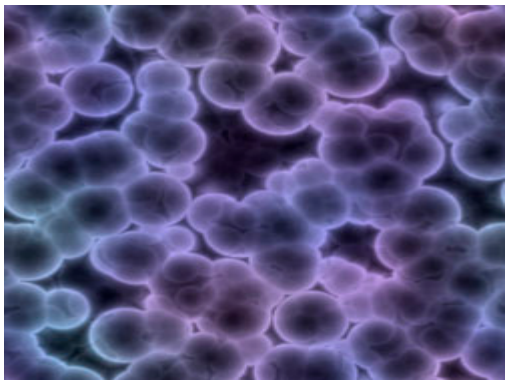
Computational systems biology of cell signalling

Results in Brief

Computational models for cell signalling

Exploiting computational and mathematical models to simulate and predict cellular responses could unveil important information about complex diseases and help design effective therapies.

HEALTH



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Signal transmission within cells is central for biological pathways and cell function in health and disease. To understand how cells make decisions, it is crucial to understand the complex interplay among proteins.

To this end, the EU-funded 'Computational systems biology of cell signalling' (Cosbics) project aimed to establish and apply a novel computational framework for analysing dynamic interactions of molecules within cells. The modelling approach followed by partners used mathematical models to quantitatively predict the spatial-temporal response of signalling pathways and subsequent target gene expression.

More specifically, the project studied two common pathways implicated in cancer (the Ras/Raf/MEK/ERK pathway and the JAK-STAT pathway). However, the tools developed for the mathematical analysis were generic and could be applied in other systems biology projects, as well. Additionally, they could predict the biochemical

behaviour of pathways in response to perturbations.

By combining mathematical modelling with biology, the Cosbics project provided new knowledge on how these two central communication networks are subverted in tumour cells. It also generated an invaluable scientific tool for designing biological experiments in academic and industrial research.

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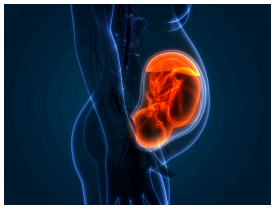

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Project Information

COSBICS

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