

## **Computational model of EGFR and IGF1R pathways in lung cancer: a systems biology approach for translational oncology**

This paper helps to understand the molecular biology of Epidermal Growth Factor Receptor and type 1 Insulin-like Growth Factor Receptor pathways in non-small cell lung cancer. Since non-small cell lung cancer makes up 85% of all lung cancer, investigating some of the key contributors to this cancer is important. The researchers used experimental data from 130 patients, all of whom had a surgical resection of primary NSCLC. The paper replicates the EGFR and IGF1R pathways in NSCLC and investigates their impact. I want to look into other pathways that interact with the above pathways to get an even better understanding of the processes related to NSCLC. A lot of ODEs are used to describe the model. A scientific UI can be developed to allow doctors to input patients' tumor data and then simulate the EGFR and IGF1R pathways and the impact of different drugs on the pathways.

Notes for presentation:

- Surgical resection of primary NSCLC is essentially just removing the tumor in the lung.
- For graphs, the top shows the initial values of the EGFR and IGF1R number of active receptors, showing over, down, and wild expression. NOTE these values are not beginning at equilibrium due to an assumption that an outside force messed with them
- So bottom graph shows that when both are expressed then the ERK pathway is highly activated resulting in the growth and survival of cancer cells

## **Integrative Analysis of Cell Cycle Control in Budding Yeast**

This paper helps to understand the yeast's cell cycle control system. The researchers created a model based on the current consensus of the yeast's cell cycle control system. They then tested the model on 100+ mutants and concluded that for the vast majority of them, the model held true (agreed with real results). There are around 10 mutants that the model does not properly predict. I could explore these mutants in greater detail by tweaking the model and seeing the results or I can update the model with data from new experimental studies. The model uses many ODE's. I can make an educational UI showing how the different mutations of yeast affect the cell cycle control system.

Notes for presentation:

- Yeast is very well understood, making mathematical models very complex which initially seems counterintuitive
- For network, this is the consensus model of the cell cycle control in yeast. This is what the researchers based their model on
- The point of this paper was to validate/invalidate the consensus model by using many mutant yeast strains

## **A comprehensive model for the proliferation–quiescence decision in response to endogenous DNA damage in human cells**

The researchers want to understand how the decision-making process of a cell to proliferate or quiescence is affected by DNA damage. I found this to be the most interesting paper because of the concept of quiescence. The researchers used live-cell imaging experiments to build a model of the molecular network. The model replicates the decision-making process given DNA damage and draws the conclusion that the restriction point and the G1/S transition are the most important when it comes to decision-making. This model uses ODE's. I could create a UI to predict the state of a cell given DNA damage. I want to further explore this decision-making process as I find it fascinating and see what else impacts the decision.

Notes for presentation:

- The decision is important to maintain the genome and prevent the spread of mutations which leads to cancer
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