My Findings

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Chapter 1

Statistical Physics and Biology

1.1 Introduction

The future of medicine, Time magazine, Jan 1999: "Ring farewell to the century of physics, the one on which we split the atom and turned silicon into computing power. It's time to ring in the century of biotechnology [1]." Despite thee tremendous importance of life science and biotechnology nowadays as the above statements proclaim, at this stage their knowledge appears to be largely phenomenological, and thus undeniably calls for fundamental and quantitative understandings of the complex phenomena. It will be timely to ring in the century of a new physical science to meet this challenge.

The concept of self-organization is a central theme in biology and there are many great review paper on the subject (like [2, 3, 4]). In short **biological components self-assemble themselves to function. To perform the biological self-organization, then oftern cross over the energy barriers that seem to be insurmountable in the view point of simple physics. To this end, there are two physical characteristics that feature in the mesoscopic biological systems introduced above. The first one is their aqueous environment and thermal fluctuations therein**. The water has many outstanding properties among all liquids. It has a very high heat capacity, meaning that it can act as a heat reservoir with a negligible temperature change. Also, it has a very high (compared to other liquids) di-electric constant. Because of this, water can reduce electrostatic energy of the interactions to the level of thermal energy. This unique property of water originates from the weak hydrogen bonds between molecules. Although, the hydrogen bounds can be broken with the thermal energy of the environment, it causes long range correlation between water molecules. As a result, the liquid water manifests a quasi-critical state where it responds collectively and sensitively to external stimuli [1, 5, 6]. The biological systems in mesoscale characterized by the *soft inter connectivity and weak interactions* may appropriately be called the **bio-soft condensed matter** [1].

1.2 Keywords

Quasi-critical state, collective behaviour, self-assembly, bio-soft condensed matter, Coarse graining, non-equilibrium thermodynamics,

Chapter 2

Papers Reviewed

In this section I will keep the notes of the papers I have reviewed, or reproduced their results.

Paper Summary

Title: Topological data analysis distinguishes parameter regimes in the Anderson-Chaplain model of angiogenesis
Author(s): Nardini, Byrne
Published on: 2021-PLOS CB

2.1.1 Introduction

This paper studies the Anderson Chaplain [7] model of angiogenesis and partitions the parameter spaces based on the morphology of the vascular structure generated by the model. In other words, let $P = R^d$ be the parameter space of the model, M the space of all possible morphology for the vascular networks. Also, define the equivalence relation $\sim$ defined on the parameter space P to be

$$\text{for } p_1, p_2 \in P \text{ we have } p_1 \sim p_2 \qquad iff \qquad \mathcal{A}(p_1) \equiv \mathcal{A}(p_2),$$

where $\mathcal{A} : P \to M$ a mapping from the parameter space to the morphology space. The $\equiv$ is yet another equivalence relation defined on the morphology space M where for $m_1, m_2 \in M$ we write $m_1 \equiv m_2$ if and only if m_1 and m_2 has the same topological characterization. These topological characterizations are computed using the topological data analysis techniques.

2.1.2 Method

Chaplain-Anderson model of angiogenesis used in this paper keeps track of the spatio-temporal evolution of three variables: endothelial tip cells, tumor angiogenesis factor, and fibronectin.

Topological data analysis: Two filtration methods were used: sweeping plane method, and flooding filtration. The filtration is performed on the binary images generated with the Chaplain-Anderson model.

2.1.3 Useful facts

- The growth factors the cancer cells release when under low nutritient and oxygen: vascular endothelial growth factor (VEGF), platelet derived growth factor (PDGF), and basic fibroblast growth factor (bFGF).

2.1.4 Points that are not clear yet

(a) In the introduction, the authors claim that "The morphology of a vascular network can reveal the presence of an underlying disease, or predict the response of a patient to treatment", without any citation of explanation. I think this needs more discussion.

2.1.5 Useful papers cited

- Papers related to biology of the tumor induced angiogenesis [8, 9].
- More modern descriptions of the angiogenesis [10, 11]
- The role of the mechanical stress on the angiogenesis [12, 13, 14]
- Some old and classic models for the angiogenesis [7, 15, 16, 17].
- More detailed theoretical models for angiogenesis [18, 19, 20, 21].
- Alternative models of angiogenesis [22, 23, 24, 25, 14, 26, 27]
- Statistical and single scale methods to quantify the vascular networks [24, 28, 29, 30, 31]
- Biological angiogenesis experiments [32]
- Topological data analysis [**? ?**]
- Applied Algebraic Topology [**? ?**]
- Application of topological data analysis [**? ? ? ?**]
- Topological data analysis and agent based models [**? ?**]

2.1.6 Results