[L2] Emerging Big Data: Chemoinformatics-Driven View of Kinase Drug Discovery

Jürgen Bajorath

Department of Life Science Informatics, B-IT, LIMES Program Chemical Biology and Medicinal Chemistry, University of Bonn, Endenicher Allee 19c, D-53115 Bonn, Germany

Kinases are among the most heavily investigated drug targets and inhibition of kinases and kinase-dependent signaling has become a paradigm for therapeutic intervention. Kinase inhibitors and associated activity data have increasing 'big data' character, which presents challenges for computational analysis, but also unprecedented opportunities for learning from compound data and for data-driven medicinal chemistry. Herein, publicly available kinase inhibitor data are evaluated and a number of characteristics are discussed. In addition, selectivity of clinical kinase inhibitors is explored computationally on the basis of recently reported cell-based profiling data. For inhibitors shared by pairs of kinases, selectivity profiles were generated and a variety of selective inhibitors were identified. Uni-directional selectivity profiles revealed inhibitors that were selective for one kinase over the other, while bi-directional profiles uncovered compounds with inverted selectivity for paired kinases.