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### “Statistics of expression analysis with RNA-Seq”

**20 March 2012, 11:00 (s.t.)**

**Venue:** 2nd Floor Seminar Room  
Institute of Molecular Biology (IMB)  
Johannes Gutenberg University Campus Mainz

All are welcome to attend

## **Abstract:**

### Statistics of expression analysis with RNA-Seq

Many applications of high throughput sequencing require statistical inference based on count data. Mapped reads are often summarized by counting their overlaps with genomic features (e. g. genes, exons and binding regions) in samples in different experimental conditions.

In this talk, I will introduce the basic technical concepts behind the methodology 'DESeq', which employs generalized linear models of the negative binomial family, as well as biological applications to differential gene expression, differential transcription factor binding, and differential exon usage ('DEXSeq').