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Poster presentation

Molecular field topology analysis and structure generation
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Molecular Field Topology Analysis (MFTA) [1] is a QSAR approach based on the local (atomic) descriptors. First, a so-called molecular supergraph is constructed which is a simple graph such that the molecular graphs of all training set structures can be represented as its subgraphs. A uniform descriptor set for the statistical analysis is obtained by superimposing each training set structure onto the molecular supergraph. Each supergraph vertex is assigned the values of effective atomic charge, van der Waals radius, H-bond donor and H-bond acceptor ability, local lipophilicity and other parameters for the corresponding atom of the training set structure. For unoccupied vertices the neutral descriptor values are used. The analysis of the impact of local descriptors on the activity for different supergraph positions is highly helpful in search for new promising structures as well as in understanding their action.

However, the efficiency of new structure design can be significantly improved by the use of structure generators. For that purpose we have developed a method of molecular graph generation in conjunction with MFTA models based on the consideration of fragmental supergraphs and structural constraints [2]. In the deterministic mode, it builds all possible connected molecular graphs that can be represented as subgraphs of MFTA supergraph and satisfy the required constraints. In the stochastic mode, a representative subset of this structure set is constructed. The proposed approach is implemented in the convenient Java-based software.

The application of MFTA and structure generation in the design of active structures is illustrated by several case studies.

References
1. Palyulin VA, Radchenko EV, Zefirov NS: J Chem Inf Comp Sci 2000, 40:659-667.
2. Melnikov AA, Palyulin VA, Radchenko EV, Zefirov NS: Doklady Chemistry 2007, 415:. in press.