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The computational challenges in Life Sciences

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Life sciences is one of few areas of research where the complexity of the problems grows faster than our ability to deal with them from a computational point of view. Massive genomic projects have yielded detail sequence information on all the species of human interest and we are now deriving meta-genomic information of complex ecosystems, including for example the human digestive system. In a near future we might face the pangenomic scenario, where sequence information of all the human beings might be accessible. In parallel, to the genomic revolution, system biology projects are putting all this sequence data in the proper cellular context, building entire networks aimed to explain the chemical complexity of life. The third axis structural genomic projects are increasing the structural knowledge on biological machines opening then the possibility to modulate on their actions and by extension on the entire cellular functioning.

During my talk I will try to draw the exciting, but scaring scenario of the research in biology, trying to outline the main topics where help from computers is needed. I will provide examples of how current computer platforms can help to derive biologically-relevant information and I will emphasize the complexity of the problem from the computational point of view.

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