

# Modelling the emergence of pre-treatment phenotypic heterogeneity in vascularised tumours

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The coexistence within the same tumour of cancer cells that express different phenotypic characteristics poses a major obstacle to successful anti-cancer therapy and management of disease relapse. A more in-depth theoretical understanding of the process at the root of such phenotypic heterogeneity can be achieved through analysis and numerical simulation of structured-population models. The focus of this talk is on non-local partial differential equations modelling the adaptive dynamics of space- and phenotype-structured cancer cell populations. The analytical and numerical results presented shed light on the evolutionary determinants of intra-tumour phenotypic heterogeneity in vascularised tumours and suggest new routes of investigation for cross-disciplinary pre-treatment studies.

## References

- [1] C. Villa, M.A.J. Chaplain, T. Lorenzi, Modelling phenotypic heterogeneity in vascularised tumours, arXiv preprint arXiv:1910.08566 (2019)
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