Bioinformatics

doi.10.1093/bioinformatics/xxxxxx

Advance Access Publication Date: 30 September 2015

Manuscript Category



Medical Bioinformatics course at Freie Universität Berlin

Report for the Medical Bioinformatics Project

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Associate Editor: XXXXXXX

Received on XXXXX; revised on XXXXX; accepted on XXXXX

Abstract

Motivation: As the amount of biological data has recently increased due to new and enhanced techniques like next-generation sequencing, the analysis of this data also needs to improve and especially speed up. As a result, new frameworks and platforms for distributed stream and batch data processing are evolving. In a university project, we developed a pipeline for the analysis of biological data from *The Cancer Genome Atlas (TCGA)* data portal, which provides - among others - the access to data from high level sequence analysis of tumor genomes. In this report we present the used methods and discuss their results.

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

$$\sum x + y = Z \tag{1}$$

2 Approach

3 Methods

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2 Sample et al.

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4 Discussion

5 Conclusion

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Acknowledgements

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Funding

This work has been supported by the... Text Text Text.

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