Thesis topic:

Systems Biology approach to unravel the molecular mechanisms involved in T-cell acute lymphoblastic leukaemia

T-cell acute lymphoblastic leukaemia (T-ALL) is an aggressive malignancy of thymocytes induced by the transformation of T-cell progenitors and is diagnosed primarily in children and adolescents. Leukaemic transformation of immature thymocytes is a multistep phenomenon driven by a number of oncogenic mutations. Although treatment outcome in patients with T-ALL has improved in recent years, significant questions about the disease pathogenesis have remained to be addressed, including a better understanding of the factors and molecular pathways that contribute to the malignant behaviour of T-ALL and how these could be exploited for therapy optimization.

The aim of this Master´s project is to achieve a better understanding of T-ALL by the computational analysis of gene expression and molecular interaction data.

The research for the thesis includes

i) Identification of genes either directly or indirectly related to T-ALL.

ii) Next, proteins encoded by these genes will be mapped onto protein-protein and regulatory interaction networks. Identifying partners of those genes/proteins and thus obtain the molecular context of T-ALL tumorigenesis.

iii) Analysis of molecular interaction networks linking T-ALL-expressed genes and molecular pathways.

Note:

1. The project is primarily computational. Thus, a keen interest in bioinformatics and computational biology is essential.

2. Depending upon the interest of the candidate, experimental lab work can be included in the thesis project.

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