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Abstract.

The Q-UEL language of XML-like tags and the associated software applications are providing a valuable toolkit for Evidence Based Medicine (EBM). In this paper the already existing applications, data bases, and tags are brought together with new ones. The particular Q-UEL embodiment used here is the BioIngine. *The main challenge is one of bringing together the methods of symbolic reasoning and calculative probabilistic inference that underlie EBM and medical decision making. Some space is taken to review this background. The unification is greatly facilitated by Q-UEL's roots in the notation and algebra of Dirac, and by extending Q-UEL into the Wolfram programming environment. Further, the overall problem of integration is also a relatively simple one because of the nature of Q-UEL as a language for interoperability in healthcare and biomedicine, while the notion of workflow is facilitated because of the EBM best practice known as PICO. What remains difficult is achieving a high degree of overall automation because of a well-known difficulty in capturing human expertise in computers: the Feigenbaum bottleneck.*

Keywords:

Evidence Based Medicine, PICO, Systematic Review, epidemiology, Artificial Intelligence, Q-UEL.

1.   Introduction and Review of Inference.

1.1. Background.

Q-UEL was developed as an interoperability language to reconcile the diverse standards and ontologies in healthcare and biomedicine [1], and also the no less diverse approaches to using probability, today [1] and historically [2-9]. Q-UEL's own preferred approach to probabilistic inference borrows from physics and semantic theory