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Domain: Vaccine Ontology

**AN OVERVIEW ABOUT THE VACCINE ONTOLOGY (VO)**

With extensive use of vaccines in both research and the clinic, it has become an urgent challenge to standardize vaccine annotation, integrate information about varied vaccine types, and support computer-assisted reasoning. To address this challenge, a collaborative community effort is initiated to develop a Vaccine Ontology (VO) to cover all aspects of the vaccine domain. Development of VO thus far has emphasized classification of vaccines and vaccine components, vaccination investigation, and host responses to vaccines. Vaccine-induced immune responses, vaccine adverse events, and vaccine protection against specific disorders are derived from the fundamental vaccine-host interaction and also represented in VO. This manuscript outlines our first VO draft. It highlights key challenges for future development in VO and sister ontologies such as Infectious Disease Ontology (IDO), Ontology for General Medical Science (OGMS), and Ontology for Biomedical Investigations (OBI), which they were planning to address jointly. VO has been used for a number of applications, including use of SPARQL scripts to query and compare different vaccines and in dramatically improving PubMed vaccine literature searching. VO is also being used to develop an ontology-based vaccine knowledgebase for efficient data integration in the Semantic Web.

Vaccine research, development, testing, and clinical use involve complex processes whose computational representation requires a large number of data types and significant data volume. A number of vaccine types are available; for example, live attenuated vaccines, subunit vaccines, and DNA vaccines. Vaccines are developed using multiple approaches including studies of gene and protein expression, molecular and cellular interactions, and tissue and whole-body responses, as well as in extensive epidemiological modeling. In the post-genomics era, many high-throughput techniques (*e.g.*, microarray or proteomics) are increasingly used to generate large amounts of data at a rapid pace. Currently there are more than 200,000 vaccine-related articles in PubMed. It is increasingly challenging to identify and annotate vaccine data

from this large and diverse literature which no one scientist or team can fully master. In addition to the wealth of peer-reviewed literature on vaccines, there are many public vaccine databases including the USA CDC Vaccine Information Statements system (http://www.cdc.gov/vaccines/pubs/vis/), the licensed vaccine information by the U.S. FDA (http://www.fda.gov/cber/vaccines.htm), and the Vaccine Resource Library (http://www.childrensvaccine.org/). These databases emphasize the clinical uses and regulatory oversight of existing vaccines. Was developed VIOLIN (http://www.violinet.org), a web-based vaccine database and analysis system to store and analyze research data concerning commercial vaccines and vaccines under clinical trials or in early stages of development. ,

GRAPH MODEL OF THE ONTOLOGY.

(A)

(B)
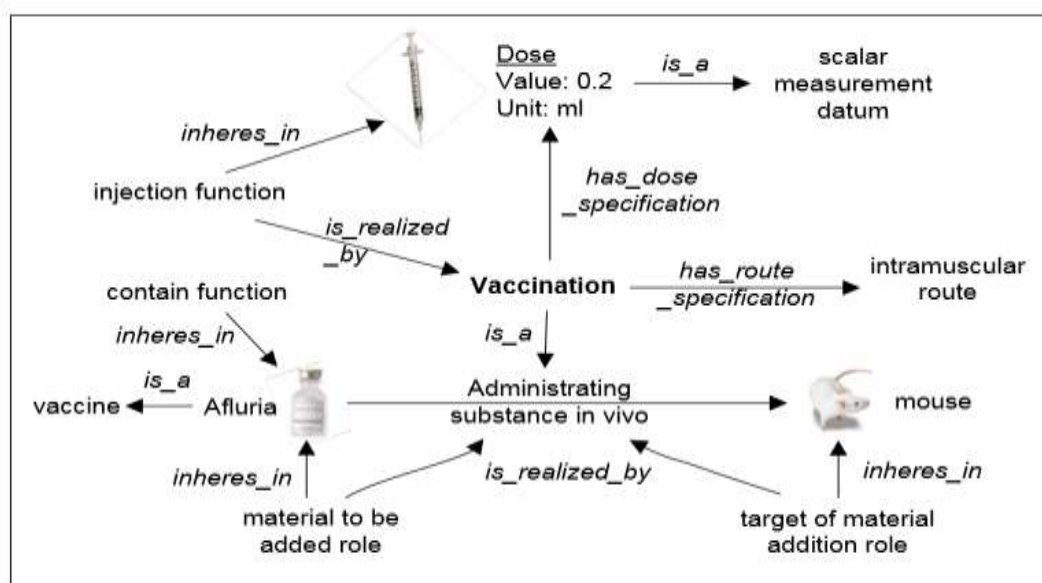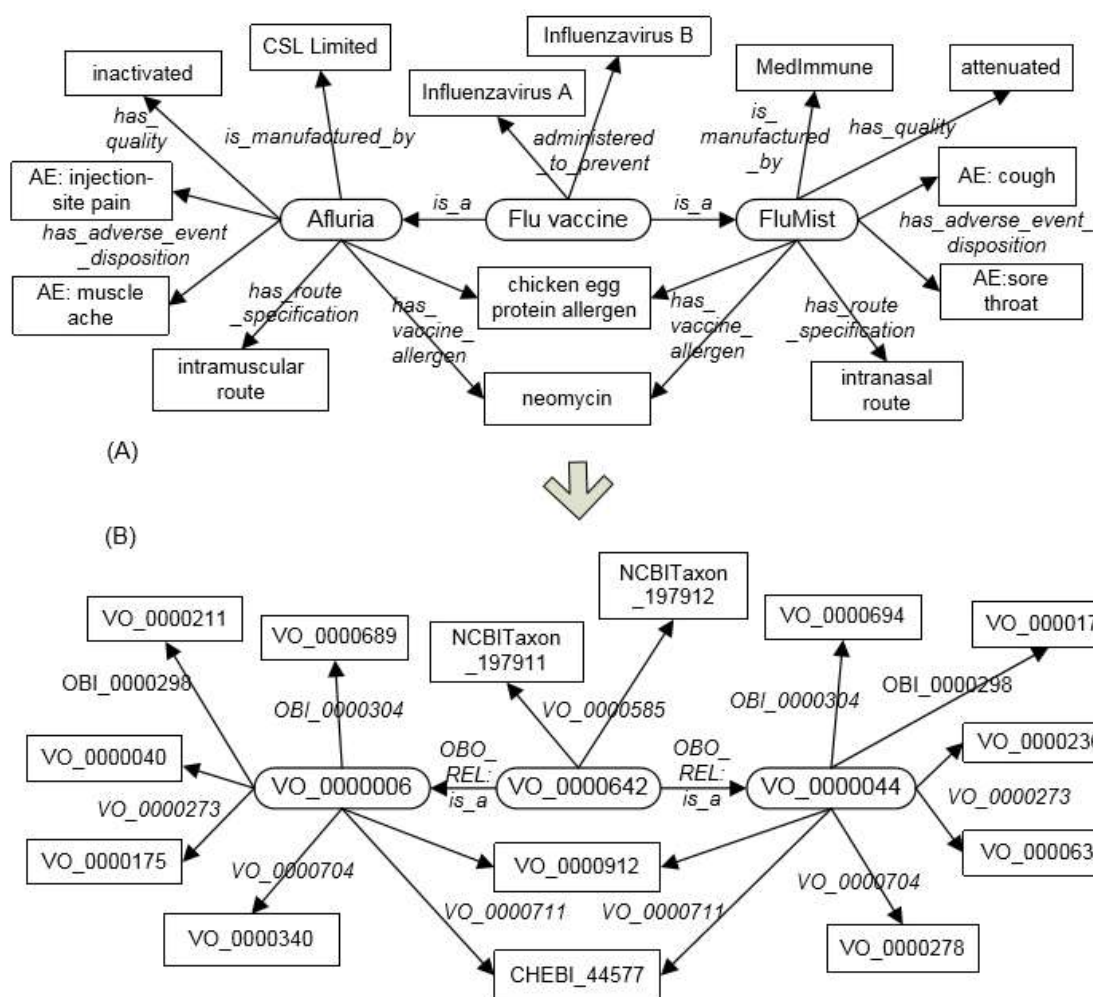
REFERENCES

[1]   The PubMed database. Available at http://www.ncbi.nlm.nih.gov/pubmed/

[2]   Xiang Z, Todd T, Ku KP, Kovacic BL, Larson CB, Chen F, Hodges AP, Tian Y, Olenzek EA, Zhao B, Colby LA, Rush HG, Gilsdorf JR, Jourdian GW, He Y. VIOLIN: vaccine investigation and online information network. Nucleic Acids Res l2008;36: D923-8.

[3]   Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, Harris MA, Hill DP, Issel-Tarver L, Kasarskis A, Lewis S, Matese JC, Richardson JE, Ringwald M, Rubin GM, Sherlock G. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. Nat Genet l2000;25: 25-9.

[4]   Smith B, Ashburner M, Rosse C, Bard J, Bug W, Ceusters W, Goldberg LJ, Eilbeck K, Ireland A, Mungall CJ, Leontis N, Rocca-Serra P, Ruttenberg A, Sansone SA,

Scheuermann RH, Shah N, Whetzel PL, Lewis S. The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. Nat Biotechnol l2007;25: 1251-5.

[5]   Smith B, Ceusters W, Klagges B, Kohler J, Kumar A, Lomax J, Mungall C, Neuhaus F, Rector AL, Rosse C. Relations in biomedical ontologies. Genome Biol l2005;6: R46.

[6]   Courtot M, Gibson F, Lister A, Malone J, Schober D, Brinkman R, Ruttenberg A. MIREOT: the Minimum Information to Reference an External Ontology Term. In: The 1st International Conference on Biomedical Ontology (ICBO 2009). Buffalo, NY, USA; 2009.

[7]   Smith B. The Logic of Biological Classification and the Foundations of Biomedical Ontology. In: Hájek P, Valdés-Villanueva L, Westerståhl D, editors. Logic, Methodology and Philosophy of Science. Proceedings of the 12th International Conference. London: King's College Publications; 2005, p. 505-520.

[8]   Harandi AM, Davies G, Olesen OF. Vaccine adjuvants: scientific challenges and strategic initiatives. Expert Rev Vaccines l2009;8: 293-8.

[9]   Consortium O. The modeling of biomedical experimental processes with OBI. . In: Bio-Ontolgies Workshop (at ISMB 2009). . Stockholm, Sweden; 2009. p. 1-4.

[10]   Zhou W, Pool V, Iskander JK, English-Bullard R, Ball R, Wise RP, Haber P, Pless RP, Mootrey G, Ellenberg SS, Braun MM, Chen RT. Surveillance for safety after immunization: Vaccine Adverse Event Reporting System (VAERS)--United States, 1991-2001. MMWR Surveill Summ l2003;52: 1-24.

[11]   Ruttenberg A, Rees JA, Samwald M, Marshall MS. Life sciences on the Semantic Web: the Neurocommons and beyond. Brief Bioinform l2009;10: 193-204.

[12]   Xiang Z, Zheng W, He Y. BBP: *Brucella* genome annotation with literature mining and curation. BMC Bioinformatics l2006;7: 347.

[13]   Hoogendam A, de Vries Robbe PF, Stalenhoef AF, Overbeke AJ. Evaluation of PubMed filters used for evidence-based searching: validation using relative recall. J Med Libr Assoc l2009;97: 186-93.