Basel Computational Biology Seminar

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Functional families in the CATH domain structure classification give insights on protein evolution and the impacts of splicing

Powerful tools for comparing protein structures and protein sequences have allowed us to analyse proteins from more than 20,000 completed genomes and identify 5500 evolutionary domain superfamilies. These superfamilies cover nearly 70% of domains from all kingdoms of life and are captured in our resource (CATH). Some structural frameworks seem particularly suited to supporting different residue arrangements in the active sites and structural variations on the surfaces of the domains which can modify protein functions. Sub-classification of CATH superfamilies into functional families allows us to examine mechanisms of function evolution in these superfamilies. We find surprising examples of convergent evolution within superfamilies where very different catalytic machineries are associated with similar enzymatic chemistries, showing that these scaffolds enable multiple routes to the same function. Furthermore, our comprehensive evolutionary classification allows to examine how new proteins have emerged at different stages of evolution and detect those domain families which shift function more frequently. In eukaryotic lineages these are frequently associated with cell-cell interactions and cell signalling. Finally, our CATH functional family classification helps in considering the impacts of splicing in human and fly.

Date: Monday, December 11th, 2017
Time: 16:00 h
Room: Lounge (level 13), Klingelbergstrasse 61 (vis-à-vis Pharmazentrum)
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