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Ruth for sensur

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etc

Abstract

Kort oppsummert hele oppgaven

Why you do this

How you do this

The results

Conclusion

Preface

Hvem er oppgaven ment for? Andre bioinformatikkstudenter

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# Introduction

## Background

Why decide to have this project…

Why should the project be done, why use time

## PROBLEM STATEMENT / AIMs

What you actually doing in the project.

Visualize quastresult and add information quast-like, that can be useful for determining which assembly is the best.

Same principle can be added.

Organize a automatized principle. Make something to compare.

## Literature review

Quast, gage assemblathon

Hvordan andre har funnet den beste løsningen

## Problem solution

Briefly about the solution. How you solved it.

Benefit of system. Quast need install etc, but not this.output structure is rather good so we reuse code for our output.

# Background

## Genome Assembly

### Sequencing

Reads

Coverage

Contig

Scaffolds

#### De novo sequencing

#### Next generation sequencing

### Assembly

#### Assembly algorithms

#### Assembly challenges

### Quality measures

#### Quast

## Bioinformatics

### Benchmarking

## Galaxy

Introduction to galaxy

# Material

All dataset used in the application here

## Datasets

## Reference genomes

## Software

# Methods

This chapter covers a description of the tool and implementation.

## Reproducing the GAGE-B results

## Galaxy

# Results

Samme som ch5

# Discussion

## Interpreting the GAGE-B results

## Analysis of galaxy tool

### Performance

### Potential use

### Weakness

## Further work

## Conclusion

Referanseliste!

Glossary =)

Appendix a  
(Plot/Figure)



figure

Appendix B  
(Tables)

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