

Designing PEAT to capture, share and analyse protein data

October 21 2010

University College Dublin researchers led by Conway Fellow, Dr. Jens Erik Nielsen have created a novel application that not only facilitates the analysis of experimental data generated in the course of a research project but also ensures that this valuable data is available for future use. The team described the application in an article published recently in the journal, *Nucleic Acids Research*.

PEAT (Protein Engineering Analysis Tool) is not simply another laboratory information management system, but has been designed to address specific tasks encountered in a typical protein engineering project while integrating data deposition in the process.

Proteins are often described as the building blocks within organisms given their central role in critical <u>cell functions</u>. When changes occur in the structure or function of proteins, diseases such as Alzheimer's or cancer can result. Consequently, a significant proportion of research efforts concentrate on dissecting, optimising or changing proteins in an effort to find new treatments for such diseases.

Vast amounts of data are generated annually through the protein engineering techniques used in the process of studying proteins. Although this valuable experimental data could be used in other research projects, there is no requirement to deposit it in a database before publishing and so it is unavailable for re-analysis or essentially 'lost' within the pages of a thesis or journal article.



Commenting on the benefits of PEAT, Dr. Nielsen said, "The task of data capture and database deposition is often seen as a tedious and unrewarding process. PEAT incentivises data storage by integrating the process with the analysis tools in a single application. I hope that researchers will see the benefits of using PEAT so that we can create and share high quality datasets on the connections between protein sequence, structure and function".

PEAT is written in the python programming language and, although still under active development, has been road tested on several projects within Nielsen's laboratory, and has been used to establish several online databases. Additional functionality specific to particular research projects can be implemented with specifically written plug-ins that allow users to tailor the functionality of PEAT to specific experiments, proteins or scientific questions.

This research is being funded through awards from Science Foundation Ireland, the Health Research Board, Higher Education Authority and a UCD Ad Astra scholarship. PEAT is available at <u>http://enzyme.ucd.ie/PEAT</u>.

More information: *Capturing, sharing and analysing biophysical data from protein engineering and protein characterization studies.* Damien Farrell, et al. <u>doi:10.1093/nar/gkq726</u>

Provided by University College Dublin

Citation: Designing PEAT to capture, share and analyse protein data (2010, October 21) retrieved 23 April 2024 from <u>https://phys.org/news/2010-10-peat-capture-analyse-protein.html</u>

This document is subject to copyright. Apart from any fair dealing for the purpose of private



study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.