Tumor Cell Migration in 3D – Features & Models

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Abstract

Using an automatic setup, we observe tumor cells as they migrate within a collagen gel. The resulting **3D** trajectories of individual cells are analyzed statistically. Features such as exponential invasion profiles, sub-/super-diffusive mean displacements squared and

Detection Setup



We use MDA-231 breast carcinoma cells and type1 collagen gels. The gels are polymerized in petri dishes with FCS medium added.

A fully automated setup tracks a group of individual cells in 3D, by recognizing characteristic optical patterns that emerge as the focal plane scans through the cell body.

Experim. Results





Cumulative probability to find cells at depths greater or equal *z*, after invading the gel for a fixed time from the surface. The profiles show an extended exponential regime.

Typical 3D trajectory of a cell, recorded for 18 hours. Velocity fluctuations (inset) from switching result between more diffusive and more ballistic phases.

leptokurtic step width distributions indicate that cell migration is not a Brownian random walk.

assuming cells with A model directional persistence, moving randomly within a porous matrix, with an optional possibility of protolytic matrix degradation, can explain the observed features.



Collagen gel

Tumor cells

Cell density n(z,t)

In bulk diffusion experiments, the cells start with a homogeneous distribution throughout the volume of the gel.

In surface invasion experi-

ments, the cells are initially

plated onto the top surface

of the gel.



The mean squared displacement $<\Delta r^2>$ versus lagtime Δt of cells in a 3D collagen gel shows a large cell-to-cell variability, including sub- and super-diffuive cases.



Exponential probability distribution of step widths between cell positions, observed at regular intervalls of 1h. Motion in z-direction is reduced.





Monte Carlo simulations of cell migration are performed on a 3D grid. Porosity is modeled by a fraction ρ of randomly distributed fields (blue) that are inaccessible to the cells (red).



Directional persistence is simulated by allowing the cells, in each step, to move only within a finite angle arround the previous

Combined Model

Experimental data are reproduced best in a model assuming agents with directional persistence that move randomly within a porous material and are able to degrade



direction.

obstacles in their path via proteolysis.



The combination model produces trajectories with statistical features close to the observations. A sample is shown to the left.



Simulated mean squared displacment (MSD) versus lagtime of Brownian walkers that diffuse in a porous medium with different volume fractions ρ of obstacles. For large ρ , the MSD saturates due to confinement.



Simulated surface invasion of Brownian walkers into a halfspace of porous material with ρ =0.85. One obtaines close-to exponential profiles in the cumulated probability $P(z,t_i)$ for different recording times t_i. In contrast, diffusion within a homogeneous medium shows non-exponential profiles (blue curve).

Proteolysis

Persistence





simulate proteolytic То matrix degradation, the cells are allowed to remove adjacent obstacles with a certain rate.

Proteolysis leads to a

obstacle density ρ . Thus,

cell migration becomes a

process. This is reflected in

a time-dependend increase

of the apparent diffusivity

(as determined from the

MSD at fixed lagtime).

decrease of

random

gradual

non-statonary



Simulated mean squared displacements of individual agents show a wide spectrum of apparent diffusivities and power law exponents.

Summary

Features & Models	Exponential Invasion	Sub- Diffusion	Super- Diffusion	Non – stationarity	Cell-to-Cell variability
Experiment	+	+	+	?	+
Porosity	+	+	_	-	+
Persistence	-	-	+	-	_
Protolysis	+/-	-	_	+	+
Combi M.	+/-	+	+	+	+