IRIS-HEP Fellow project

Role of Myocardin-Related Transcription Factors in the Smooth Muscle Cell gene program

Volodymyr Shabanov

About me

My name is Volodymyr Shabanov, a 4th year student at Faculty of Biology, V. N. Karazin Kharkiv National University. I have a great interest in bioinformatics and over the years I have attended courses specializing in DNA barcoding, phylogenetic analysis etc.

I would like to learn more about RNA analysis as an IRIS-HEP Fellow. I believe that through the Fellowship program I can acquire new skills and it will allow me to gain experience in bioinformatics.

Introduction

Understanding the effect that genes have on the human body is crucial in modern medicine and is a subject of many studies [1]. Specific genes can affect the activity of other genes and fundamentally change the cellular processes. Research of effects that genes of interest and their transcriptome might have on cellular activity could help creating more effective treatment methods,

This project is dedicated to the gene MYOCD that encodes myocardin. Myocardin is a protein that is contained in smooth muscle cells and cardiac muscle cells and is responsible for differentiation of muscle cells and it participates in regulatory processes [3]. Although MYOCD is extensively studied [2] [4], we are still far from full understanding of its functions.

Project

In this project,we analyze the effect of over-expression of myocardin on other genes in smooth muscle cells (SMC) from the human coronary artery using the RNA-Seq method.

SMC were treated with adenoviruses that express nothing (control group) or over-express myocardin (treatment group). There were 4 virus induced and 4 control samples. RNA was extracted from these cells and sequenced with paired-end reads on an illumina machine.We will compare these two groups to find a list of genes that show differential expression and predict the functional role of these affected genes.

Methods

We will use *fastQC* and *multiQC* for sequence quality control. If any sequence data filtering will be required, we will use *trimmomatic* to trim low quality sequences. For quantification of the transcripts, we will use *Salmon* that performs read mapping to a human genome and counting reads corresponding to specific genes. This process will give us raw count data that will be analyzed for differential gene expression signals using *DESeq2*. At the end, we will use *WebGestaltR* for functional analysis of the differentially expressed genes.

Plan

Week 1

Study the literature on sequence quality control, install *fastQC* and *multiQC* and read software manuals.

Week 2

Make sequence quality control using *fastQC* and *multiQC*.

Week 3

Study the literature on differential gene expression analyses, install DESeq2 and read its manual.

Week 4-8

Perform the analysis of the gene expression data with DESeq2.

Week 9-10

Analyze the functional role of the differentially expressed genes with WebGestaltR.

Week 11-12

Proofread the results, prepare a report on the results of research.

References:

1. Heintzman, N., Hon, G., Hawkins, R. et al. Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature 459, 108–112 (2009). https://doi.org/10.1038/nature07829

2. Wang, Z., Wang, D.Z., Pipes, G.T. and Olson, E.N., 2003. Myocardin is a master regulator of smooth muscle gene expression. Proceedings of the National Academy of Sciences, 100(12), pp.7129-7134.

3. Huang J., Wang T., Wright A. C., Yang J., Zhou S., Li L., et al.. (2015). Myocardin is required for maintenance of vascular and visceral smooth muscle homeostasis during postnatal development. Proc. Natl. Acad. Sci. 112, 4447–4452. doi: 10.1073/pnas.1420363112

4. Mokalled M. H., Carroll K. J., Cenik B. K., Chen B., Liu N., Olson E. N., et al.. (2015). Myocardin-related transcription factors are required for cardiac development and function. Dev. Biol. 406, 109–116. doi: 10.1016/j.ydbio.2015.09.006