

Regensburg Lectures in Medical Bioinformatics

“Determination of RNA-protein interactions”

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Introduction

It is becoming increasingly clear that RNA-binding proteins are key elements in regulating the cell's transcriptome. Thus, unraveling the interaction network of the RNA-binding proteins by determining their binding sites is becoming an increasingly important topic. CLIP-seq is one of the major tools to determine binding sites but suffers from high false negative rate due its expression dependency. This critical hinders the use of public CLIP-data. We will show in several examples how use of raw public CLIPp data can lead to false biological reasoning and how advanced machine learning approach can overcome this problem. I will further discuss our results from our new Nature paper, showing that the human RNA helicase DHX9 predominantly binds to IRAlu elements and such suppresses the negative effect of Alu inflation in transcripts.

Friday, 15.09.2017, 12.15 p.m.
Hörsaal 53 (Westliche Naturwissenschaften, EG)

Host: Prof. Dr. Rainer Spang