Stochastic individual based models with application to modelling of cancer therapy

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- drift towards higher fitness (canonical equation)
- evolutionary branching (splitting of populations to reduce competition)









A. Bovier (IAM Bonn)

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- Generator acting on functions $f:\mathcal{M}_p(\mathcal{X}) \to \mathbb{R}$ by

$$Lf(\nu) = \int_{\mathcal{X}} [f(\nu + \delta_{x}) - f(\nu)] b(x) (1 - m(x)) \nu(dx)$$

$$+ \int_{\mathcal{X}} [f(\nu - \delta_{x}) - f(\nu)] \left[\frac{d(x)}{d(x)} + \int_{\mathcal{X}} c(x, y) \nu(dy) \right] \nu(dx)$$

$$+ \int_{\mathcal{X}} \int_{\mathcal{X}} [f(\nu + \delta_{x+y}) - f(\nu)] m(x) M(x, dy) \nu(dx).$$













Here the functions d, b, c, p, m have the following meaning:

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- M(x, dy): probability distribution of the type of a mutant child of an individual of type x.









Application to modelling of cancer evolution and therapy

Can these models be applied to cancer and its treatment?

This would require: :

- Identification of the key mechanisms and players effecting the evolution of a tumour under treatment
- Quantitative identification of parameters
- Efficient numerical simulation of the model



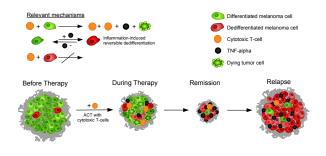






Immunotherapy of melanoma

Over the last years, we have tried to do all this for specific immunotherapies of melanoma in a mice model that was implemented at Bonn University Hospital. Starting point were experiments by Landsberg et al. where the following scenario was observed:





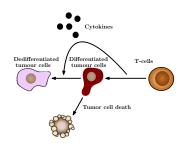


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A first model

New feature to be included in the model:

- genetically identical individuals can express different phenotypes
- phenotypes switch randomly within lifecycle ("bet hedging")
- switch rates can be changed by the presence of other "individuals" ("phenotypic plasticity")









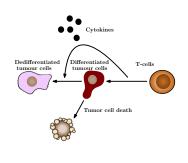


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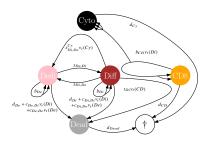
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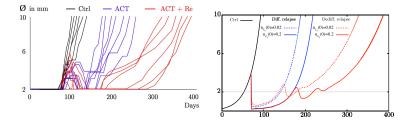






Comparison of experimental data

obtained by Landsberg et al. with simulations for biologically reasonable parameters



Left: Blue and red curves show therapy with and without reactivation of T-cells.

Right: Blue curves correspond to simulations where the T-cell population becomes extinct (can be seen as therapy without reactivation) and red curves to survival of T-cells (can be seen as therapy with reactivation).







Combination treatment

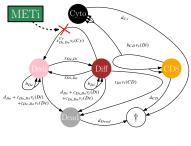
- Glodde studied evolution of melanomas under adoptive cell transfer therapy (ACT) combined with MET-inhibitor INC280
- Therapy protocol: HCmel12 melanoma cells are transplanted into the mouse and left to grow
 - ▶ after 16 days (tumour size 3-4mm diam) cytotoxic T-cells are injected
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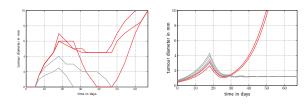






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First try



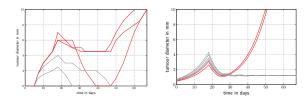
Problem: Therapy appears more effective for large tumours contrary to experiments!







First try



Problem: Therapy appears more effective for large tumours contrary to experiments!

Solution:

- Include the effect of T-cell exhaustion to slow down immune response
- Include spatial structure of the tumour

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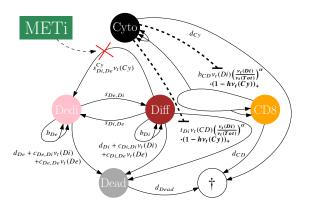








Exhaustion and spatial structure











The full generator

$$\begin{split} &(\mathcal{L}\phi)(\nu_{t}) \\ &= \left(\phi\left(\nu_{t} + \delta_{Di}\right) - \phi(\nu_{t})\right)\left(1 - m\right)b_{Di}\nu_{t}(Di) \\ &+ \left(\phi\left(\nu_{t} - \delta_{Di} + \delta_{Dead}\right) - \phi(\nu_{t})\right)\left(d_{Di} + c_{Di,Di}\nu_{t}(Di) + c_{Di,De}\nu_{t}(De) + c_{Di,KO}\nu_{t}(KO)\right)\nu_{t}(Di) \\ &+ \left(\phi\left(\nu_{t} + \delta_{De} - \delta_{Di}\right) - \phi(\nu_{t})\right)\left(s_{Di,De} + s_{Di,De}^{Cy}(Cy)\right)\nu_{t}(Di) \\ &+ \left(\phi\left(\nu_{t} + \delta_{De}\right) - \phi(\nu_{t})\right)\left(1 - m\right)b_{De}\nu_{t}(De) \\ &+ \left(\phi\left(\nu_{t} - \delta_{De} + \delta_{Dead}\right) - \phi(\nu_{t})\right)\left(d_{De} + c_{De,Di}\nu_{t}(Di) + c_{De,De}\nu_{t}(De) + c_{De,KO}\nu_{t}(KO)\right)\nu_{t}(De) \\ &+ \left(\phi\left(\nu_{t} + \delta_{Di} - \delta_{De}\right) - \phi(\nu_{t})\right)s_{De,Di}\nu_{t}(De) \\ &+ \left(\phi\left(\nu_{t} + \delta_{KO}\right) - \phi(\nu_{t})\right)\left(d_{KO}\nu_{t}(KO) + mb_{Di}\nu_{t}(Di) + mb_{De}\nu_{t}(De)\right) \\ &+ \left(\phi\left(\nu_{t} - \delta_{KO}\right) - \phi(\nu_{t})\right)\left(d_{KO} + c_{KO,Di}\nu_{t}(Di) + c_{KO,De}\nu_{t}(De) + c_{KO,KO}\nu_{t}(KO)\right)\nu_{t}(KO) \\ &+ \left(\phi\left(\nu_{t} - \delta_{Dead}\right) - \phi(\nu_{t})\right)d_{Dead}\nu_{t}(Dead) \\ &+ \left(\phi\left(\nu_{t} - \delta_{De}\right) - \delta(\nu_{t})\right)t_{Di}\nu_{t}(Di)\nu_{t}(CD)\left(1 - h\nu_{t}(Cy)\right) + \left(\frac{\nu_{t}(Di)}{\nu_{t}(Tot)}\right)^{\alpha} \\ &+ \left(\phi\left(\nu_{t} - \delta_{CD}\right) - \phi(\nu_{t})\right)d_{CD}\nu_{t}(CD) \\ &+ \left(\phi\left(\nu_{t} - \delta_{CD}\right) - \phi(\nu_{t})\right)d_{CD}\nu_{t}(CD) \end{split}$$









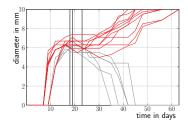
Results including T-cell exhaustion, spatial structure







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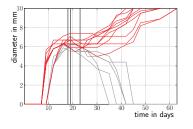


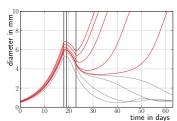






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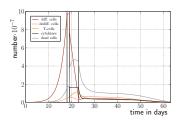


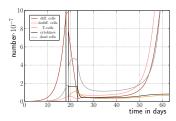




Late relapse

• Stochastic effects play a role even in large populations











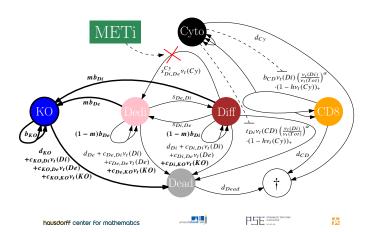
Glodde et al engineered several melanoma variants that do not express the gp100-antigen and are resistant to T-cell treatment.

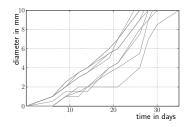


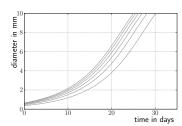




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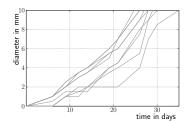


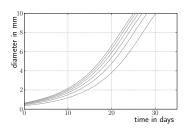


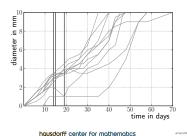


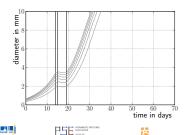




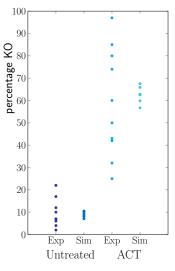














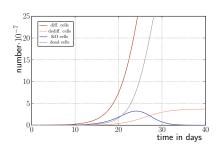


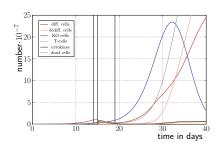






KO simulations





- Without treatment the knockout is suppressed by the wildtype
- Under therapy the knockout prevails

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No competitive pressure when the wildtype is in remission



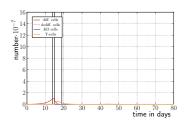


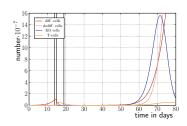






KO mutants, natural mutations













Conclusion

- Experimental data can be described by the probabilistic/deterministic model
- New key aspects have been identified: T-cell exhaustion, spatial structure
- Random fluctuations determine the success of therapy
- Phenotypic switch and genetic selection as mechanism to escape therapy









Thank you for your attention!











Baar M, Coquille L, Mayer H, Hölzel M, Rogava M, Tüting T and Bovier A. A stochastic individual-based model for immunotherapy of cancer. Scientific Reports 6, 24169 (2016)



Landsberg J, Kohlmeyer J, Renn M, Bald T, Rogava M, Cron M, Fatho M, Lennerz V, Wölfel T, Hölzel M and Tüting T.

Melanomas resist t-cell therapy through inflammation-induced reversible dedifferentiation. *Nature* 490:412–416 (2012)



Glodde, N.

c-MET inhibition improves T-cell immunotherapy of mouse melanomas but cannot prevent outgrowth of genetic antigen loss variants.

Ph.D. Thesis, Bonn Univ. 2016



Glodde, N.,, Hölzel, M.

Reactive neutrophil responses dependent on the receptor Tyrosine Kinase c-Met limit cancer immunotherapy.

Immunity 47:1-14 (2017)



Hölzel M, Bovier A, Tüting T.

Plasticity of tumour and immune cells: a source of heterogeneity and a cause for therapy resistance? *Nat Rev Cancer* 13:365–376 (2013)





