Biomedical and Health Informatics Lecture Series

Thursday, April 21, 2011
1:30 - 2:20 p.m., Room E-216

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"Semantics of Bioinformatics Components and Models"

In this talk I will summarize recent work from our group, which studies the semantics of biological processes. All of our work uses semantic web technologies (OWL & RDF) and reference ontologies to allow us to specify semantics via annotations to biological models of processes. We study processes over a wide variety of scales—from small to big and from fast to slow. Once we have semantic annotations, we can carry out more intelligent information retrieval of annotated components and models, as well as some forms of consistency checking. I will present recent results from our group both in (a) synthetic biology parts retrieval and (b) consistency checking of pathway biosimulation models (from BioModels). Finally, I will discuss our future plans to apply these ideas across multiple libraries of biosimulation models (CellML, BioModels, JSim), as well as to the Virtual Physiological Human project.

John Gennari, PhD, received his doctorate in Computer Science (in artificial intelligence) in 1990, and has been carrying out research in biomedical informatics since 1994, when he began working as a research scientist in the Stanford Medical Informatics group. His primary research focus is in knowledge representation and especially knowledge sharing. John is extensively published in the Biomedical Informatics literature, in application areas as diverse as clinical trial protocol management, health care guidelines, and cell-signaling pathways. Dr. Gennari joined the BHI faculty in 2002.

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NOTE: Podcasts from MEBI 590 Lecture Series talks for this quarter are available at
http://courses.washington.edu/mebi590/schedule.htm

Podcasts from previous quarters are available at
http://courses.washington.edu/mebi590/past.lecture.schedules.html