Detecting Cell Attractors in Cancer

C. Santamaría[♮] G. Rubio[♮] and B. García–Mora[♮1]

([♮]) Instituto Universitario de Matemática Multidisciplinar, Universitat Politècnica de València, Camino de Vera, 46022 Valencia, Spain.

Abstract

Despite advances in cancer survival rates, we are still far from genuinely curing cancer. It is a fact that therapies often do not work, and after an apparent cure, the disease reappears with greater aggressiveness [1]. A growing number of researchers are questioning the current theoretical framework since it does not provide the answers capable of bringing about genuinely significant advances in healing. In a recent book that collects several contributions on the subject [2], we read that "the current paradigm, namely that a number of specific genes, when mutated or misregulated, cause cancer, has not by itself led to a cure for cancer–a failure clearly not due to lack of financial investments or intellectual effort. Therefore, a new theoretical framework for causally understanding and treating cancer is required." In this sense, "clinical outcomes are not in agreement with the prevailing paradigm (...) no plausible 'cancer mutations' are found in a tumor, or rationally designed, target-selective drugs do not work as expected or even make the tumor more aggressive".

The Boolean networks approach has a successful tradition from a theoretical point of view for modelling biological processes, including cancer [3]. With the recent advent of single-cell analysis techniques, the possibilities of experimentally testing its results have increased dramatically. In addition, single-cell procedures allow Boolean networks to explore the internal processes of cells. In this framework, we present an approach to exploring cancer, based on an algorithm to locate what has been called cellular attractors [4]. We apply our approach to a sample of bladder carcinoma obtained at Hospital La Fe in Valencia (Spain), with an estimated population of 9,214 cells and 21,373 genes.

References

[1] Huang, S., The Logic of Cancer Treatment: Why It Is So Hard to Cure Cancer; Treatment-Induced Progression, Hyper-Progression, and the Nietzsche Effect, In: *Rethinking Cancer: A New Paradigm for the Post-genomics Era*, ed B Strauss, M Bertolaso, I Ernberg and M J Bissell (Cambridge,MA: MIT Press, 2021)

[2] Strauss, B., Bertolaso, M., Ernberg, I. and Bissell, M. J. eds, Rethinking Cancer: A New Paradigm for the Post-genomics Era. Cambridge, MA, MIT Press, 2021.

[3] Thieffry, D., Kaufman, M., Regulatory circuits: From living systems to hyper-chaos. A special issue dedicated to the memory of René Thomas *J. Theor. Biol.*, (474): 42–47, 2019.

[4] Ernberg, I., The Cell Attractor Concept as a Tool to Advance Our Understanding of Cancer, In: *Rethinking Cancer: A New Paradigm for the Post-genomics Era*, ed B Strauss, M Bertolaso, I Ernberg and M J Bissell (Cambridge,MA: MIT Press, 2021)

[1] email@correspondingauthor