

## Curriculum Vitae/Resume

### Swetha Garimalla

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**Citizenship:** US Citizen

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## EDUCATION

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**Georgia Institute of Technology**, Atlanta, GA      Expected: May 2018  
Doctorate of Philosophy in Biological Sciences  
Minor: Statistics

**Carnegie Mellon University**,      May 2010  
Pittsburgh, PA  
Master of Science in Computational Biology

**Carnegie Mellon University**, Pittsburgh, PA      May 2008  
Bachelor of Science in Biological Sciences  
Minor: Chemistry

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## TECHNICAL SKILLS

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**Computer Programming:** Java, Perl, R, C++, C, Python, Bash  
Shell, Matlab, Mathematica, BioNetGen, Ruby, PHP, CSS, HTML,  
jQuery, Javascript, Common Lisp, CSS, Scala, CUDA C  
**Laboratory:** DNA extraction, isolation and analysis, ELISAS, enzyme  
assays, fluorescence microscopy, fractionation of cells, PCR and  
sequencing, protein isolation and purification, recovering specific  
cellular material, recrystallization, SDS-PAGE gel electrophoresis.

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## PUBLICATIONS/PRESENTATIONS

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Yin W, **Garimalla S**, Moreno A, Galinski MR, Styczynski MP. "A tree-like Bayesian structure learning algorithm for small-sample datasets from complex biological model systems." *BMC Systems Biology*. 2015 Aug 28.

**Garimalla S**, Kieber-Emmons T, Pashov AD. "The Patterns of Coevolution in Clade B HIV Envelope's N-Glycosylation Sites." *PLoS One*. June 24 2015.

Hogan WR, **Garimalla S**, Tariq S. "Representing the Reality Underlying Demographic Data." *International Conference on Biomedical Ontologies (ICBO)*, University at Buffalo, NY, July 28-30, 2011. Full length conference proceeding paper, accepted.

Hogan WR, **Garimalla S**, Tariq SA, Ceusters W. "Representing Local Identifiers in a Referent-Tracking System." (extended abstract), *International Conference on Biomedical Ontology*, Buffalo NY, July 28-30, 2011.

Pashov, Anastas, **Swetha Garimalla**, Behjatolah Monzavi-Karbassi, and Thomas Kieber-Emmons. "Carbohydrate targets in HIV vaccine research: lessons from failures." *Immunotherapy* 1.5 (2009): 1-18.

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## RESEARCH

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### **Georgia Institute of Technology** – June 2014 – Present

- Research involving the characterization of long-lived plasma cells (LLPC) through the integration of cell-type specific transcriptomic and epigenetic data, as well as LLPC bone marrow niche proteomic data from healthy control patients. The long-term goal of this project is to gain a more holistic understanding of the processes that are involved in the development and differentiation of B-cells into long-lived plasma cells in healthy in contrast with unhealthy (lupus, multiple myeloma, etc.) patients.
- Research involving the integration of various types of biological data (including transcripts, miRNA, and proteins) are received from MaHPIC (Malaria Host-Pathogen Interaction Consortium) related to various stages of *Plasmodium cynomogli* infection non-human primates, *Macaca mulatta*, to model *Plasmodium vivax* infection in humans. The goal of this project was to gain a more holistic understanding of host-pathogen interaction and host response during the malaria infection cycle.

### **University of Michigan** – February 2012 – May 2014

- Research involving development of a linear B-cell epitope predictor that can accurately predict linear B-cell epitopes given the primary amino acid sequence of a given protein. This is meant to only be a portion of a large-scale project to develop a discontinuous B-cell epitope predictor that will be able to predict non-linear B-cell epitopes given a primary amino acid sequence of a protein with Dr. Yongqun He.

- Research comparing coevolution of epitopic regions in comparison to nonepitopic regions under supervision of Dr. Yongqun He.

### **University of Arkansas Medical School – May 2009 – July 2011**

- Research involving the development of Biomedical Ontologies and Referent Tracking Systems for electronic health records under the direction of Dr. William R. Hogan
- Research involving HIV epitope prediction for vaccine development research through correlation with variability of residues and presence of mannose sites in relation to the presence of epitopes under direction of Dr. Thomas Kieber-Emmons and Dr. Anastas Pashov.
- Research involving protein expression of various proteins and their corresponding pathways between samples of breast cancer tissue and tissue that surrounds the cancer in order to determine where the proteins that show the greatest difference in expression are largely related to metabolic processes - more specifically, the glycolytic pathway, which has been noted to play a bigger role in energy production in cancer cells as has been described by the Warburg hypothesis under supervision of Damir Herman

### **Carnegie Mellon University - October 2007 – June 2010**

- Aided in the modification of virus capsid assembly simulator in the field of parameter optimization under instruction of Dr. Russell Schwartz.
- Worked on a solo project in which I designed the algorithm for this project. Utilized parameter optimization and machine learning techniques to predict the probability of a residue and/or motif in a protein being a part of a B-cell epitope to draw information on the possibility and future direction of vaccines for HIV.

### **University of Pennsylvania - June 2007 - August 2007**

- Analyzed, programmed and determined the correlation between gene expression data and cis-regulatory modules (CRMs) under the direction of Dr. Sridhar Hannenhalli and supervision of Dr. Larry N. Singh. I wrote and modified several software modules in C++ under LINUX and conducted extensive data analysis of gene expression across different cis modules.
- Worked on creating a program in Perl to determine correlation between gene expression/repression data and spatial location of genes under the direction and supervision of Dr. Sridhar Hannenhalli. This project also involved extensive data analysis and validation of gene expression data.

## **Center for Genomic Sciences - September 2006 - February 2007**

- Aided in the study of molecular mechanisms of potential genes and their role as pertaining to the formation of biofilm and virulence of *Streptococcus pneumoniae* and *Pseudomonas aeruginosa* under direction and supervision of Dr. Nalini Mehta.
  - Aided in the study, determination, and characterization of core genes for strains of *Streptococcus pneumoniae* and *Streptococcus aureus* under direction of Dr. Luisa Hiller
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## **PROFESSIONAL PROJECTS**

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### **University of Michigan – May 2012 – Present**

- Automated analysis processes for various wet lab tests.
- Conducted the computational analysis of NextGen Sequence exome capture data.
- Architect of database and system, and developer for a multi-user information system that is utilized by the lab to keep track of cases, tests, results, and workflow.
- Creating and automating an analysis protocol for NextGeneration exome sequencing data.

### **Protech Solutions - August 2011- May 2012**

- Training programmers in basic bioinformatics techniques
- Bioinformatics consultant for ontology development
- Worked on developing a Protege Plug-in that supports the automatic modularization of OWL ontologies. using PATO as our modularization tool and integrating it in to Protege as a plug-in. As PATO was not considered to be used within an ontology development environment this project considers the full work-flow; it involves extracting, reusing and editing the modules. .
- I worked on developing a Protege Plug-in that supports the automatic extraction of "slices" from OWL ontologies. The plug in makes extensive use of the OWL API, SPARQL and Biportal Web services.

### **University of Arkansas for Medical Sciences – June 2009 – July 2011**

- Research involving the development of Biomedical Ontologies and Referent Tracking Systems for demographic data that is relevant to electronic health records
  - Development of Biomedical Ontologies and Referent Tracking Systems for representation of encounter, diagnosis, and procedural data that is relevant to electronic health records.
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