

# *Curriculum Vitae*

## Michael Hamilton

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### Education

- PhD Computer Science, Colorado State University, Fort Collins, CO. (in progress)
- MSc Computer Science, Colorado State University, Fort Collins, CO. 2010
- BS Computer Science, Minor Mathematics, Colorado State University, Fort Collins, CO. 2006
- Russian Linguist Certification, Defense Language Institute, Monterey, CA. 2000

### Academic Appointments

- **Graduate Research Assistant** Colorado State University, 8/2007 - present
  - Predicting alternative splicing events in *Arabidopsis* using kernel methods
  - Identifying differentially expressed genes and splice forms from RNA-Seq data
  - Predicting calmodulin-binding proteins and interaction sites
- **NIH Summer Research Fellow** NIH/NLM/NCBI, Bethesda, MD, 5/2009-8/2009
  - Analyzing codon usage in the malaria parasite *Plasmodium*
- **NSF Summer Research Fellow** Max Planck Institute, Tübingen, Germany, 5/2008-7/2008
  - Structured output prediction of protein binding sites
- **Research Fellow** Iowa State University, Computational Biology Summer Institute, 6/2007-8/2007
  - Generating a structural model of human telomerase reverse transcriptase using *in silico* techniques
  - Predicting interaction sites on the model and assessing their biological relevance
- **Graduate Teaching Assistant** Colorado State University, 6/2006-present
  - Reinforcing students' exposure to Python, C, BASH, data structures, and algorithm analysis
  - Coordinating programming labs that emphasize clear and efficient implementation practices
- **Student Scientist (undergraduate research)** Colorado State University, 5/2006-8/2006
  - Conducting protein-protein interaction research using supervised machine learning techniques
- **Student Scientist (undergraduate research)** Colorado State University, 6/2005-8/2005
  - Reverse-engineering an Eclipse plug-in for testing UML designs
  - Designing and implementing a GUI to illustrate the sequence diagram of the testing process

# Publications

## Journals

- A.S.N. Reddy, Mark F. Rogers, Dale N. Richardson, Michael Hamilton, and Asa Ben-Hur. Deciphering the plant splicing code: Experimental and computational approaches for predicting alternative splicing and splicing regulatory elements. *Frontiers in Plant Genetics and Genomics* 3, 2012.
- C.D. Ross, B. McCarty, M. Hamilton, A. Ben-Hur, and E.D. Ross. A promiscuous prion: Efficient induction of [URE3] prion formation by heterologous prion domains, *Genetics*, 2009.

## Conferences

- M. Hamilton, A.S.N. Reddy, and A. Ben-Hur. Kernel methods for calmodulin binding and binding site prediction. In: *ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, 2011.<sup>†</sup>
- J. Lee, M. Hamilton, C. Gleeson, C. Caragea, P. Zaback, J. Sander, X. Li, F. Wu, M. Terribilini, V. Honavar, and D. Dobbs. Unexpected similarities in structure and nucleic acid binding sites of diverse telomerase proteins revealed by combining structure prediction and machine learning approaches. *Pacific Symposium of Biocomputing*, 2008.
- Trung Dinh Trong, Sudipto Ghosh, Robert B. France, Michael Hamilton, Brent Wilkins. UMLAnT: An Eclipse plugin for animating and testing UML designs. *Eclipse Technology Exchange Workshop*, in conjunction with *OOPSLA*, San Diego, USA, October 15-16, 2005.

## Refereed Posters and Extended Abstracts

- M. Hamilton, A.S.N. Reddy and A. Ben-Hur. SVM methods for prediction of calmodulin binders and binding sites. *Intelligent Systems for Molecular Biology*, 2010.
- Michael Hamilton and Asa Ben-Hur. A structured outputs method for predicting protein binding sites. *International Workshop on Mining and Learning with Graphs*, Helsinki, Finland, 2008.<sup>†</sup>
- Identifying DNA, RNA and protein binding interfaces in human telomerase. *16th Annual Growth Factor and Signal Transduction Symposium: Senescence, Aging and Cancer*, 2007.<sup>†</sup>
- Combining structural modeling, evolutionary information, and machine learning to improve prediction of nucleic acid binding sites in telomerase. *Fifth Annual Rocky Mountain Bioinformatics Conference*, 2007.
- Generating models as a platform for comparing functional and structural elements of telomerase. *Midwest Symposium on Computational Biology and Bioinformatics*, 2007.

<sup>†</sup> – presented

## Memberships

- Upsilon Pi Epsilon
- American Statistical Association
- International Society for Computational Biology
- Association for Computing Machinery

## References

Upon request