

Henry R. Moncada

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OBJECTIVE Job application

EDUCATION **Ph.D Computational Science,**
University of Texas at El Paso (UTEP), El Paso, TX, US, May 14, 2018, (GPA: 3.9)
“Parallelization and Scalability Analysis of the 3D Spatially Variant Lattice Algorithm”
Master of Science in Computational Science,
University of Texas at El Paso, El Paso, TX, US, May 14, 2016, (GPA: 3.9)
“Towards the Scalability and Hybrid Parallelization of a Spatially Variant Lattice Algorithm”
Master of Science in Applied Mathematics
University of New Mexico (UNM), Albuquerque, NM, US, Aug 1, 2009, (GPA: 3.83)
“Paratransgenic Vectors and their Potential Influence on the Dynamics of Chagas disease”
Bachelor of Science, Physics
Universidad Nacional Mayor de San Marcos (UNMSM), Lima, Peru, 1998
“Study of Structural Property for Reflectivity Modeling System Superlattices”

COMPUTER SKILLS Operating Systems: *Linux, Windows*

High-Level language (HLL) :

- *Proficient in C/C++, Python 2.7/3, FORTRAN 77/90, and Matlab/Octave*
- *Familiar with R and Maple/Maxima*
- *Familiar with MPI/OpenMP - for CPU multicore clusters*
- *Familiar with CUDA - graphical processing units (GPUs)*
- *Familiar with OpenCL/OpenACC/Trilinos-Kokkos - Heterogeneous platforms (CPUs & GPUs)*

Version Control Software :

- *GIT and Subversion (SVN)*

Concurrent and Parallel Programming Tools

- *Parallel Performance Evaluation*
 - *Lightweight Profiling Library for MPI (mpiP)*
 - *Cray Pertools*
 - *Tuning Analysis Utilities (TAU)*
- *Computational Math Libraries*
 - *Basic Linear Algebra Subprograms (BLAS) & Linear Algebra PACKage (LAPACK)*
 - *Fastest Fourier Transform in the West (FFTW)*
 - *SuiteSparse(CSPARSE)*
 - *Portable, Extensible Toolkit for Scientific Computation (PETSc)*
 - *Kokkos - Trilinos Core Kernels Package.*

LANGUAGES

Spanish, *native language*
English, *speak fluently and read and write with high proficiency*

RESEARCH EXPERIENCE

Postdoc Volunteer, Bioinformatics Department - UTEP

- *Systemic Bioinformatic analysis requires shepherding files through a series of transformations, called a pipeline or a workflow. These workflow data products are used to extract data and highlight relevant information than biologists examine which then validate targeted experiments and support hypothesis or help to formulate a new one. These new custom bioinformatic analysis tools require programmers to implement new methods and/or put together existing ones to build new data analysis frameworks (data flows commonly known as bioinformatic pipelines). These transformations are done by executable command-line third-party software written for Unix/Linux-compatible operating systems. The increasing amount of DNA sequences has intensified the need for robust workflows for interpreting a range of biological phenomena.*

Fall 2017 and Spring 2018 - Oak Ridge National Laboratory & University of Texas at El Paso

- *I had been working on the computer code implementation of the 3D Spatially Variant Lattice (SVL) algorithm.*
 - *The SVL written program codes were implemented on TACC Stampede 2 supercomputer.*
 - *The SVL code was written using C in conjunction with PETSC and FFTW tools.*
 - *We study the Scalability and performance of the SVL on Stampede 2 architecture (KNL and SKX).*

Summer Internship 2017, Oak Ridge National Laboratory - Computational Science Institute - Future Technologies Group

- *I had been working on the benchmark of the High-Performance Geometric Multigrid (HPGMG) and PETSC 2D Spatially Variant Lattice (SVL) algorithm.*
 - *The following computer tools were used,*
 - *PIN for the instrumentation framework and MIC instruction-set architectures were used to benchmark a serial version of the HPGMG and SVL code.*
 - *PIN will provide an API that extracts away the underlying instruction-set idiosyncrasies and allows context information such as register contents to be passed to the injected code as parameters.*
 - *PIN saves and restores the registers that are overwritten by the injected code, so the application continues to work.*
 - *This work was developed using ORNL HPC server EXCL and NEWARK/MEGATRON supercomputer.*

Summer Internship 2015, Border Biomedical Research Center Bioinformatics Department-UTEP

- *I have been working on the development PYTHON and WED-PYTHON application for DNA - Genomics and Sequence Analysis.*
- *A performance evaluation using HTCondor job scheduler for workload management and multiple submission jobs.*
 - *Project focus on development python bioinformatics computational tools to predict genomic structures and analyze molecular sequences for the G protein-coupled receptors (GPCRs). GPCR constitute a large protein family of recep-*

tors that sense molecules outside the cell and activate inside signal transduction pathways and cellular responses.

- There are an incredible amount of GPCR-DNA data available to be analyzed and used on the computational model.
- A performance evaluation of HTCondor job scheduler system using Python and BLAST to evaluated DNA sequences.

Summer Internship 2014, Electronic Structure Group - Physics Department - UTEP

- In the summer 2014, I was working on the performance evaluation and analysis of the Naval Research Laboratory Molecular Orbital Library (NRLMOL) code, Poisson subroutines in Fortran.
 - The NRLMOL code is a set of parallel programs developed by Mark Pederson and collaborators written in FORTRAN 77 with updated subroutines written in FORTRAN 90 and C.
 - It is used on the calculation of electronic structure for large molecules and clusters, group symmetry and PBE exchange-correlation functional, etc.
 - NRLMOL is an existing massively parallel code based on multicore processors that can reach a very good flops performance which I compiled and executed using NERSC-HOPPER petaflop system on Cray XE6 supercomputer.
 - The goal of the internship was to develop an understanding of NRLMOL code on a high-performance platform, and moreover identify possible bottlenecks and give suggestions for their improvement.
 - A performance evaluation was done with the help of PERFTOOLS, which is a performance evaluation library available at NERSC. PERFTOOLS is used to profile the NRLMOL code.
 - The profile information is used to identify possible performance bottlenecks, load imbalance and tracing as well as to determine the possible locations and causes of those bottlenecks.
 - The results given by PERFTOOLS about the NRLMOL code can be used to improve the performance of the NRLMOL and develop a potential and efficient simulation for a particular HPC platform.

Math Department, UNM, Albuquerque-NM

- Bacterial Symbiosis and its influence on the Dynamics of Chagas Disease.
 - Developed a numerical approach to simulate the introduction of genetically modified bacterial symbiont into natural populations of Chagas disease vectors.
 - This approach utilizes the coprophagic behavior of these insects, which is the way in which the symbiont is transmitted among bug populations in Kissing Bugs nature.
 - Implement the numerical simulation in MATLAB

Physics Department, UNMSM, Lima-Peru

- Study of Structural Property for Reflectivity Modeling System Superlattices.
 - Implement a numerical model in FORTRAN based on the dynamical diffraction theory to model the experimental reflectivity.
 - Numerical model includes material mixing at the interface, interface roughness and random variation of component thickness.

- The numerical model reveals the structural parameters of the device, such as the multilayer period, the individual layer thickness, the width of the interface and the optical constants.
- The numerical model is used to study superlattices devices composed of hydrogenated amorphous silicon/silicon carbide ($a\text{-Si:H}/a\text{-Si}_{1-x}\text{C}_x\text{H}$) and silicon/germanium ($a\text{-Si:H}/a\text{-Ge:H}$), deposited by the plasma-enhanced chemical vapor deposition (PECVD) technique, were analyzed using small-angle X-ray diffraction.

Geophysical Institute of Peru (IGP), Lima-Peru

- Department of Emergency-Training program and earthquake data management and earthquake effect in real time.
 - Record daily earthquake data collection, earthquake wave propagation gives information about the earthquake location of earthquake effect in real time.
 - Estimation of earthquakes location by measuring of the wave ground response of the compressive P wave, the shearing S wave.
 - Rolling surface wave motions recorded by seismographs stations.

DOCTORAL RESEARCH TOPIC

The purpose of this research is to design a faster implementation of the spatially variant that improves its performance when it is running on a parallel computer system. The spatially variant is used to synthesize a spatially variant lattice for a periodic electromagnetic structure. The spatially variant has the ability to spatially vary the unit cell orientation and exploit its directional dependencies. The spatially variant produces a lattice that is smooth, continuous and free of defects. The lattice spacing remains strikingly uniform when the unit cell orientation, lattice spacing, fill fraction and more are spatially varied. This is important for maintaining consistent properties throughout the lattice. Periodic structures like a photonic crystal or metamaterial devices can be enhanced using the spatially variant to unlock new physics applications. Our current effort is to write a portable spatially variant code for parallel architectures. To develop and write the code, we pick a general-purpose programming language that supports structured programming. For the parallel code, we use FFTW for handling the Fourier Transform of the unit cell device and PETSc (Portable, Extensible Toolkit for Scientific Computation) for handling the numerical linear algebra operations. Using Message Passing Interface (MPI) for distributed memory helps us to improve the performance of the spatially variant code when it is executed on a parallel system.

SKILLS

Problem Solving

- Excellent analytical and logical reasoning skills. Able to multi-task. Can learn new skills quickly. Able to lead or work within a group environment.

Teaching skill

- Enjoy working and helping students to increase their motivation to study math and physics and develop and improve new learning skills to solve math and physics problems.

HONORS

- Kappa Mu Epsilon (Math Honor Society)
- SIAM Student Chapter vice-president 2013
- SIAM Student Chapter president 2014

- UTEP SIAM Seminar coordinator (2015, 2016)
- Member of Student Advisory Committee for the International Student Fellowship at the First Baptist Church El Paso (2014)
- Recipient of Good Neighbor Scholarship during the following year period 2012-2016

PUBLICATIONS *Reflectivity modeling of Si-based amorphous superlattices; Superlattices and Microstructures. E. L. Zevallos Velsquez, **H. Moncada L.**, UNMSM-Per, M. C. A. Fantini USP-Brazil, Reflectivity modeling of Si-based amorphous superlattices; Superlattices and Microstructures, Vol 28, No 3, 2000.*

*XSEDE Conference, 2016 Miami, FL. Poster Presentation, Towards the Scalability and Hybrid Parallelization of a Spatially Variant Lattice Algorithm **Henry. R. Moncada L.**, Shirley V. Moore, Raymond C. Rumpf*

*Under Review: Parallelization and Scalability Analysis of the 3D Spatially Variant Lattice. **Henry R. Moncada**, UTEP; Shirley V. Moore, ORNL; Raymond C. Rumpf, UTEP.*

REFERENCES

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Senior Research, Computer Science and Mathematics Division, Oak Ridge National Laboratory.

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Professor, Department of Electrical and Computer Engineering, Director EM Lab Schellenger, University of Texas at El Paso.

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Professor, Mathematical Sciences, Director, Bioinformatics and Computational Science Programs Director, BBRC Bioinformatics Core, University of Texas at El Paso.