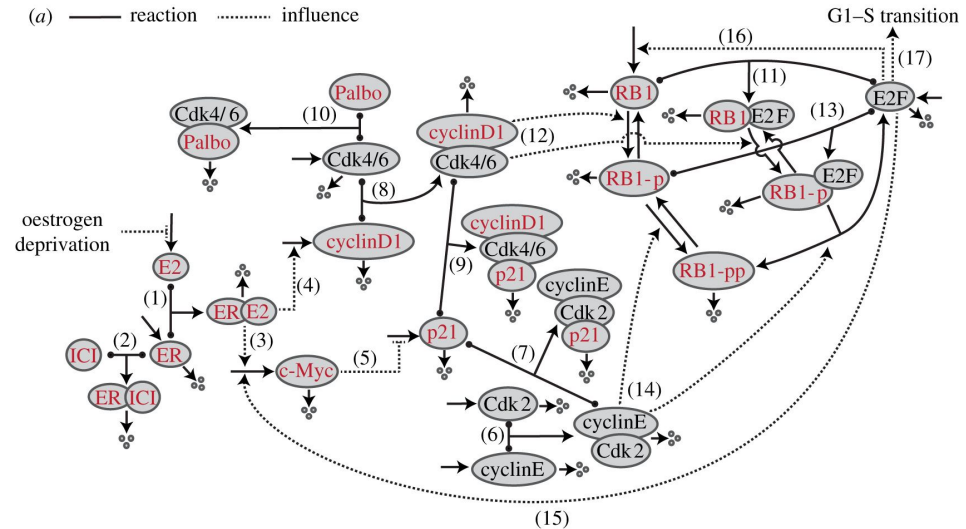


Mathematical Modeling of breast cancer cells in response to endocrine therapy and Cdk4/6 inhibition

Andrea Tonina e Gloria Lugoboni
30/01/2024

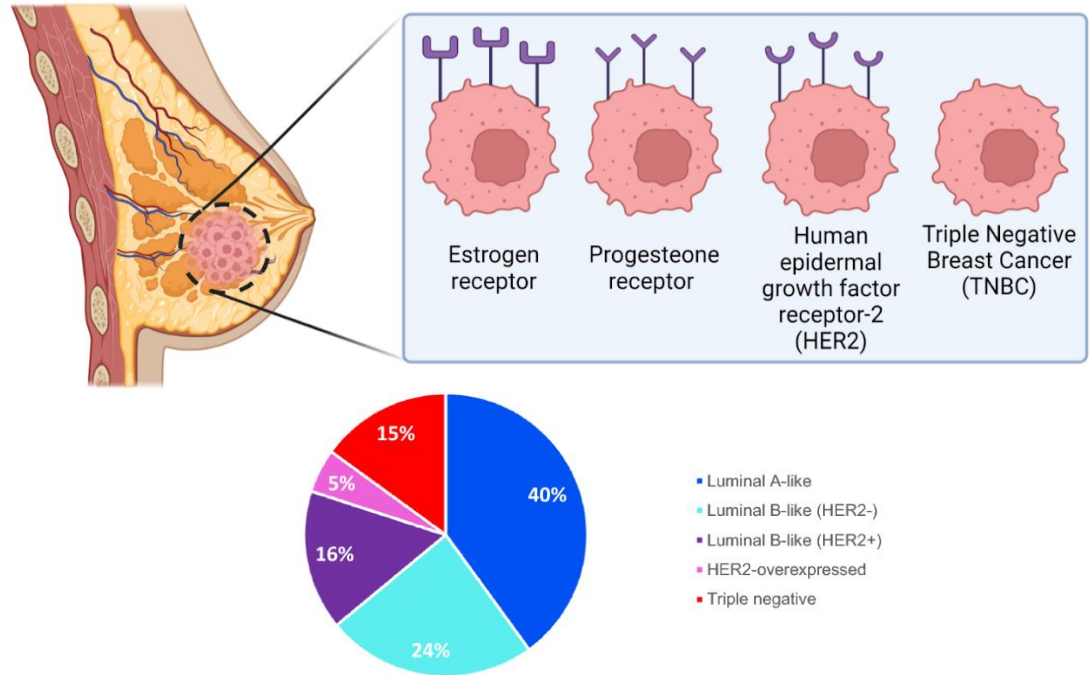


Introduction

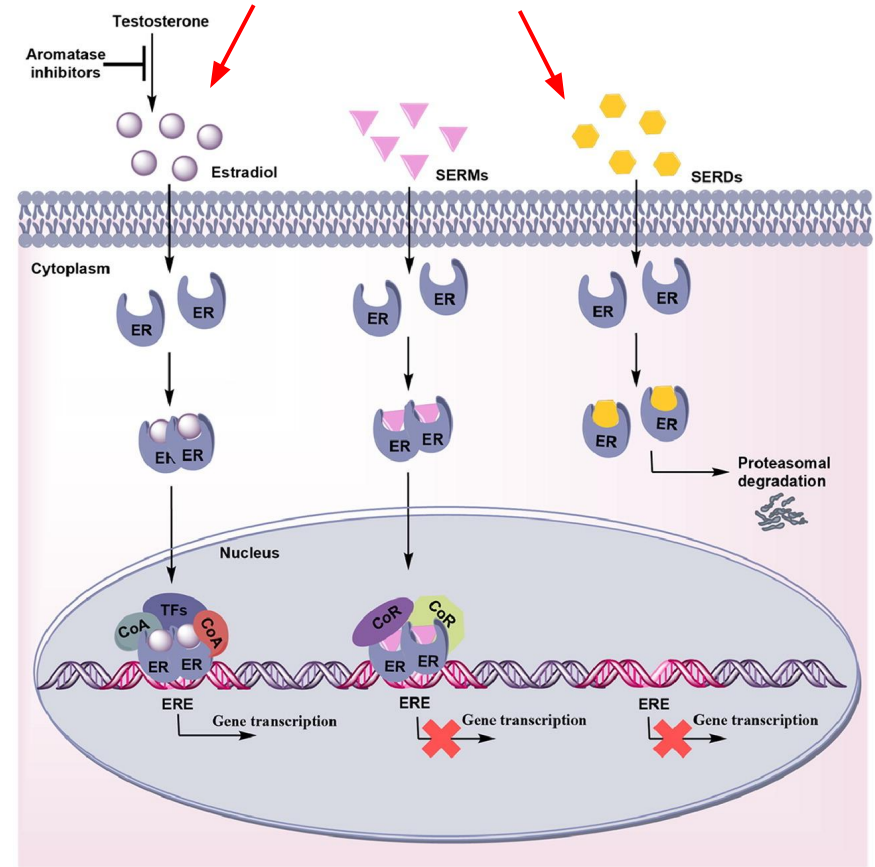
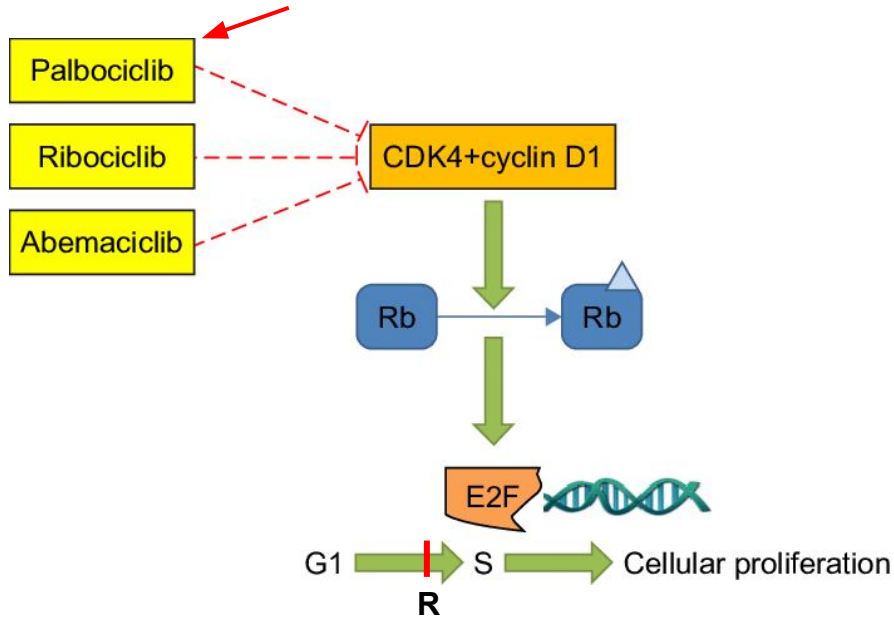
- Breast cancer
 - General overview
- Endocrine therapies and Cdk4/6 inhibition
 - Cyclin-dependent kinases Cdk4/6 and Palbociclib
 - Endocrine therapies

Breast cancer

- One of the most common cancer of this generation
- Divided into 5 main subtypes based on gene expression
 - Luminal A and Luminal B are ER-positive (aberrant proliferation)

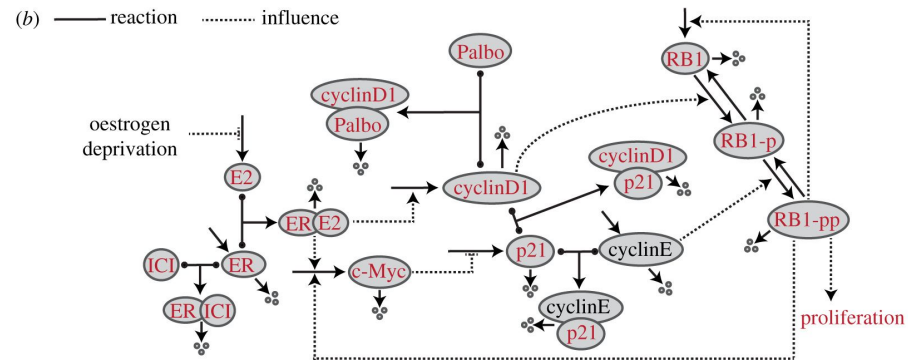
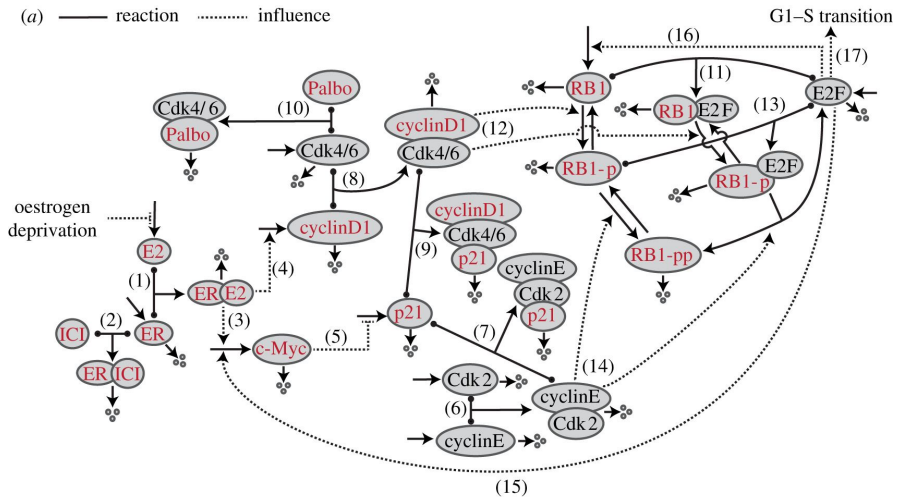


Therapies



Abemaciclib: A CDK4/6 inhibitor for the treatment of HR+/HER2- advanced breast cancer, Silvia Corona et al, Drug Design Development and Therapy Volume 12, 2018
 Hitisha K. Patel, Teeru Bihani, Selective estrogen receptor modulators (SERMs) and selective estrogen receptor degraders (SERDs) in cancer treatment, Pharmacology & Therapeutics, 2018

Model structure



Model description: 14 ODE of first order, 16 variables, 62 parameters

Our implementation

Deterministic approach

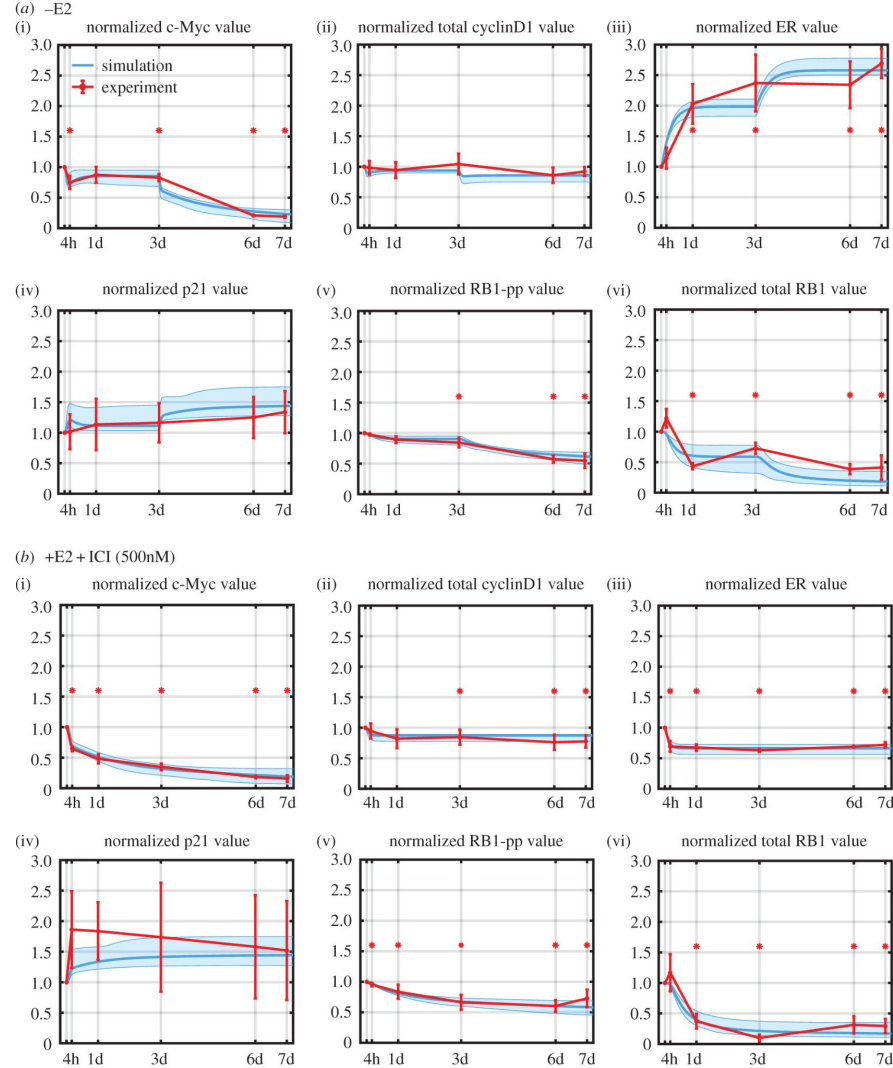
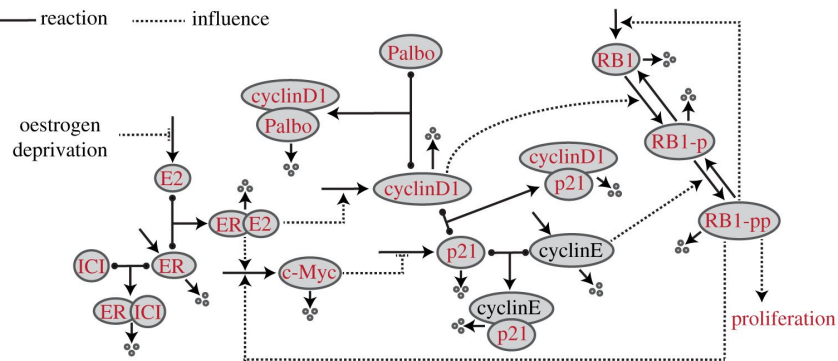
- ODE solver: ode23s
- Initial states and parameters were obtain from the original paper

Stochastic approach

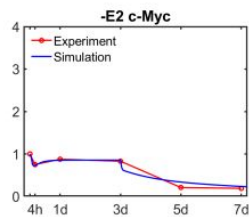
- ODE were converted into a set of reactions
- Deterministic rates converted into stochastic rates
- RSSA

Results 1: The proposed model structure can largely explain the experimental data

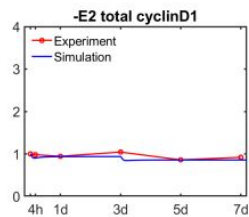
(b) — reaction influence



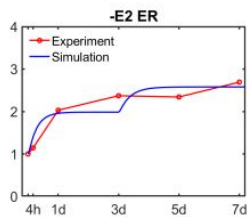
Our results



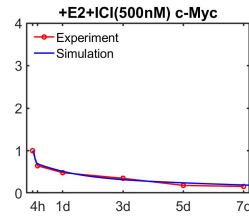
(a) *normalized c-Myc value*



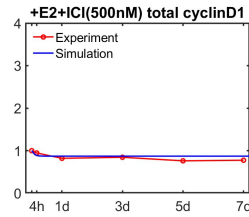
(b) *normalized total cyclinD1 value*



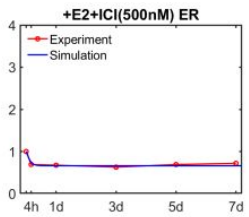
(c) *normalized ER value*



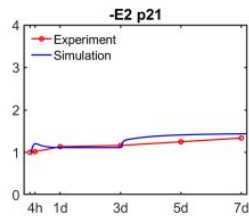
(g) *normalized c-Myc value*



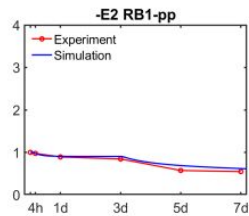
(h) *normalized total cyclinD1 value*



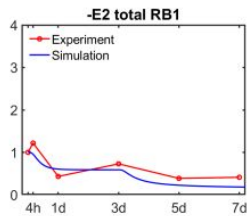
(i) *normalized ER value*



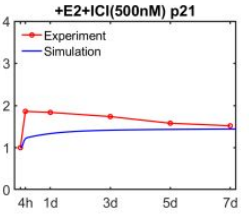
(d) *normalized p21 value*



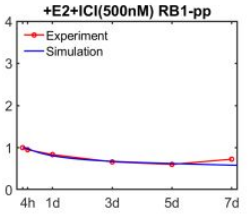
(e) *normalized RB1-pp value*



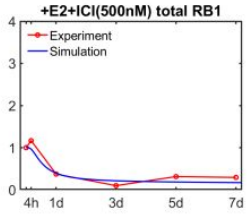
(f) *normalized total RB1 value*



(j) *normalized p21 value*

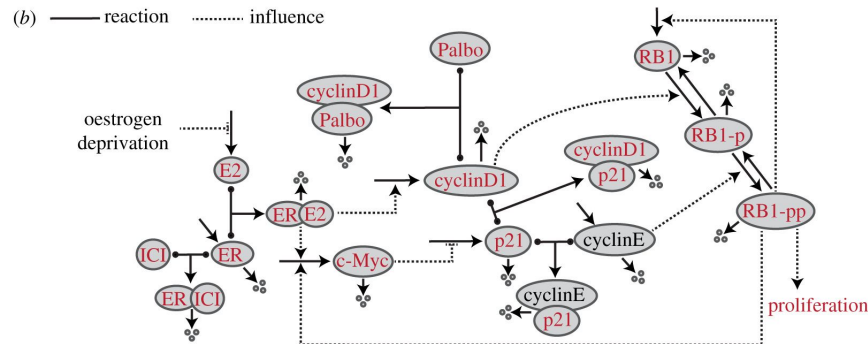
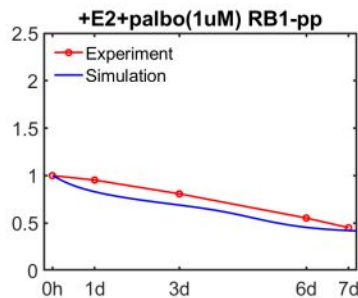
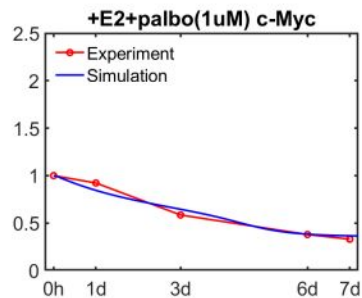
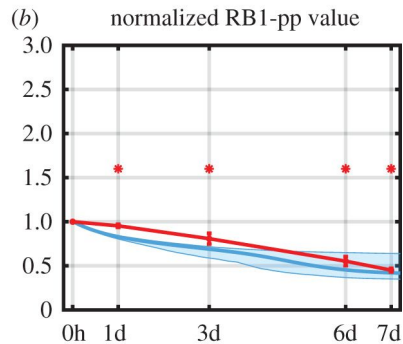
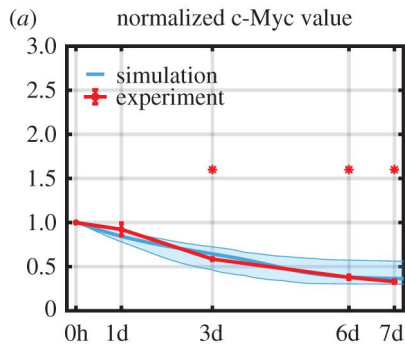


(k) *normalized RB1-pp value*

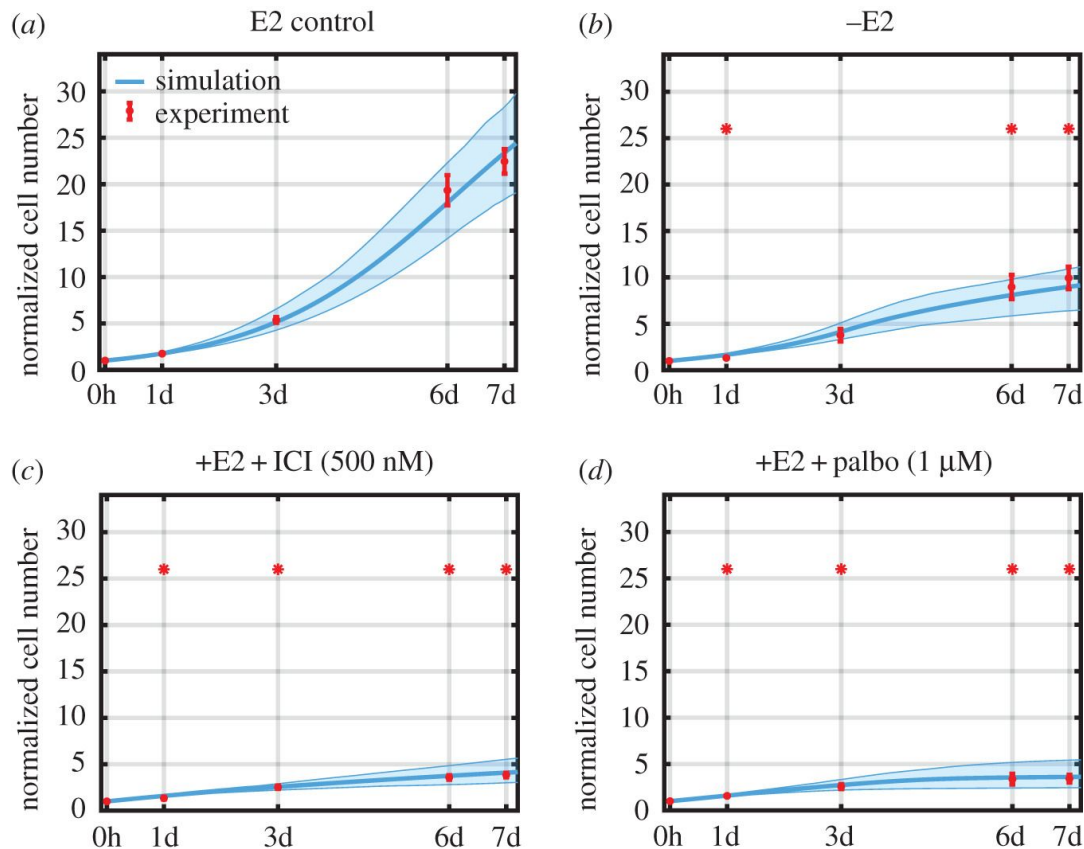


(l) *normalized total RB1 value*

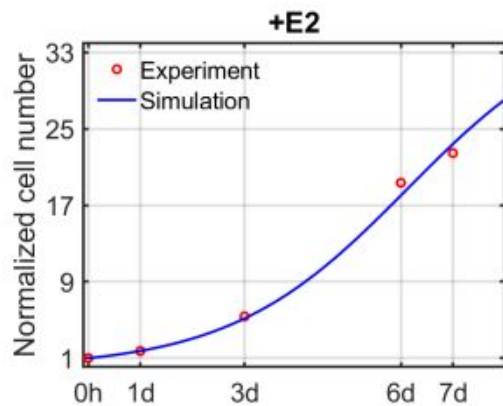
Results 2: Adding a new drug to the model requires limited new data



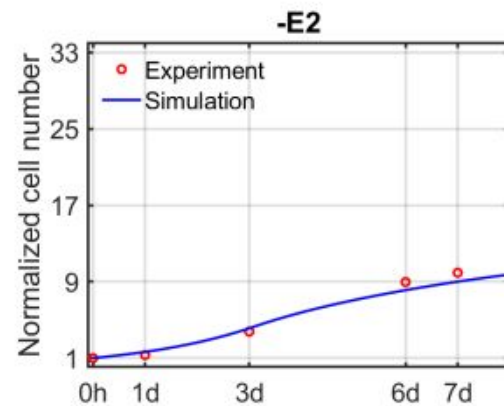
Results 3: The proliferation results can be explained by the RB1-pp level



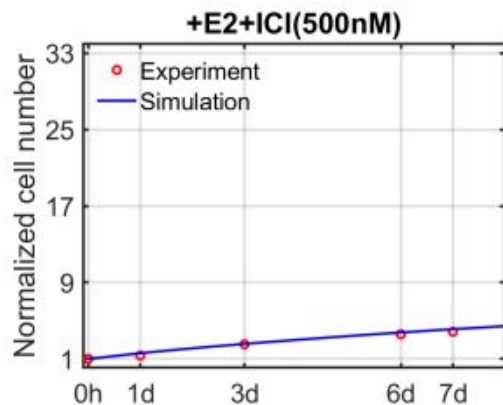
Our results:



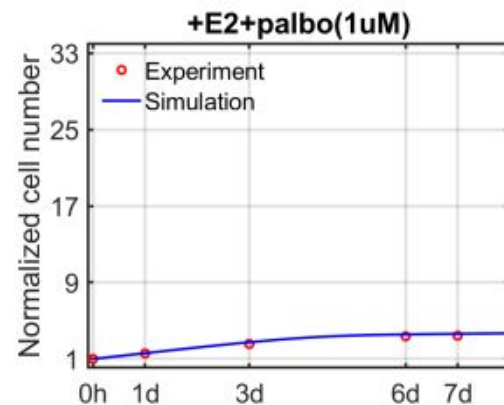
(a) *E2 control*



(b) *-E2*



(c) *+E2+ICI*



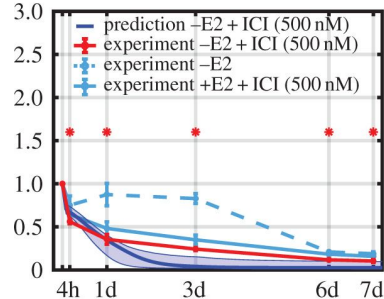
(d) *+E2+palbo*

Results 4:

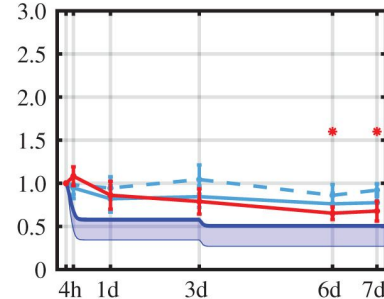
The model can predict the effect of combination treatment

-E2 + ICI (500 nM)

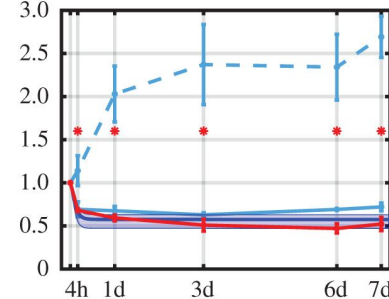
(a) normalized c-Myc value



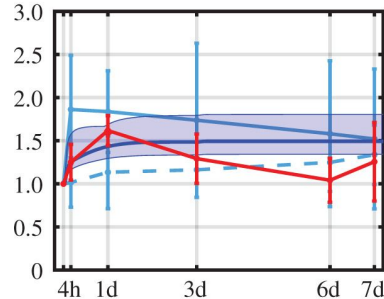
(b) normalized total cyclinD1 value



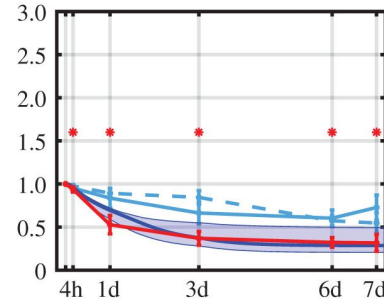
(c) normalized ER value



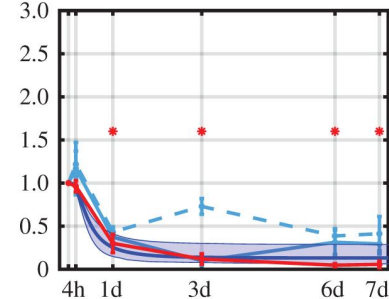
(d) normalized p21 value



(e) normalized RB1-pp value



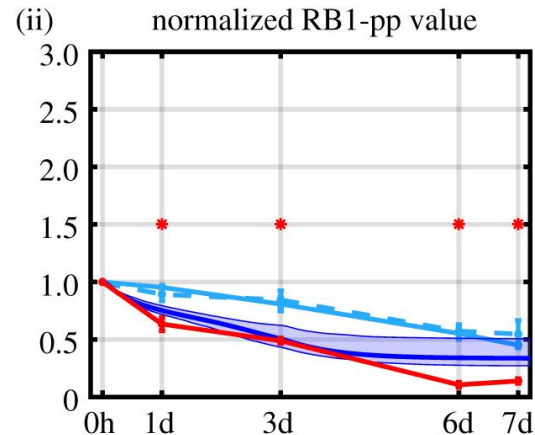
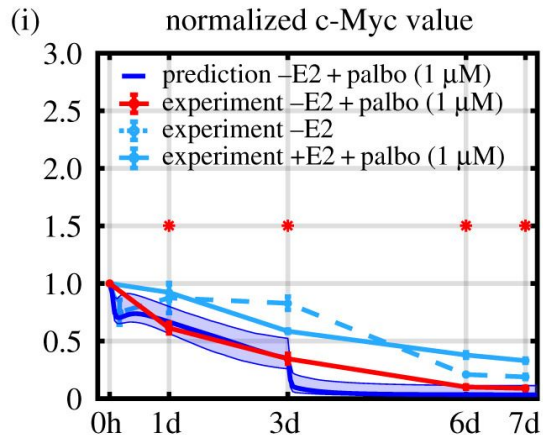
(f) normalized total RB1 value



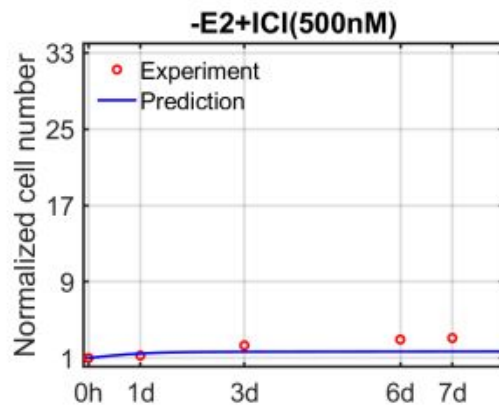
Results 4:

The model can predict the effect of combination treatment

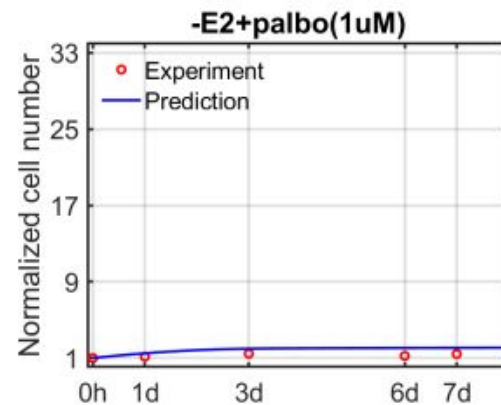
(a) -E2 + palbo (1 μ M)



Our result:
On proliferation
levels with
combination of
therapies

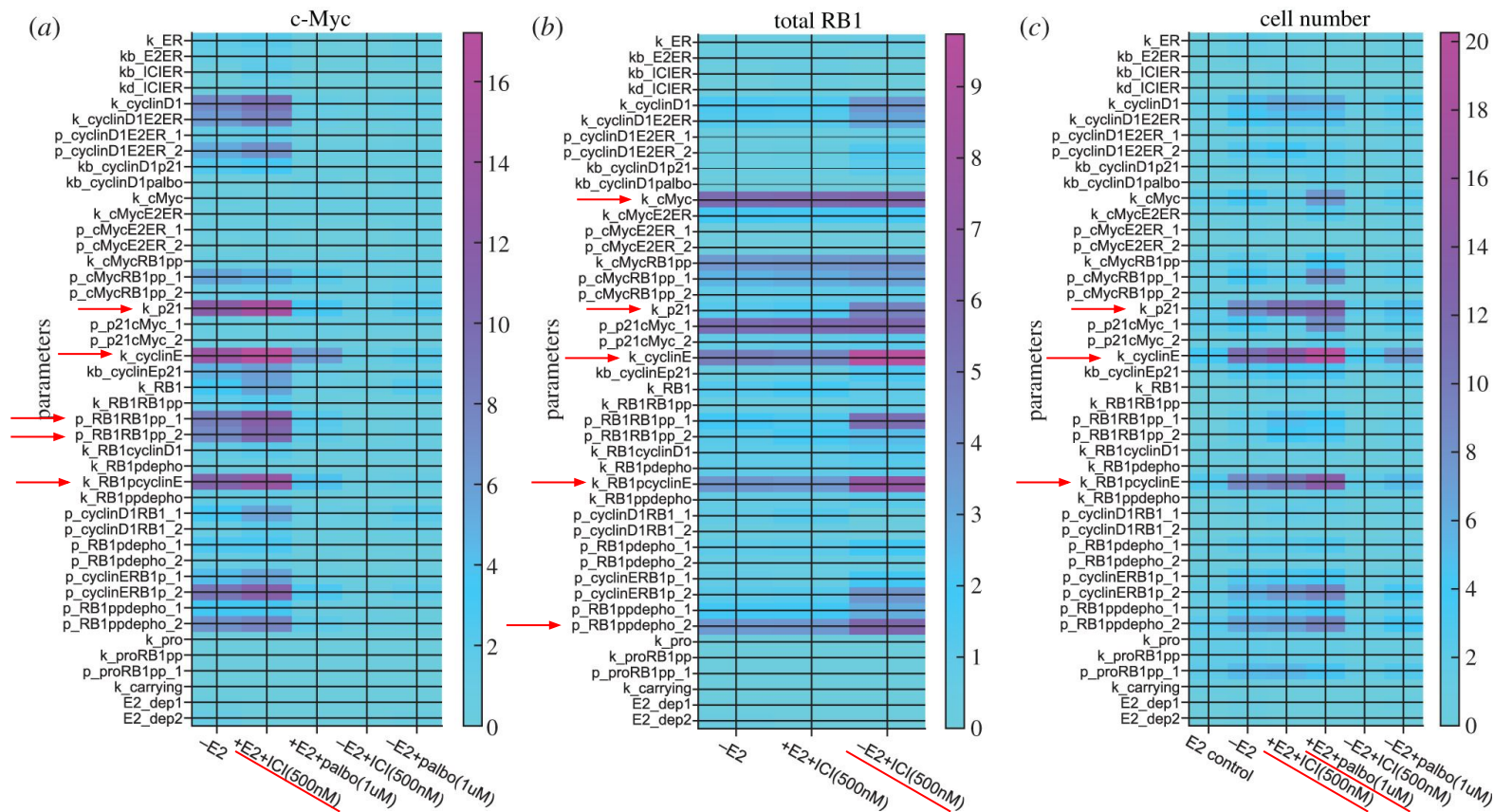


(a) $-E2+ICI$



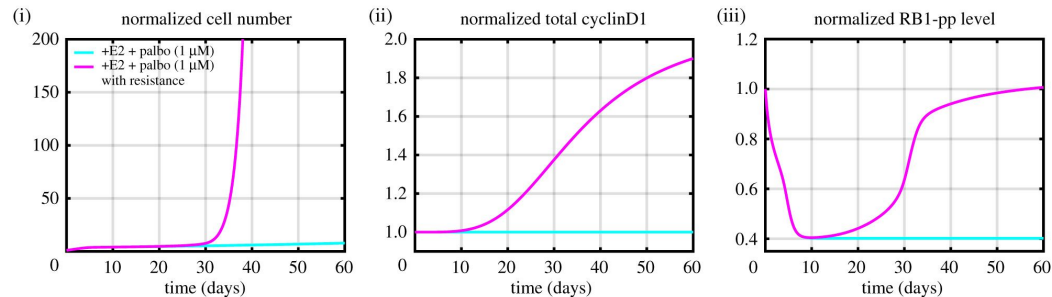
(b) $-E2+Palbo$

Results 5: Local sensitivity analysis of protein levels and proliferation

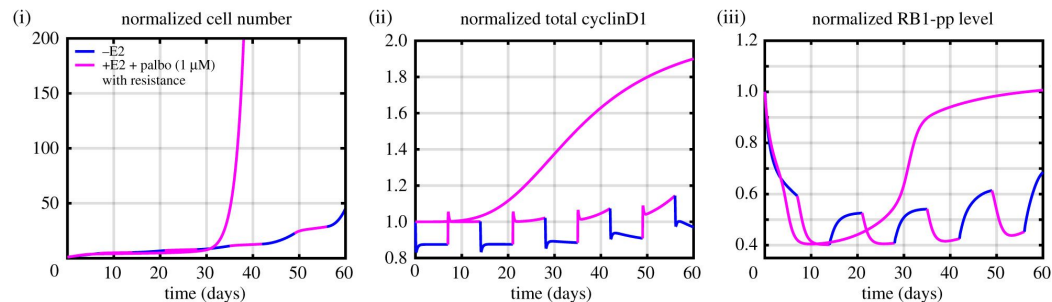


Results 6: The model can be used to explore the effect of sequential therapies

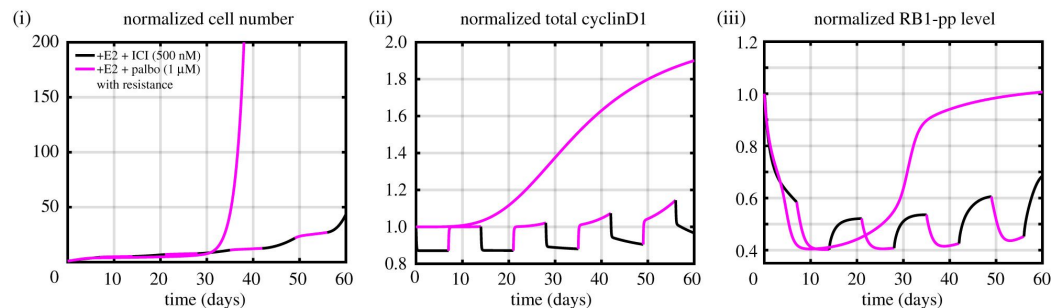
(a) +E2 + palbo (1 μ M) versus +E2 + palbo (1 μ M) with resistance



(b) alternation: -E2 7 days \rightarrow +E2 + palbo (1 μ M) with resistance 7 days

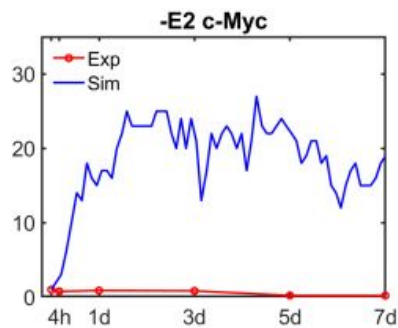


(c) alternation: +E2 + ICI (500 nM) 7 days \rightarrow +E2 + palbo (1 μ M) with resistance 7 days

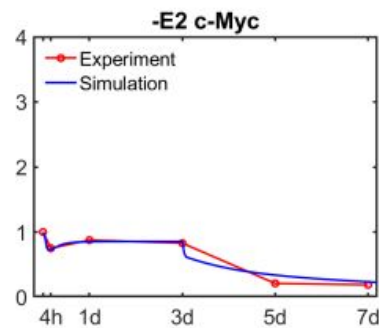


Discussion:

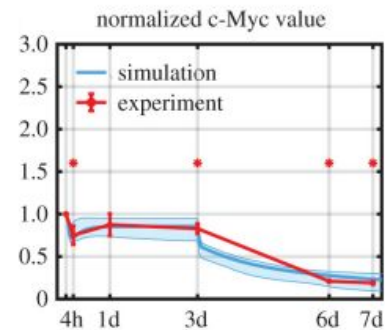
- Mathematical model is able to describe the aberrant ER signaling that takes place in these cancer cells
- The model was found to be predictive for cell proliferation and protein levels regulating ER signaling, both in terms of monotherapies and combined therapies
- Make assumptions on the predictive ability of the model regarding the utilization of cycle therapies in the context of resistance onset



(a) *Stochastic simulation*

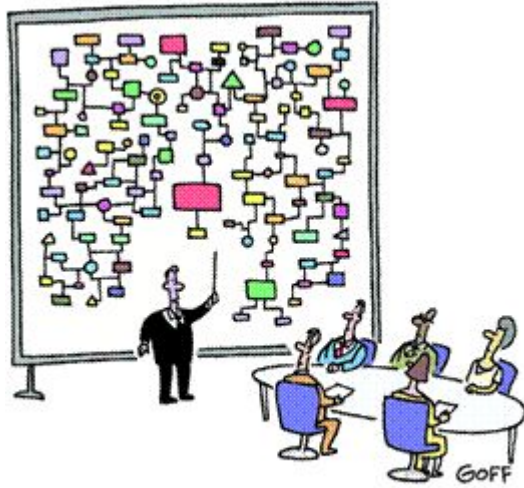


(b) *Deterministic simulation*



(c) *Original paper*

Figure 14: Comparison between the results of the stochastic simulation, the deterministic simulation, and the original paper in terms of the levels of the proteins c-Myc.



"And that's why we need a computer."

Thank you!

