bioinformatics Algorithms Solutions

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Bioinformatics - Wikipedia

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Bioinformatics is a blend of biology, computer science, and mathematics. Modern biology generates massive quantities of big data. Hidden in this data might be the next cancer therapy, the definitive proof that a certain gene is responsible for a disease, or the information needed to replicate a crucial biological process—and you could be on the team that discovers it.

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RNA-Seq is a technique that allows transcriptome studies (see also Transcriptomics technologies) based on next-generation sequencing technologies. This technique is largely dependent on bioinformatics tools developed to support the different steps of the process. Here are listed some of the principal tools commonly employed and links to some important web resources.

List of RNA-Seq bioinformatics tools - Wikipedia

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APPLIED MATHEMATICS - washington.edu

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efficient numerical evaluation to arbitrary precision, for all complex values of parameters.

Mathematical Functions—Wolfram Language Documentation

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Oxford Nanopore MinION Sequencing and Genome Assembly

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Roche - Annual Report 2018

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