The neXtProt knowledgebase on human proteins: current status

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ABSTRACT

neXtProt (http://www.nextprot.org) is a human protein-centric knowledgebase developed at the SIB Swiss Institute of Bioinformatics. Focused solely on human proteins, neXtProt aims to provide a state of the art resource for the representation of human biology by capturing a wide range of data, precise annotations, fully traceable data provenance and a web interface which enables researchers to find and view information in a comprehensive manner. Since the introductory neXtProt publication, significant advances have been made on three main aspects: the representation of proteomics data, an extended representation of human variants and the development of an advanced search capability built around semantic technologies. These changes are presented in the current neXtProt update.

INTRODUCTION

neXtProt (http://www.nextprot.org) is a web-based knowledge platform focusing on human proteins. Similarly to Model Organism Databases (MODs) which serve to collate data and provide an impetus for research on model species, the goal of neXtProt is to serve as a one-stop-shop for research on human proteins by providing a representation of the current state of knowledge in a manner that is at once both comprehensive and of high quality. Since the first publication on neXtProt (1), we have continued to expand the database. We have developed close collaborations with two major user groups: proteomics researchers, who use mass spectrometry techniques to identify the different protein forms present in biological samples and biomedical researchers working on elucidating how genetic variations in protein-coding sequences can lead to disease. Our recent work has been mostly focused on integrating data from these two areas of human biology, with extensive quality control procedures. Major efforts have been undertaken on the search and retrieval capacities of neXtProt in order to take into account the richness of annotations and evidences so as to support the retrieval of proteins based on highly precise criteria as well as to allow programmatic data access. The next sections of this paper describe these improvements in detail.

NEW neXtProt CONTENT

neXtProt continuously adds new content to the database. Table 1 displays the information contained in neXtProt as of October 2014. The major data sources include Bgee (2), HPA (3), Peptide Atlas (4), SRMAtlas (5), UniProtKB (6), GOA (7), dnSNP (8), Ensembl (9), COSMIC (10), DKFGFP-cDNA localization (11,12), Weizmann Institute of Science’s Kahn Dynamic Proteomics Database (13), and IntAct (14).

In addition to the data presented in Table 1, neXtProt provides (i) mappings of proteins to their Ensembl genomic transcripts on the human genome; (ii) associations with over 800 000 identifiers, including cDNA clone names encoding for the proteins, Affymetrix and Illumina DNA probe sets; (iii) cross-references to CCDS (15), HPRD (16); and (iv) abstracts of all articles from PubMed that are cited in human UniProtKB/Swiss-Prot entries as well as some cited by other resources such as Entrez Gene (GeneRIFs) (17), MINT (18), and PDB (19) and which have been computationally mapped to the relevant protein entry by the UniProt consortium, totaling over 400 000 references. We have also recently integrated a 3D structure visualization applet—BioViz—developed by BIONEXT (http://www.bionext.com). The current version of the applet allows users to zoom, select regions or position-specific annotations (such as post-translational modifications (PTMs)) and view them in the context of the 3D structure, in addition to...
FOCUS ON PROTEOMICS

HUPO, the Human Proteome Organization (http://www.hupo.org), is an international group that connects all laboratories using proteomics as an approach to characterize human proteins in healthy and disease samples. HUPO's Human Proteome Project (HPP; http://www.thehpp.org (20)) aims to make a comprehensive inventory of all proteins with respect to their existence, the different isoforms expressed, post-translational modifications as well as their abundance, distribution and subcellular localization. neXtProt has been selected as the knowledge resource for the HPP project (21). As such, neXtProt’s role within the HPP project is to integrate the results of the mass-spectrometry (MS) identification studies that are flagged as being part of HPP; provide metrics concerning the progress of the project (which proteins still need to be identified by proteomics); and represent the extent of our knowledge of human proteins’ properties and functions in the best possible manner.

PeptideAtlas (5), developed at the Seattle Proteome Center, is a close collaborator on the HPP project (4). PeptideAtlas collects raw results from proteomics experiments and reinterprets them using a uniform computational pipeline, the Trans-Proteomic Pipeline (22), with a stringent false-discovery rate cut off of 1%. PeptideAtlas provides peptide identification in biological samples, i.e. protein existence validation. PeptideAtlas has proteomics data from multiple tissues and fluids: plasma, urine, brain, kidney, heart, liver, lung, digestive system, pancreas, spleen, eye, breast, adrenal gland, urinary bladder and female and male reproductive systems. On its proteomics page, neXtProt presents peptides identified in experiments integrated by PeptideAtlas. Moreover, neXtProt displays the tissues in which a peptide was identified in the Evidences column of the table view. Another project of the Seattle Proteome Center is the SRMAtlas, an atlas of peptides detected by Selected Reaction Monitoring (23). This technique is currently the most precise method for quantifying peptides by mass spectrometry. SRMAtlas provides tools (i.e. synthetic peptides spectra) to allow protein identification and quantification in biological samples. As of October 2014, neXtProt displays the peptides validated by SRMAtlas (Figure 1).

neXtProt also integrates data directly from high-throughput studies. We have integrated 21 papers with post-translational modifications, covering several different types of modifications: phosphorylation, N- and O-glycosylation, sumoylation, ubiquitylation, acetylation and methylation. Again, only high quality data is loaded, based on stringent criteria that vary from paper to paper, but that usually require a protein false discovery rate (FDR) of 1% of less.

FOCUS ON VARIANTS

Across the whole spectrum of human population, there are millions of variations in protein sequences (24), most of which having no consequence on health. However a great challenge that derives from easier access to exome and...
whole genome sequencing is trying to identify those mutations that may cause a pathologic effect or increase the risk to certain diseases. With our expertise on human protein function, we have embarked on a project of annotation of protein variants implicated in hereditary cancers. To do so, we are developing an annotation platform to annotate protein function and mutant phenotypes, which is still at the prototypical stage and will be presented in a future publication. In order to annotate protein variants as exhaustively as possible, we have integrated mutations from the COSMIC database (10), and are in the process of integrating those from ClinVar (25). The variants we are integrating are those that affect protein sequence, and are of type: substitution, insertion and deletion.

Disease and cell line mappings

neXtProt strives to support interoperability with other resources by using standard vocabularies and ontologies whenever possible. When this is not possible, we construct vocabularies and mappings that we make publicly available on our FTP site. COSMIC uses its own internal classification system to describe diseases and cell lines. This led us to develop two resources, the Cosmosaurus and the Cellosaurus, to address this issue.

The Cosmosaurus: a mapping between COSMIC and the NCI Thesaurus

We have created a mapping between COSMIC and the NCI Thesaurus (26). This mapping is named ‘Cosmosaurus’. In COSMIC, each sample is described using four fields: ‘Primary site’, ‘Site subtype’, ‘Primary histology’ and ‘Histology subtype’. The Cosmosaurus treats each distinct combination of these four fields as a synonym (SY) for a NCI entry, defined by its NCI Thesaurus term (ID) and accession (AC). The mapping was developed in-house, with the invaluable help of COSMIC biocurators. An example of a Cosmosaurus mapping is shown below. In this case, four different combinations of COSMIC sample descriptions are mapped onto a single NCI term. The version of July 2014 contains 1706 COSMIC terms mapped to 736 NCI Thesaurus terms.

| ID          | Colorectal Tubular Adenoma |
|-------------|-----------------------------|
| AC          | C27456                      |
| SY          | large intestine, caecum, adenoma, tubular |
| SY          | large intestine, left, adenoma, tubular |
| SY          | large intestine, NS, adenoma, tubular |
| SY          | large intestine, right, adenoma, tubular |

The Cellosaurus: an extensive glossary of cell lines

Many of the data annotated in COSMIC come from cell lines. Unfortunately, there was no comprehensive standardized resource describing cell lines. To address this, we have developed a new controlled vocabulary, the Cellosaurus, which, as far as we know, is the most comprehensive resource on cell lines (Bairoch, in preparation). The Cellosaurus is constantly growing; the version of September 2014 contains over 32,000 cell lines from 240 species (74% from human, 14% from mouse), 21,000 synonyms and 23,000 publication references to over 6500 publications. COSMIC samples originating from a cell line are mapped to a Cellosaurus unique identifier.

FOCUS ON SEARCH AND DATA RETRIEVAL

We have completely restructured the neXtProt data model and infrastructure. The objective of these changes was to allow neXtProt users to precisely extract information that they are interested in; to manage list of proteins (originating from the results of searches, or created by users); and build analysis tools on top of neXtProt. Figure 2 gives an overview of the new neXtProt architecture and the technologies used.

With the new architecture, all the data in neXtProt is now accessible via a REST API. The REST API decouples the database from all our services; in particular, the search and...
Figure 2. The new neXtProt infrastructure. neXtProt implements the following software and packages: Spring: open source web application over Java (spring.io); Spring JDBC templates: thin API between database and data objects (http://docs.spring.io/spring/docs/3.0.x/spring-framework-reference/html/jdbc.html); PostgreSQL: database where sequences, annotations, evidences and terms, as well as user resources (profiles, saved lists and queries) are stored (http://www.postgresql.org); Lucene/solr: full-text search engine for simple search queries (http://lucene.apache.org and http://lucene.apache.org/solr); Jena: graph search API for complex search queries (http://jena.apache.org); and Virtuoso: to store RDF data and perform complex SPARQL search queries (http://virtuoso.openlinksw.com).

Figure 3. The neXtProt list manager can be used to save lists, make operations such as combining them, and export the entries contained in a list. The full entries can be exported, or only certain data, such as accession numbers, the overview, the general annotations, etc.
Figure 4. Example of a neXtProt advanced search. This query retrieves entries corresponding to proteins having a PDZ domain and that interact with at least one protein expressed in the brain. The query returns 129 entries. Results can be sorted according to gene name, protein name, protein family name, chromosome, accession number or protein length. The results can also be saved as list, and that list exported in different formats such as text, XML or JSON.

Figure 5. Examples of SPARQL queries available in the advanced search page. The examples cover a wide range of different queries and many incorporate counts of objects (for example, retrieve proteins having three disulfide bonds).
port files. Problems identified in a dataset are immediately communicated to the data source contributing to a virtuous circle and resulting in improved data quality. Many checks are also performed at each neXtProt release to ensure data integrity and retrievability, tool functionality as well as the proper implementation of new features.

**DATA AVAILABILITY**

Like any other neXtProt annotation, the variant data is available in our export files in XML and PEFF formats (described in (1)) on our FTP site ([ftp://ftp.nextprot.org/](ftp://ftp.nextprot.org/)). They can also be accessed from our API at [http://api.nextprot.org](http://api.nextprot.org). This content is available under the Creative Commons Attribution-NoDerivs License.

**CONCLUSIONS**

neXtProt is being built as a participative platform and we look forward to receiving users’ input for the future development of neXtProt. Next developments include the continued expansion of the types of data captured in neXtProt. We also wish to support users who will take advantage of our API to incorporate some of neXtProt data into new bioinformatics applications. This will allow these applications to benefit from our efforts in providing high-quality curated knowledge on human proteins.

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