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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

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science, bioinformatics
combines biology, computer
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Prolonged antibiotic therapy
for the bacterial infections has
resulted in high levels of
antibiotic resistance. Initially,

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bacteria are susceptible to the antibiotics, but can gradually develop resistance. Treating such drug-resistant bacteria remains difficult or even impossible. Hence, there is a

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As a crude approximation,
current sequencing methods
consist of 3 consecutive steps

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designed to extract a molecular diagnosis from a DNA sample. First is a wet step in which the patient's DNA undergoes chemical manipulation to detect what base pairs are present.

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...

The NGS method, by its
nature, can generate a
significant amount of poor,

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failed, or false-positive sequences that are not usually seen in other molecular testing methods. One purpose of a bioinformatics pipeline is to filter sequences from view that do not meet the

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laboratory's predefined quality standards.

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Thus, I define translational bioinformatics research as the development and application of informatics methods that connect molecular entities to clinical entities. In this collection, Dr.

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Kann and colleagues have assembled a wonderful group of authors to introduce the key threads of translational bioinformatics to those new to the field.

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Compared to other methods,
ECMarker is an interpretable
model aiming to reveal

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underlying molecular mechanisms (e.g. gene regulation) while predicting phenotype. Many existing machine learning models still aim to learn a black box with high accuracy, which is not

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straightforward to provide any biological insights as described above.

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and metabolomic technologies generate massive amounts of data your genome alone contains some 6 billion pieces of code in the form of the letters A, G, T and C. Finding genetic and molecular variants

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within these data that are related to disease is like searching for the proverbial needle in a haystack.

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T. Lengauer, C. Hartmann, in
Comprehensive Medicinal
Chemistry II, 2007. 3.15.9
Outlook. This chapter
summarizes the state of the art
in a wide variety of areas in
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can contribute to providing useful information for the analysis of the molecular basis of diseases, the search for target proteins, and the analysis of the effect of drug therapies.

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1 Introduction. Gene
expression profiling by RNA-
sequencing has become
routine tool in biomedical

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research. Similarly, on the clinical side, RNA-seq has now been introduced as a cost-effective diagnostic tool (Cummings et al., 2017; Kremer et al., 2017). Moreover, recent technological advances

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have made the assessment of gene expression at single-cell level (scRNA-seq) feasible, opening new ...

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opportunities within industry and, as genomics enters the clinical arena, within hospitals, as well. Molecular and Computational Biology

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science and other related fields just regard bioinformatics as one specific application of their theories and methods due to the inability to provide precise solutions to complex

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molecular biology problems.
(2) Biologists focus on
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Research Core Facilities
(BRCF), and the faculty in the
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data of BC and surrounding
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and Systems Biology Methods
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introduces integrative
approaches in translational
bioinformatics and systems
biology to support the practice
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My research laboratory

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studies the molecular epidemiology of cardiovascular disease, utilizing metabolomic, genomic and bioinformatics methods in a "systems biology" approach to identify

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pathogenesis.

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