

Benjamin BOYER

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Work Experience

- PhD in Theoretical Biochemistry (CNRS) 2010-14

Realized at the LBT (laboratoire de Biochimie Theorique, Paris), this work included:

- Creation and implementation of new algorithms for 3D modeling and study of molecules, specifically DNA and helical protein.
- Using, maintaining and developing Ptools, a C++ and Python library for molecular modeling and docking.
- Communicating and collaborating with people in different field of expertise, in an international context (including 6 month of work at the Technical University of Munich)

- Teaching (Université Paris Diderot) 2010-14
Python Programming, Javascript, Molecular modeling

- Six month internship at the LBT (CNRS) 2010
on developing coarse-grain docking methods with flexible DNA for predicting protein-DNA complex.

- Six month internship at Roslin Institute (Scotland) 2009
on simulating the flow in biological pathway with Petri net. First part consisted of developing the method using Python for prototyping and Java for developing a plug-in. The second part consisted at implementing and optimizing (parallelism, interfacing with C,...) the method in BioLayout express3D, a Java software for visualizing gene expression in 3D.

- Three month internship at Institut Jacques-Monod 2008
in the research team “Modeling in integrative biology” on a meta-genomic analysis of the Sargasso Sea using Python and Bash.

Education

- Phd in Theoretical Biochemistry (CNRS) 2010-14
- Master in Bio-informatics at the University Denis Diderot-Paris 7 2008-10
- Licence's degree in Bio-informatics at the University Denis Diderot-Paris 7 2005-08

Publications

Yang D, Boyer B, Prévost C, Danilowicz C, Prentiss M. 2015. *Integrating multi-scale data on homologous recombination into a new recognition mechanism based on simulations of the RecA-ssDNA/dsDNA structure*. Nucleic Acids Res. 43:10251-63.

Boyer B, Ezelin J, Poulain P, Saladin A, Zacharias M, Robert CH, Prévost C. 2015. *An integrative approach to the study of filamentous oligomeric assemblies*, with application to RecA. PLoS One. 10:e0116414.

O'Hara L., Livigni A., Theodoridis T., Boyer B., Angus T., Wright D., Chen S., Raza S., Barnett M., Digard P., Smith L., Freeman T. 2016. *Modelling the structure and dynamics of biological pathways*. PLoS Biology Vol: 14