

# Bethe Colloquium

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## Genomic Research goes Computational

The life and medical sciences have seen a revolution in the last decade. Initiated in the 1990s with the Human Genome Project, genomic research has significantly accelerated since 2007 when next generation sequencing (NGS) technologies were introduced. NGS is seen as the single most important driver of innovation in the life sciences in the next 10 to 25 years. The number of human genomes sequenced by 2015 already reached 300,000 and in the same year US-president Barack Obama announced a US-based project sequencing 1 million American citizens. A few weeks ago, the pharma company Astra Zeneca announced to sequence even 2 million human beings. At the same time the Beijing Genome Center is on its way sequencing all species existing in China. All these advances have triggered three main developments: first, biology becomes more and more computational. Mathematics and informatics play an ever-increasing role in genomic research and therefore in the life sciences. This biological data avalanche without computation and meaningful algorithms - even including deep learning algorithms - would be meaningless. Second, biology becomes quantitative. Indeed, genomic technologies allow the generation of truly quantitative data. And third, data-driven hypothesis generation and machine learning-based decision making slowly but steadily replaces classical approaches based on thoughts, postulates and speculation. I will give an overview of these developments and will also bring them into the perspective of our own goals applying genomics to questions in neurodegeneration and immunology.

### Lecture Hall 1

Physikalisches Institut - Nussallee 12 - 53115 Bonn

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