BioISI Research Seminar

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Computational design of protein binders for the molecular recognition of biomarkers

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Protein biomarker detection techniques have become a basic tool in cancer management due to their fast, non-invasive analysis procedures. Typical probes for protein detection are antibodies, but their opimization is costly, time consuming, and does not allow for a control over the specificity of their binding site.
In this work we overcome the problem of designing probes capable of targeting a specific protein binding site by the computational design of peptides and nanobodies, as promising alternatives for biomarker recognition. We developed computational protocols for the generation of high affinity binders. The affinity of a starting binder towards the target biomarker was optimized iterarively by using an algorithm based on a combination of replica exchange molecular dynamics, clustering analysis, binding energy calculation, and replica-exchange Monte Carlo. We optimized peptides capable of capturing beta-2-microglobulin and lysozime, and nanobodies for the recognition of the breast cancer biomarker HER-2. Subsequently, we performed ad-hoc screening protocols for the thermal and colloidal stability of the selected mutants, as well as for the stability of the biomarker-binder complexes. All systems are being validated experimentally by our collaborators).

Host: Patricia Faísca - PBS

When: 17th March 2016, 12h00
Where: Building C3, Room 3.2.13
Faculdade de Ciências da Universidade de Lisboa - Campo Grande, Lisboa (Portugal)

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