Predicting tumor growth using a statistical layered population abstraction

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Joint work with Gregory Batt and Blaise Genest

Tumor Model



Tumor Simulator

[B. Waclaw, I. Bozic, M. Pittman, R. Hruban,B. Vogelstein & M. Nowak, 2016, A spatial model predicts that dispersal and cell turnover limit intratumour heterogeneity, *Nature*]

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Every Cell represented, grid based.

- -Growth (cellular division if space available around + mobility). Natural growth of tumor: nbr cells cubic in time.
- -Treatment everywhere (e.g. « ray »)
- -Treatment in surface (e.g. « medicine »)



• Obtain a simpler/faster abstraction from Tumor Simulator to evaluate speed of growth/death.

If no topological dependencies, easy to obtain equations. But growth and surface death depends on positions of cells.



Our model



Layers linear with radius (follow the t³ natural growth)

Each layer has a variable for cell concentration in that layer (100 values)

Probability Tables

Locality : Layer depends on previous, self and next layer



Results

Results 1: growth (mean)

Growth model (means)



Blue / green : initial model Blue : Used for training Red : replay+prediction of our model

Growth (distribution)

Growth (100 runs of original and abstraction, Layer 6)



Running Time



• Original : 14.3 seconds





ADD A CURVE FOR OUR PROGRAM

Results 2: treatment (mean)



Treatment (distribution)

Growth+death (100 runs of original and abstraction, Layer 3)



time

Results 3: surface treatment

Treatment

treatment (death on surface)

Treatment reaches the surface cells mostly



Can replay from same configurations

Not enough data yet for better abstraction

Future work

Future work

- Predict outcome of alternations between treatment and no treatment
 - We need more/better data!
 - produced data actively rather than by observation
- Consider more realistic Tumor models

(e.g. Drasdo's models)

Future work

• Consider multi level models (more accurate for treatment):

• Lower level: treatment with TRAIL (signaling pathway for each cell) [Palaniappan et al. 2017, Bioinformatics]

