Reporting activities in bioinformatics research

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Chapter 1

Research and Publication Overview

1.1 Next-generation Sequencing

In our group at the Straubing Center of Science we develop bioinformatics solutions for next-generation sequencing (NGS) data, e.g., new methods and algorithms for analyzing (meta-)genomic and (meta-)transcriptomic data of microorganisms, as well as genome assembly and functional annotation.

In November 2015, we have one paper under review and one paper has been published recently [1]. In this manuscript we developed an experimental protocol that retains the high genetic resolution granted by high-throughput sequencing methods while effectively removing many low abundance sequences that are likely due to PCR and sequencing errors. According to this protocol, we split samples and submit both halves to independent PCR and sequencing runs. The resulting sequence data is graphically and quantitatively characterized by the discordance between the two experimental branches, allowing for a quick identification of problematic samples.

Moreover, another paper is currently in preparation, which will be submitted for publication by the end of year.

1.2 Protein classification, design, and drug discovery

Moreover, we aim at developing new methods and pipelines for protein classification [2, 3, 4, 5, 6, 7, 8], e.g., annotation, but also for protein engineering [9, 10], and the discovery of new drugs and inhibitors [11, 12]. Currently one manuscript is in preparation and will be submitted for publication in spring 2016.

1.3 Bioinformatics for molecular diagnostics

Our groups is also active in the field of bioinformatics solutions for molecular diagnostics applications. There we have mainly two research fields, namely HIV and Cancer. Moreover, we conducted also some studies dealing with other kind of diseases, e.g., diabetes and neurological disorders.

1.3.1 HIV

In our group, we develop machine learning and statistical models for the prediction of drugs resistance [13, 14, 15, 16, 17] and co-receptor tropism in HIV. Moreover, we focus on models for cross-resistance [18] prediction as well as subtype specific differences in HIV [19]. During the last year we published three papers dealing with HIV-1 co-receptor tropism in clinical settings [20], as well as computational models for improved prediction accuracy [21, 22]

1.3.2 Cancer

A second major research field in our group is the development of non-invasive models for the prediction of cancer [23], but also other specific conditions [24, 25], e.g., fibrosis [26] together with the University
1.3.3 Other diseases

We also develop models for the prediction of other types of diseases, e.g., diabetes and neurological disorders [27, 28, 29, 30, 31]. In a recently published study [32] we aimed to identify potential associations between liver injury markers and diabetes in a population-based study.

1.4 Computer Science

We are also active in other topics from the field of computer science, e.g., in particular in DNA computing. In DNA computing we have a special focus on DNA watermarking for biotechnological applications [33, 34, 35, 36, 37]. However, we also investigate in other research directions from the field of computer science, e.g., IT security [38, 39, 40, 41, 42, 43, 44, 45, 46].
Bibliography


