海外特別講演

Peer Bork, PhD

Senior group leader and joint head of the Structural and Computational Biology unit, EMBL Heidelberg

Biosketch

Peer Bork, PhD, is senior group leader and joint head of the Structural and Computational Biology unit at EMBL, a European research organization with headquarters in Heidelberg where he also serves as strategic head of bioinformatics. In addition, he holds an appointment at the Max-Delbrueck-Center for Molecular Medicine in Berlin. Dr Bork received his PhD in Biochemistry (1990) and his Habilitation in Theoretical Biophysics (1995). He works in various areas of computational biology and systems analysis with a focus on function prediction, comparative analysis and data integration. His group has published more than 500 research articles in international, peer-reviewed journals, among them more than 50 in Nature, Science and Cell. According to ISI (analyzing 10 years spans), Dr. Bork was for many years the most cited European researcher in Molecular Biology and Genetics and is among the top 5 in Biochemistry and Biology. He is on the editorial board of a number of journals including Science and PloS Biology, and functions as senior editor of the journal Molecular Systems Biology. Dr Bork co-founded five biotech companies, two of which went public. More than 30 of his former associates now hold professorships or other group leader positions in prominent institutions all over the world. He received the "Nature award for creative mentoring" for his achievements in nurturing and stimulating young scientists. He was also the recipient of the prestigious "Royal Society and Academie des Science Microsoft award" for the advancement of science using computational methods and obtained a competitive "ERC advanced investigator grant".

The human gut microbiome: Variation, stratification and associations with disease

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The human microbiome, that is all the microbes living in and around us, has recently become accessible by deep environmental shotgun sequencing (metagenomics) of large cohorts (Qin et al., Nature, 2010). The most prominent human habitat of our invisible microbial companions is the gut; it harbors hundreds of species which have important functions but have also been associated to more than 30 human diseases. I will illustrate the diagnostic potential of microbial markers using colon cancer as an example. Those associations are not always consistent across the human population and we indeed recently identified three microbial community types at the genus level across several industrial countries, which we dubbed enterotypes (Arumugam et al., Nature, 2011). We also analyzed (meta)genomic variation in gut microbial communities at the strain level and found that these variation patterns could serve as a fingerprint of an individual (Schloissnig et al., Nature, 2013). Finally we studied functional variation and determined the antibiotics resistance potential of individuals with clear differences between countries reflecting differences in antibiotics use both by human and in food production (Forslund et al., Genome Res., 2013). Taken together, stratification and variation of the gut microbiome is prominent at different levels, preparing the grounds for biomarker identification in numerous applications.