[L11] Electronic-Structure Informatics for Virtual Screening of Antagonists to Biogenic Amine Receptors of Silkworms

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We have been applying electronic-structure calculations in order to evaluate molecular descriptors for unsupervised and supervised learnings [1-5]. We call this approach “electronic-structure informatics”. In this approach, we define and calculate quantum chemical descriptors for evaluating molecular similarity [1-5], for deriving prediction models using multi-regression analysis [3], for characterizing three-dimensional patterns of ligand-protein interaction [4], and for classifying scents of molecules [5].

In this presentation, we report another application of electronic-structure informatics, aiming at discovery of antagonists to biogenic amine receptors of silkworms. Ohta et al. has recently investigated activity of 32 chemicals to regulate feeding behavior of silkworms by referring to known antagonists to the receptors [6]. We derive a predictive model describing biological activity of the molecules by numerically evaluating molecular descriptors through density-functional theory calculations. The coefficients of determination (the R^2 value) in the multi-regression analysis referring to Ohta’s experimental measurement is 0.764. This statistical analysis shows that the HOMO-LUMO gap ($\Delta\varepsilon_{HL}$), molecular volume (V_m), and solvation energy (ΔE_{solv}) are important quantum chemical descriptors.

Potential antagonists to the biogenic amine receptors are searched from our electronic-structure database, which stores numerical values obtained by DFT calculations on natural compounds registered in the KNApSAcK database by Kanaya et al. [7,8]. By referring to the criteria on $\Delta\varepsilon_{HL}$, V_m, and ΔE_{solv}, we suggest several compounds as new antagonists controlling the feeding behavior of silkworms.

Bibliography:

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