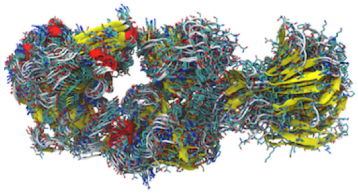

IV ASBioSim – Advanced School on Biomolecular Simulation: Protein Engineering with Rosetta, from fundamental principles to tutorials
05 to 10/May, 2019, Recife/PE, Brazil

Integrative biology to unravel the flagellar motility apparatus of *Leptospira*

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Abstract:

The bacterial flagellum is a complex multi-protein machine that drives translational movement in almost all motile species. Coupled with sensory transduction systems, bacteria can react to environmental cues, swimming towards beneficial sites and away from noxious ones. Spirochetes are a Phylum of bacteria that includes agents of several deadly ailments (syphilis, leptospirosis, etc). In stark contrast to most flagellated bacteria, Spirochetes bear endo-flagella, *i.e.* with filaments that remain confined within the periplasm instead of penetrating the outer membrane. Spirochetal flagella are nevertheless essential for swimming, probably by some kind of link to the singular screw–like cell morphology. *Leptospira* species display only two endo-flagella, sub-terminally attached to each end of the cell and, resulting in an attractive model to study spirochetal locomotion. Swimming direction is correlated to the sense of motor rotation on the flagella basal bodies. In addition, purified filaments show a typical highly super-coiled architecture, as in a spring. In contrast to the well-studied filament from *Salmonella enterica*, which is assembled by polymerization of a single protein species (FliC), the filaments from *Leptospira* are much more complex, including four isoforms of flagellin, and several different sheath proteins. Many questions remain regarding the structure of the spirochetal flagellar filament and how endo-flagella trigger whole cell rotation. We have started addressing these questions by an integrative approach, combining genetic manipulation of *Leptospira biflexa*, high-resolution crystallography of flagellar components and cryo-electron tomography of its entire filament. We have thus unveiled a unique asymmetric architecture of the sheath proteins around the flagellin core, inducing a supercoiled filament structure.