Third Year PhD in Physics Report

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1 Research Summary: Project and Side-Project

1.1 Main Project: Chromatin Compaction; a combined computational and experimental approach

Understanding the mechanistic details underlying DNA compaction is a very important question in Biophysics. In order to fit in the cell nucleus, the DNA winds itself around proteins, the histones, to form nucleosomes, which are the building blocks of chromatin. While the first level of compaction, the nucleosome, has been studied in atomic resolution, the topology of the chromatin fibre remains debated.

During my third year as a PhD student, I focused on the electrostatic interactions in chromatin. The high electric charge present on nucleosomes, their size and porosity make electrostatics and solvation crucial factors, affecting their interaction at all distances. Therefore, they have very important repercussions on the topology of the chromatin fibre at different orders of DNA compaction, and, by consequence, on genome replication and transcription. I conducted a comprehensive analysis concerning the interactions between nucleosome pairs at various distances. In addition to numerical estimates of the electrostatic interaction energy of nucleosomes at different relative distances and orientations, obtained within the Poisson-Boltzmann framework, I looked into the approximation of these energies by analytical asymptotic expressions. I also studied the contribution of solvation to nucleosome electrostatics and conducted a quantitative analysis on its porosity. Finally, I compared my findings with Zeta Potential experiments on nucleosomes in varying ionic conditions.

Furthermore, I conducted work specifically focused on the electrostatic interactions between the negatively charged DNA backbone, and the positively charged histone tails. The positioning of the histone tails impacts nucleosome stability, sometimes opposing the attractive pull of the histone core, locally deforming the DNA, and tuning DNA unwrapping. My analysis showed non-trivial, conformation-dependent interactions between histone tails and DNA, which greatly affect nucleosome dynamics, and deserve more attention in the study of nucleosome and chromatin dynamics. Specifically, I observed the following effects: In the regions where the histone tails protrude between the two DNA gyres, the latter are pushed closer together and away from the core. The H2A N-terminal tail can affect transcription, acting as an obstacle to PolymeraseII. The C-terminal tail causes visible changes in the electric field even with small conformational changes, highlighting its critical role.

1.2 Side-Project: Theoretical Mueller Matrix Microscopy

In collaboration with Dr. Aymeric Le Gratiet and Prof. Colin J. Sheppard.

We study the Mueller matrix and the Coherency matrix (a linear combination of the Mueller matrix and the Pauli matrices) in the context of light propagation and the application of these matrices in label-free microscopy. We investigate the properties of the Coherency matrix and interpret the physical information on light and physical samples that can be extracted from it. During the past year, we have made progress in the following research questions:

- We studied the characteristic polynomial of the Coherency matrix and proposed a method to extract its eigenvalues, based on the algorithm recently proposed by T. Tao and collaborators (ArXiv p. 1908.03795v3 (2019)).
- We studied backscattering through a medium on a perfect mirror, and proposed that backscattering from a uniform medium can be modeled as an effective uniform medium situated on a perfectly reflective substrate.
- We showed that use of a beam splitter in a reflectance polarization imaging system gives a Mueller matrix similar to the Sinclair-Mueller matrix for exact backscattering, and that the effect of the reflectance by the sample is canceled by the action of the beam splitter, so that the remaining features represent polarization effects present in addition to the reflection process.

2 List of Publications

[1] A. L. Gratiet, L. Lanzano, R. Marongiu, **Artemi Bendandi**, P. Bianchini, and A. Diaspro, “Phasor approach of mueller matrix optical scanning microscopy for label-free biological tissue orientation imaging,” *Under Review*, 2020.

[2] **Artemi Bendandi**, A. S. Patelli, A. Diaspro, and W. Rocchia, “The role of histone tails in nucleosome stability: an electrostatic perspective,” *Under Review*, 2020.

[3] C. J. R. Sheppard, **Artemi Bendandi**, A. L. Gratiet, and A. Diaspro, “Polarization in reflectance imaging: Effect of a beam splitter,” *Under Review*, 2020.

[4] C. J. R. Sheppard, **Artemi Bendandi**, A. L. Gratiet, and A. Diaspro, “Eigenvectors of polarization coherency matrices,” *Journal of the Optical Society of America A*, vol. 37, p. 1143, June 2020.

[5] **Artemi Bendandi**, S. Dante, S. R. Zia, A. Diaspro, and W. Rocchia, “Chromatin compaction multiscale modeling: A complex synergy between theory, simulation, and experiment,” *Frontiers in Molecular Biosciences*, vol. 7, Feb. 2020.

[6] C. J. R. Sheppard, **Artemi Bendandi**, A. L. Gratiet, and A. Diaspro, “Polarization in reflectance imaging,” *Journal of the Optical Society of America A*, vol. 37, p. 491, Feb. 2020.

[7] A. L. Gratiet, M. d’Amora, M. Duocastella, R. Marongiu, **Artemi Bendandi**, S. Giordani, P. Bianchini, and A. Diaspro, “Zebrafish structural development in mueller-matrix scanning microscopy,” *Scientific Reports*, vol. 9, Dec. 2019.