Depiction of molecular fragments, their properties and chemical space for citizen science drug discovery

Project description

Citizen science has become more abundant during the past decade. A striking example is the scientific discovery game ***Foldit***, an online 3D jigsaw puzzle where players are invited to shake and wiggle the 3D structure of proteins in order to find the most stable conformations. The project has brought biological results and lead to collaborative development of new algorithms. The type of problem Foldit is tackling shares similarities, in terms of complexity, with drug design, justifying to undertake a citizen science approach to rational drug design.

The goal of the project is to develop a serious game that will allow the player to participate in human-centered rational drug design. The problem of optimization of drugs is complicated to undertake automatically because the chemical landscape that needs to be explored is multidimensional and the modifications do not sum up in a linear way. Challenges resemble those in protein folding, where foldit has shown that human analysis and intuition surpass computer algorithms. The scientific field to be explored comprises molecular structure, nonbonded interactions (between drug and target) and rational drug design.

A crucial step is to tackle the representation of chemical properties and space to guide players. The project involves the following:

- Representation of chemical properties and fragments. This feature will allow the player to intuitively apprehend 3D and 2D properties.
- Definition of druggable fragments space. Definition of suitable fragments for each type of drug-target interaction.
- Representation of the chemical space as a 2D map to be included in the game. This feature will allow the players to expand chemical space in the direction of unexplored possibilities and should facilitate collective intelligence.

Key preliminary work has already been carried out with the design of the UnityMol platform (unitymol.sourceforge.net) and the proof-of-concept serious game DocMolecules (https://youtu.be/5x2nazXoiKw), providing a solid foundation for this project.

About the host institute

The "Institut de Biologie Physico-Chimique" was created in 1930 by the Foundation Edmond de Rothschild. In association with the CNRS (Centre National de la Recherche Scientifique), a leading international scientific institution it offers an exceptional environment to scientists early in their career, with a dynamic international exposure animated by regular seminars and meetings. The Laboratoire de Biochimie Théorique is internationally recognized for developing and applying computational methodologies to solve biologically relevant problems. Its members are active in the fields of docking, atomistic and coarse-grained simulations tackling problems as protein/protein and protein/DNA interactions, dynamics and function of membrane proteins, protein folding and aggregation.

Closing date: 25 March 2017

Interested candidates should send a detailed CV and a statement of research interests as PDF documents, and have three reference letters sent to taly@ibpc.fr.

Executive summary:

When?	36 months starting September 2017
Where?	Laboratoire de Biochimie Théorique, Paris, France.
Team Leader:	Antoine Taly
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