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Many infectious diseases are due to viruses that are able to enter and reproduce themselves in a living organism, such as the human body. Moreover, viruses can migrate from one organism to another causing infectious diseases, which have tremendous societal and economic impact. The means of virus migration can be different, for example, through an air, solid or liquid medium. Moreover, viruses can cause common flues, which often do not require treatment. However, many death-threatening diseases have been attributed to particular viruses. A well-known example of such diseases is the Ebola virus, which has posed an international health threat. Another example is HIV, which causes AIDS. These are only two of many possible examples, where current treatment can be inefficient. Therefore, it is important to understand how viruses are formed and ways of dissociating their structure or hindering efficiently their function within organisms.

A virus consists of a capsid, which is formed by proteins known as capsid proteins. These proteins form oligomers, which self-assembly into capsids resembling nano-containers of high symmetry (e.g., icosahedral capsids, rod-like capsids) that can carry genome, for example, single-strand (ss) or double-strand (ds) RNA or DNA. Viruses are the simplest form of life being able to naturally enter a cell and self-replicate within the cell. Knowing better how they form, what their mechanical properties are, and what conditions are required for dissociating their strurcture, certainly provides the fundamental knowledge for developing more efficient antivirus therapies. Additionally, viruses are an excellent example of self-assembly, which has been already realised in vitro. Thus, the self-assembly of virus capsids could also inspire the advanced manufacturing of bio-inspired soft materials, which can also behave like viruses entering naturally into a cell and delivering the chemical agents where is needed. Moreover, understanding the self-assembly of virus capsids contains also a philosophical aspect: Can we achieve the functionality of basic living organisms based on the self-assembly of biological molecules?

Apart from highly symmetric structures encountered in nature, such as the case of viruses, there are other forms of protein aggregates that are equally harmfull for organisms by hindering the normal function of various biological processes in the human body. For example, α-synuclein is a highly presynaptic protein, which can form pathological aggregates being associated with amyloidogenic neurodegenerative diseases. The accumulation of α-synuclein is the major component of these pathological aggregates in the central nervous systems, known as Lewy bodies. These aggregates are linked with Parkinson's and Alzheimer's diseases, dementia with Lewy bodies, diffuse Lewy body disease, and multiple system atrophy. Similarly to virus capsids, it is interesting to understand the mechanisms of pathological aggregation and identify conditions of preventing the formation of such structures or find ways to dissociate these pathological aggregates. The fundamental knowledge of the mechanisms underlying these processes will aid at the design of efficient thearapies for amyloidogenic neurodegenerative diseases.

In the proposed research, we will employ computer simulations to elucidate the mechanisms of protein self-assembly in the context of virus capsids and α-synuclein aggregates. The length and time scales required to describe such processes are very large to justify the use of all-atom simulations even if we could use the world's largest supercomputers. For this reason, we use coarse-grained models, where unnecessary degrees of freedom are smeared out. The aim is to understand and describe fundamental aspects of these processes, which are relevant for a broad range of protein aggregation phenomena in solution conditions, as well as at different interfaces. Computer simulations based on coarse-grained models can capture the universal mechanisms that control the self-assembly and aggregation processes. Moreover, they can identify the most probable molecular pathways towards intermediate and final self-assembly structures. An important advantage of computer simulation is the exquisite ability to define accurately and control various parameters that influence self-assembly and aggregation processes. This offers the possibility of isolating key elements of the mechanisms, and, also, identifies individually effects due to change of thermophysical conditions, application of mechanical stress, increase in protein concentration, etc. Our research is based on a model which is applicable in a broader area of protein aggregation phenomena providing a fundamental tool for interpreting such phenomena. Hence, many researchers in this field will benefit via a better understanding of these phenomena, while we expect that our coarse-grained model will be used for a broader range of systems in the context of protein aggregation and self-assembly. Our computer simulations will be implemented and run on state-of-the-art computers equiped with graphic cards (GPGPUs) and multiple CPUs.