Statement of research

PROJECT: *Computer Prediction of Constitutive and Alternative Splicing*

We have recently developed a new computational approach called the Binary-Abstracted Markov Models or BAMM for genomic sequence classification. This approach is the basis of the PhD dissertation of my recent student, Dr. Samuel Shepard, which he defended in April 2010. The dissertation itself is already published at *http://etd.ohiolink.edu/view.cgi?acc_num=mco1271271172* and has been highlighted in various online media articles. Using the example of exon/intron discrimination we demonstrated how the genomic non-randomness of mid-range scales could be effectively utilized for sequence classifications. The paper describing our BAMM approach was published: Shepard S., McSweeny A., Serpen G., Fedorov A. "Binary-absrtacted Markov models and their application to sequence classification." *Nucleic Acids Research*, *2012, 40(11):4765-4773*.