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Education

1993	**Post.Doc.**,	SUNY Upstate Medical University, Syracuse NY, Cardiac Arrhythmias
1992	**Ph.D.**,	Montreal University, Quebec, Canada, Computational Biomedical Engn.
1985	**M.S.**,	Laval University, Quebec, Canada, Physics
1982	**B.S.**,	Laval University, Quebec, Canada, Engineering Physics

Positions held

2013-	Complex Biosystems Inc.	Baldwinsville NY.
2013-2014	Visiting professor of Pharmacology	SUNY Upstate Medical University
2006-2012	Associate professor of Bioengineering	Binghamton University
2005-2006	Associate professor of Radiology	SUNY Upstate Medical University
1998-2005	Assistant professor of Pharmacology	SUNY Upstate Medical University
1994-1998	Research assistant	SUNY Upstate Medical University
1987-1989	Software Engineer	Clinical research institute, Montréal Canada
1985-1987	Computer Science Consultant	DMR (now Fujitsu), Québec & Montréal, Canada

Professional experience

Complex Biosystems Inc., product development: Scientific data viewer, development instruments, Jan. 2013-

Develop scientific data viewer in C/C++, based on the OpenGL and X-Motif libraries. The viewer is supplemented with development instruments, i.e.: tools to generate instructions as well as graphics windows, source code analyzer, and minimal debug facilities. Currently in test in several of our contracts.

Contact: See contracts below

Complex Biosystems Inc., service development: HPC platform for scientific and engineering applications, Jan. 2013-

Conceived the HPC platform service that consists in: (i) server configuration, (ii) server commissioning, (iii) added functionality for simulation and visualization in science & engineering, (iv) remote support with high availability insurance.

Contact: See contracts below.

Complex Biosystems Inc, contracts with: Department of Pharmacology SUNY Upstate Medical, HPC platform for pharmacology applications, April 2015-

Repaired, commissioned and now support HPC server for the Pharmacology Department of the SUNY Upstate Medical University. This is a rack mounted server with 4 and 12 cores AMD processors, local disks in each blade, hardware raid controllers and a 10 GB interconnect. The server includes functionality to: compile & run parallel jobs, analyze performance, visualize large volume of 3D data, and analyze simulation results. This server is currently used to: simulate light interaction with tissue, reproduce fluorescence properties of molecular light emitting voltage sensitive probes, simulate traveling electrochemical waves in cardiac tissue, process of laser scanning confocal microscopy images for geometric modeling.

Contact: Arkady Pertsov, see list of references.

Complex Biosystems Inc, contract with: Department of Radiology SUNY upstate medical, Dec 2016-

- *HPC platform for Nuclear Medicine applications, Dec 2016 - March 2017.*

  We networked and aggregated high end workstations into a cluster. Each work station is equipped with processors totaling 8 to 32 cores each, computing GPUs, graphic GPUs, 64 to 128 GB of memory. The cluster is set up for development and production. The nodes run on LINUX Ubuntu, one of them also run Windows 10 (dual boot). Resource management software, slurm `https://slurm.schedmd.com/`, supports job management.

  The cluster is linked to clinical PET scanners through a DICOM server we implemented. It is used for PET image reconstruction, visualization, and the Nuclear Medicine simulation, e.g., high energy radiation interaction with human body.

  Contact: Andrzej Krol, see list of references.

- *Custom software development. Application to simulate gamma-camera receptors, Feb 2017-*

  The application simulates gamma-photons traveling in LSO, LYSO, BGO or BSO crystals; their conversion to optic photons; and the optic of photons transport in crystals. The application was developed around the C++ Geant4 Library `http://geant4.cern.ch/`, and our product, xScheme, for visualization.

  The simulator takes into consideration the optic properties of the crystal surface (e.g roughness) and reflectors surrounding them. At this time we reproduced data generated by the National Berkely laboratory. Simulations are undergoing to determine the mechanical work to do on the crystal surfaces in order to minimize the dispersion of photon arrival time on photomultipliers placed on the crystal surfaces. Results will be presented at the SPIE Medical Imaging conference of Feb 2018

  Contact: Andrzej Krol, see list of references.

- *Custom software development. Optimize, for radioactive tracer dose, the PET image reconstruction pipeline of the Siemens Biograph scanner. February to May 17*

  The objective of this study was to determine whether the Siemens Biograph PET scanner owned by the SUNY Upstate Medical University could be operated in a manner to generate diagnostic quality images with a lower radioactive tracer dose. Through a research agreement

with Siemens the Department has access to the software library at the basis of their scanner image reconstruction.

This library is installed on the Radiology LINUX cluster (see above) and enables us to perform a full reconstruction from photon counts on the PET gamma-camera receptors. Using this infrastructure, in collaboration with Krol I: analyzed the reconstruction pipeline, modified its original version, and reconstructed images at half (simulated) radioactive tracer dose, indeed 5 different versions. Most important changes were filtering prior to back projection and conditions for convergence in the OSEM algorithm. Reconstructed images were loaded in the radiology imaging system (PACS) through our DICOM server for evaluation. Certified Radiologists concluded that one of our option produced images of diagnostic quality at half radioactive tracer dose.

Contact: Andrzej Krol, see list of references.

- *Custom software development. Implement high performance PET image reconstruction software aiming at reducing radioactive tracer dose. August 17-*

  The objective of this study is to improve the quality of PET image reconstructions such that radioactive tracer dose could be reduced without compromising the images diagnostic value. This is particularly important for the young population since bombarded with high energy radiation over an extensive period of time and at a critical development phase. The reconstruction is implemented within the infrastructure described in the above contract, on the Radiology LINUX cluster, and for commercially available GE, and Siemens scanners.

  Krol's lab developed a new PET image reconstruction algorithm, PAPA, (Inverse problem 2012; 28:115005, Medical Physics 2015;42(8):4872) that outperforms existing algorithms. The originality of the algorithm lies in the coupling of the reconstruction problem with a regularization of total intensity variation with well suited preconditioning. While these features improve image quality, they dramatically complicate the implementation. Indeed to date there exists no implementation that meet the practical constraints of clinical use, the most important of which being the reconstruction time. Furthermore, the study is complicated by the fact that in commercial systems the projectors needed in the reconstruction include the gamma-camera receptors functional response. Vendors of scanners do not make that information available to us. Although through a research agreement, GE and Siemens made the projectors available but only in a Matlab code.

  In this context our contract has 2 phases. First write Matlab code with the projectors given in a Matlab library to show PAPA improve image quality in a practical clinical context. Second, write C/C++ code with projectors solely based on the scanner geometry to show the reconstruction problem can be solved in a manner to meet all clinical constraints. The first phase is well advanced with preliminary results available. The second phase is in a planning stage. The plan is to write MPI/OpenMP code, that will run on a parallel server with Intel math co-processors, and data structures that optimize data flow from high performance memory to processors. The study is the subject of an NIH grant

  Contact: Andrzej Krol, see list of references.

Complex Biosystems Inc., Custom software development contract/partnership with: Brain Biosciences July 2017-

Implement state of the art PET image reconstruction algorithm in a Novel small PET scanner

designed by Brain Biosciences (http://www.brain-bio.com). The scanner aims at imaging small objects e.g. brain, or limbs, and at reducing the cost of this technology. The photomultipliers of this scanner will eventually be replaced by silicon based photomultipliers. Since more stable functional receptor response does not offer significant advantages, and accurate projectors formulated exclusively with geometric information and receptor sensitivity can be very accurate. At this stage we generated sinograms form list made files. We are in the process of generating a prototype reconstruction with Matlab code. A high perfomance C/C++ image reconstruction code will follow. The project is still undergoing.

Contact: David Beylin, Andrzej Krol, See list of references.

Complex Biosystems Inc., product development: Simulation of traveling electrochemical waves in excitable tissue, Jan 2013-

This product and associated services are expected to become the bare bone of Complex Biosystems Inc. initiated in my Ph.D, development was pursued in my postoctoral studies and then throughout my academic career. When I started the company we had a mesoscopic scale system that generated reliable predictions regarding the molecular mechanisms of arrhythmias, and contributed to the discovery of new targets.

Since the foundation of the company, this application been extended for organ scale simulations. Functionality been added to generate geometric models from medical images of muliple modalities, mesh physiologic structures with high quality hexahedral meshes, and solve nonlinear PDEs associated to traveling electrochemical waves on large physiologic structures. Originally designed for cardiac tissue the scope of application been extended to the gut.

Associated services are medical device design, and drug discovery. We already been approached by companies offering laboratory rodents to the academic institutions and pharmaceutical companies.

Contact: My CV shows several abstract on this subject. Peer reviewed journal papers will appear shortly. Interested parties are welcome send us request for information.

Bioengineering Department SUNY Binghamton, innovations in computer modeling, July 2006 - Dec 1012

Completed the discovery and implementation of novel processes (Bull Math Biol 2013;75(5):752-773, last paper in a sequence of 4 papers, see CV) to deduce protein kinetics from bioelectric data collected in isolated cells. The processes extract unknown parameters and functions of voltage of nonlinear receptors or channel gating models from bioelectric data collected in isolated cells. It does so unambiguously through an inverse method that overcome all limitations inherent to nonlinear least square fitting. Since the process can be applied in: physiologic, disease, or genetically altered conditions, and in absence or presence of therapeutic compounds, they provide quantitative information on the effect of therapeutic compounds on complex biological conditions

In a modeling framework, protein kinetic is an input in the partial differential equation (PDE) system quantifying the dynamics of traveling electrochemical waves. As such the processes are a corner stone in the discovery of therapeutic interventions (drug or device based) because they enable us to capture with great accuracy how cell respond to electrochemical stimuli. The patent is currently under review, and is followed by a community effort initiated by us and the Masonic Medical Research Laboratory (https://www.mmrl.edu, Jonathan Cordeiro) to characterize excitable tissue with these processes.

Beside we advanced our means to solve the nonlinear PDEs associated to traveling electrochemi-

cal waves with better algorithms to: mesh geometric structures, build matrix systems and solve them in a timely fashion. We validated the model prediction with the spatiotemporal evolution of electrochemical wave fronts in slabs of cardiac tissue excised from pig hearts. (Raba R. and Beaumont J., Multi-scale Analysis of the Mechanisms of Arrhythmia. World congress on mathematical modeling and computational simulation of cardiovascular and cardiopulmonary dynamics. NIH sponsored symposium. Richmond Virginia May 31 to June 3rd, 2011.)

Contact: Saleet Jafri, James Bassingthwaighte, Randal Rasmusson, Josh Leon, whom are active researchers in this field. See list of reference

Department of Pharmacology SUNY Upstate Medical, Modeling and simulation for the discovery of cardiac antiarrhythmic therapeutic options, Jan 1992 - July 2006

Member of a cardiology group, first involved as postdoc, and then as Faculty member. My role in the group was to generate simulation predictions with a model of traveling electrochemical waves in cardiac tissue that I developed. At that stage, the model was of mesoscopic scale with simulation capabilities in two-dimensions only. Still the application was quite demanding requiring close to 1 million nodes, 50,000 time steps with about 30 state variables. I wrote C/MPI code that ran on massively parallel computers of the NSF Teragrid, and on a SUN enterprise server I acquired with an NIH grant (see next item below).

Several important discoveries were wade with this system. Namely we: (i) elucidated the dynamic properties of electrochemical vortices which enabled us to understand how arrhythmias are initiated and why they are difficult to terminate with electrical stimuli; (ii) put forth the idea that the disorganized excitation recorded throughout the heart was driven by one or few vortices, which finding was corroborated experimentally; (iii) found that vortex dynamics was governed by few key membrane proteins, and that specific alteration of their kinetics could lead to vortex termination; and (iv) alteration of the kinetics (following model specifications) of one of these targets, the inward rectifier channel, with an inorganic blocker, indeed lead to vortex termination with hig success rate (see CV for papers on the subject). Overall this effort shows the potential of computer modeling for systematic drug discovery.

Contact: Saleet Jafri, James Bassingthwaighte, Randal Rasmusson, Josh Leon, whom are active researchers in this field. See list of reference

Department of Pharmacology SUNY Upstate Medical, HPC modeling facility, 1999-2005

Put in place, funded (NIH and NSF), and supported a computer modeling core at the SUNY Upstate Medical University. The facility included a parallel SUN Enterprise server, 2 storage arrays, a tape library with bar code readers, and robotic tape loader. It was interconnect to PCs in wet laboratories controlling acquisition systems to gathering data in isolated cells, cell cultures, multicellular preparations, and isolated whole hearts. It supported automated backups, and on demand archival. In addition, the core supported web based tools for sequence alignments and protein configuration calculation force fields simulations. Overall it provided services to a large number of biomedical scientists across multiple disciplines, i.e., Modeling, Pharmacology, Cardiology, Cell & molecular Biology, and Chemists. I put in place the infrastructure, and then trained a system administrator that support the operation.

Contacts: Arkady Pertsov, Barry Knox, Steeve Taffit, see list of references.

Clinical research institute of Montréal, product development: Pneumological sounds data base, and analytical system, 1987-1989

Developed a pneumological sounds data base for clinicians, with front end manager, graphical user interface, drivers to listen to the sounds and signal processing tools to extract features on the signals that were related to various diseases signatures.

Contact: Louis Gilles Durand, I could recover the contact upon request

DMR, now Fujitsu, analyst, and implementation of development environment, 1985-1987

The company sells software development services, a development methodology and consultation services to structure development activities. The company is renowned for its development methodology and was purchased by Fujitsu for this reason. The methodology includes process and data modeling with various diagrams, and support to organize the source code in structured data base.

My duties were to: write software design specifications for programmers following this methodology, and implement on-site development environment. Through these assignments I learned to develop code in a structured manner and to document it well. It was tremendously beneficial for the rest of my career.

Contact: Josh Leon my Ph.D. thesis advisor can testify that I can develop quality code. See list of references.

Specific skills

Programming languages: C 20 years, C^{++} 2 years, OpenGL 4 years, MPI 12 years, OpenMP 3 years, and Cuda 3 years

Performance analysis: gprof, PAPI, and TAU, 4 years for all.

Software development method: Object oriented Booch method, 2 years. Rapid application development (RAD) 3 years

Management Writing design specifications for programmers, (4 years)

Medical Software application in the medical field, 18 years.

Operating systems development/administration LINUX 12 years, flavors: SuSe, Ubuntu, Centos. Windows 7-10 with Visual studio 3 years.

high performance computing hardware Intell/AMD chips & compilers Infiniband interconnect, 10 years for all

HPC development environment Job scheduling, data migration across various type of storage, I/O's across different platforms/OS, efficient use of memory, 12 years for all.

Imaging & visualization in general Graphic cards, GPUs, visualization software, imaging algorithms (segmentation, surface & features extraction, registration), 10 years for all.