# Cologne Evolution Colloquium

## Andrea Sottoriva

**CRC 1310    Predictability in Evolution**

## The Institute of Cancer Research, London

### Measuring and predicting cancer evolution from patient genomic data

High-throughput genomics has the potential to revolutionise oncology by laying the ground for personalised medicine. However, translating cancer genomic findings into the clinic has often proven challenging. This is partly due to the astounding complexity of cancer genomes, as well as the presence of extensive intra-tumour heterogeneity in human malignancies. Cancer genomic data portray a very complicated picture of the genetics of neoplasms that is often hard to make sense of in light of tumour biology, hence the difficulty in translating results into real patient benefit. The cancer evolution paradigm poses that tumours change over time following Darwinian rules. Relatively simple evolutionary rules of mutation and selection can give rise to extremely complicated patterns. In this seminar, I will discuss how to identify the rules that drive tumour evolution in individual patients using a combination of mathematical modelling applied to high-throughput genomic data from human cancers. The identification of evolutionary rules within a mathematical framework allows making predictions on the future course of the disease in single patients. The ultimate aim is anticipating a cancer's next step, with fundamental implications for treatment optimisation and disease management

Wednesday, January 30, 2019, 17:00
Institute for Biological Physics, Zülpicher Str. 77a
Seminar Room 0.03, Ground Floor

Hosted by Andreas Beyer