UNIVERZITA KOMENSKÉHO V BRATISLAVE

FAKULTA MATEMATIKY, FYZIKY A INFORMATIKY

GENOME COMPARISON BASED ON RAW READ AND PAIRED READ DATA.

DIPLOMA THESIS

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VLADIMÍR MACKO

Univerzita Komenského v Bratislave

Fakulta matematiky, fyziky a informatiky

Genome comparison based on raw read and paired read data.

Diploma thesis

Poďakovanie:

Abstrakt

Kľúčové slová:

Abstract

Keywords:

Obsah

Zoznam obrázkov

Zoznam tabuliek

Introduction

Kapitola 1

Genome differences

1.1 Definitions 2-3p

Here we define theory necessary to for this thesis.

1.2 Comparative genomic 1-2p

Here we show some of current methods used in comparative genomic, which studies the differences between genomes.

1.3 Probabilistic approach 2-4

1.4 Genome alignments 3-4

Brief mentions of current genome alignments approaches.

1.5 Evaluation 2-3

Here we discuss what metrics we want to improve and what is the measure of success for our solution.

Kapitola 2

Read statistics

Here we evaluate some statistics about commonly used data. Here we evaluate current used methods and set benchmarks for our solution.

2.1   Reads 1-2

Here we evaluate data for reads and we set our expectations about these data.

2.2   Paired reads 1-2

Here we evaluate data for paired reads and we set our expectations about these data.

2.3   Benchmarks 3-4

Here we benchmark some used tools for our problem.

Kapitola 3

Catchy name for our tool that will be implemented.

Kapitola 4

Discussion 3

Here we will discuss.

Literatúra

[1] Sample paper.

Appendix A

TODO