

# Summary Report of Bioinformatics Seminar (MTAT.03.242) Presentation, Spring 2013

Your name / ID / email

## Abstract

This report includes the summary of presentation which was presented in Bioinformatics seminar (2013 spring) at Department of Computer Science. Today's presentation "BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions" was given by Raivo Kolde from Dept. of CS.

## Summary

**THIS IS JUST A FORMAT for you to have an idea what you can write in here.**

The talk was about the tool BSmooth, a tool available in R statistical package. He explained with the basics about DNA methylation and its role in gene regulation this laid a good foundation to the topic to be presented. This tool is used for the analysis of whole genome Bisulphite sequencing data. The power of this tool is shown by analysing four different datasets. The BSmooth tool aligns the reads to the genome using Bowtie, there is a QC check, and then performs smoothing. Smoothing is a phenomenon where.... The results of the article were summarized as ..... He further discussed about the drawbacks of this tool and the tools performs the tasks ..... He then presented the results obtained from testing the tool against different datasets and showed that ..... At last he discussed about the ..... applications and their evaluation against the datasets and showed some analytical results.....

## Question and Answers

Q1. What is BSmooth?

A1.

Q2. Explain smoothing? Can you suggest an alternative to smoothing?

A2.

Q3. What was your take home message?

A3.