University of Basel

DBM Basel
Department of Biomedicine

COMPUTATIONAL INFERENCE OF KINASE ACTIVITIES IN BREAST CANCER MODELS

Growth of up to 80% of all breast tumors is dependent on estrogens that activate estrogen receptor alpha (ERα) signaling, cell proliferation and survival. Thus, endocrine therapies that block ERα transcription program have been successfully used in clinics for decades. However, tumor cells can develop resistance. One important mechanism involves mutations in the ligand-binding domain of ERα, which make the receptor constitutively active and reduce therapy effectiveness. We have collected large in vitro data from MCF7 ER+ breast cancer cell line with and without clinically relevant mutation and measured phosphoproteomic data with active 2D and 3D. The data set contains samples treated with estradiol (E2), which is an activator of ERα; as well as samples subjected to clinically relevant treatments. The aim of this project is to identify differentially abundant (phospho)proteins across multiple comparisons and subsequently infer kinase activity using motif-based approach. Thus, this project will generate a comprehensive atlas of treatment responses of ER+ breast cancer models in 2D and 3D.

Your Profile

We are looking for a highly curious and motivated master student with good communication skills and a strong interest in oncology and computational biology who is willing to indepently work on and develop a research project. The laboratory language is English.

How to apply

Please send your full application consisting of a motivation letter and CV by E-mail to: m.bentires-alj@unibas.ch , michal.kloc@unibas.ch and ana.quirosgonzalez@unibas.ch

References

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