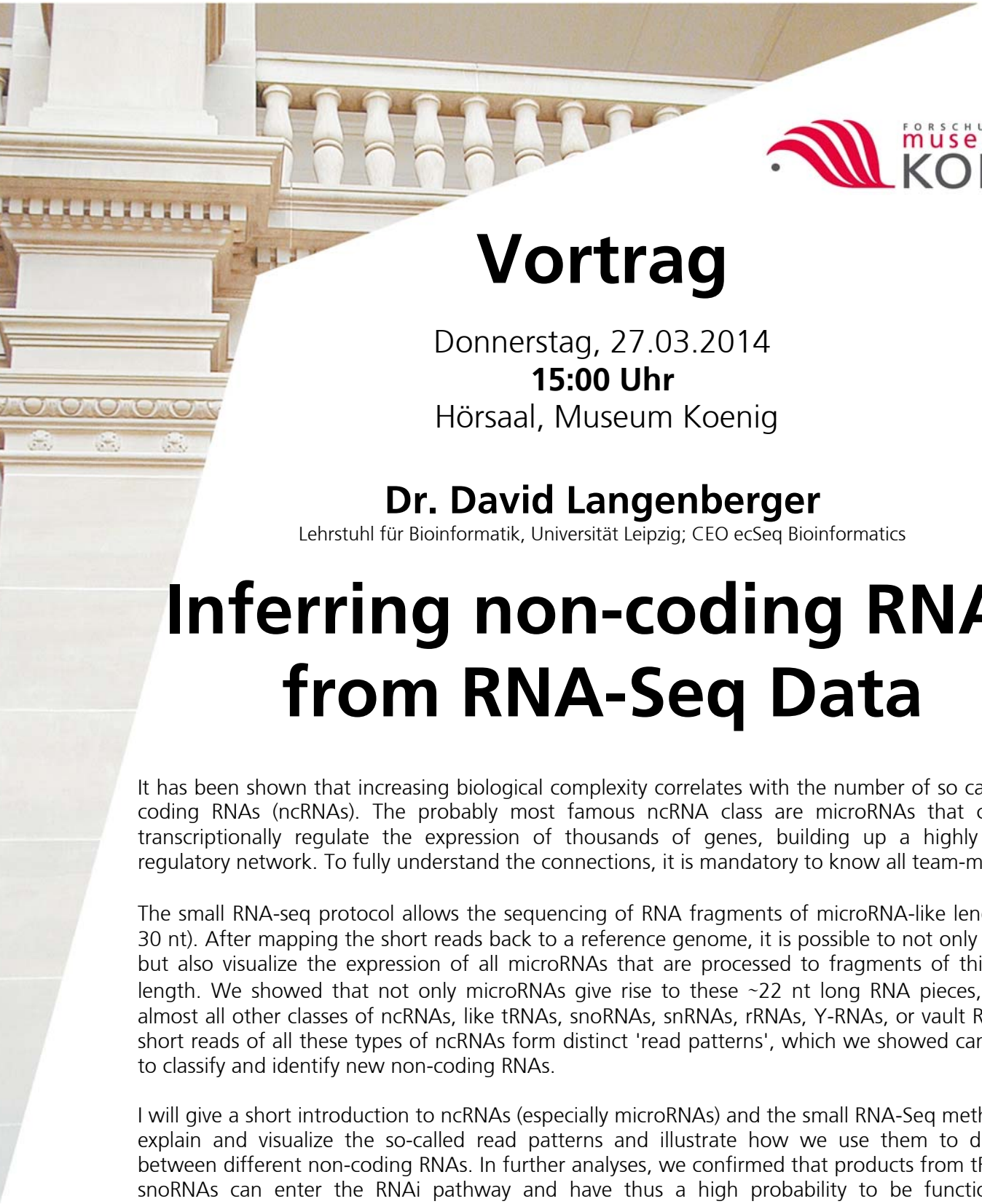

Vortrag

Donnerstag, 27.03.2014
15:00 Uhr
Hörsaal, Museum Koenig

Dr. David Langenberger
Lehrstuhl für Bioinformatik, Universität Leipzig; CEO ecSeq Bioinformatics

Inferring non-coding RNAs from RNA-Seq Data

It has been shown that increasing biological complexity correlates with the number of so called non-coding RNAs (ncRNAs). The probably most famous ncRNA class are microRNAs that can post-transcriptionally regulate the expression of thousands of genes, building up a highly complex regulatory network. To fully understand the connections, it is mandatory to know all team-mates.

The small RNA-seq protocol allows the sequencing of RNA fragments of microRNA-like length (~18-30 nt). After mapping the short reads back to a reference genome, it is possible to not only measure, but also visualize the expression of all microRNAs that are processed to fragments of this specific length. We showed that not only microRNAs give rise to these ~22 nt long RNA pieces, but also almost all other classes of ncRNAs, like tRNAs, snoRNAs, snRNAs, rRNAs, Y-RNAs, or vault RNAs. The short reads of all these types of ncRNAs form distinct 'read patterns', which we showed can be used to classify and identify new non-coding RNAs.

I will give a short introduction to ncRNAs (especially microRNAs) and the small RNA-Seq method. I will explain and visualize the so-called read patterns and illustrate how we use them to distinguish between different non-coding RNAs. In further analyses, we confirmed that products from tRNAs and snoRNAs can enter the RNAi pathway and have thus a high probability to be functional in a microRNA-like manner. This finding adds a completely new layer to the regulatory network.

Finally, I will present the free web service DARIO and give a short demonstration of how it can be used to analyze small RNA-Seq experiments online.