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Bioinformatics / ? b a ? . o ? ? ? n f ? r ? m æ t ? k s / is an interdisciplinary field that develops methods and software tools for understanding biological data, in particular when the data sets are large and complex. As an interdisciplinary field of science, bioinformatics combines biology, computer science, information engineering, mathematics and statistics to analyze and interpret ...

Bioinformatics — Wikipedia

Bioinformatics and computational biology involve the use of techniques including applied mathematics, informatics, statistics, computer science, artificial intelligence, chemistry and biochemistry ...

Bioinformatics

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The department of Bioinformatics (BiGCaT) is part of NUTRIM the school of Nutrition and Translational Research in Metabolism at Maastricht University.

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The master's program in bioinformatics is a direct response to a paradigm shift taking place in medicine and biological sciences. Further research in these areas rests on the evaluation of masses of biological data: here, the use of computers, combined with accurate mathematical models and efficient algorithms is essential.

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Bioinformatics is a research area where computer science, information technologies and statistical methods are applied to the processing of biological data. Post-genomic technologies are producing huge amounts of biological data, and bioinformatics the key science in the task to make sense of them. The current challenge of the bioscientist is to be able to easily handle all this information.

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There are a ton of ways to do this in base R, but the dplyr syntax for this is a bit more simple. ...

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English: Bioinformatics is the application of computer science and information technology to the field of biology and medicine. Bioinformatics deals with algorithms, databases and information systems, web technologies, artificial intelligence and soft computing, information and computation theory, software engineering, data mining, image processing, modeling and simulation, signal processing ...

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Abstract. La recerca en biologia no es pot entendre avui sense la computació. A causa, sobretot, del desenvolupament de les tecnologies genòmiques, la biologia ha passat en molt poc temps, de ser una ciència en la qual l'esforç humà s'orientava principalment envers l'obtenció d'unes poques dades, a ser una ciència que genera un volum enorme de dades sense pràcticament intervenció humana.

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We set up a fast approach to debias impurity-based variable importance measures for classification, regression and survival forests. We show that it creates a variable importance measure which is unbiased with regard to the number of categories and minor allele frequency and almost as fast as the standard impurity importance.

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Structural variations (SVs) are large genomic rearrangements that contribute to genomic diversity as well as genomic disorders. 4 Due to their varying lengths, SVs are difficult to detect accurately, especially when analyzing the relatively short reads generated by next-generation sequencing (NGS). Although several SV detection tools have been developed, each is limited to specific types of ...

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