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Modeling tumor development in liver

As recently demonstrated for liver regeneration after drug-induced damage, organization and growth processes can be systematically analysed by a process chain of experiments, image analysis and modeling [1]. In that paper our group was able to quantitatively characterize the architecture of liver lobules, the repetitive functional building blocks of liver, and turn this into a quantitative mathematical model capable to predict a previously unrecognized order mechanism. The model prediction could subsequently be experimentally validated. Here, we extend this model to the multi-lobular scale and study, guided by experimental findings, cancerogenesis in liver. We explore the possible scenarios leading to the different tumor phenotypes experimentally observed in mouse. Our model considers the hepatocytes, the main cell type in liver, as individual units with a single cell based model and the blood vessel system as a network of extensible objects. The model is parameterized by measurable values on the cell and tissue scale and its results are directly compared to the experimental findings.

References

[1] Hoehme, et al. (2010) Prediction and validation of cell alignment along microvessels as order principle to restore tissue architecture in liver regeneration. Proc. Natl. Acad. Sci (USA) vol. 107 no. 23 10371-10376