The nature of evolution within normal and neoplastic tissue is a subject of debate. I will present a highly flexible computational model that allows evolutionary dynamics resulting from diverse spatial structures to be compared in a single, minimal framework. Combining stochastic simulations with mathematical analysis, I will explain how tissue architecture governs the potential for subclonal expansion, the prevalence of selective sweeps, and spatial patterns of genetic heterogeneity. I will describe the conditions under which genetic diversity is most predictive of tumour progression, and I will discuss applications in optimising treatment protocols and understanding cancer risk variation. These findings help explain the observed multiformity of cancer and normal tissue evolution and contribute to establishing a theoretical foundation for predictive oncology.