Jacques Beaumont Ph.D. (http://www.clxbs.com)

Personal information

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Education

1993	**Post.Doc.**,	SUNY Upstate Medical University, Syracuse NY, Modeling & simulation in Cardiology
1992	**Ph.D.**,	Montreal University, Quebec, Canada, Biomedical Engineering
1985	**M.S.**,	Laval University, Quebec, Canada, Physics
1982	**B.S.**,	Laval University, Quebec, Canada, Engineering Physics

Interest

Take a leadership position in life science applications, i.e.: imaging, device and drug design

Positions filled

2014-	Owner, R&D engineer	Complex Biosystems Inc.
2013-2014	Visiting Professor	SUNY Upstate Medical University
2006-2012	Associate Professor of Bioengineering	Binghamton University
2006-2012	Adjunct associate professor	Bioengineering Syracuse University
2005-2006	Associate Professor of Radiology	SUNY Upstate Medical University
1999-2005	Assistant professor of Pharmacology	SUNY Upstate Medical University
1992-1999	Postdoc, research assnt, senior scientist.	SUNY Upstate Medical University
- 1992	Software Engineer	Clinical Institute of Montreal, Fujitsu

Professional experience

LINUX computing platforms: set up, repair, and support 2001-
Created, supported and obtained NIH funding for a computer modeling core at the SUNY upstate medical university. This includes: large LINUX server, storage arrays, tape library, biomedical acquisition stations (12) networked with HPC equipment. Deployed multiple services e.g.: force field molecular modeling, protein structure visualization, sequence alignment, genome sequencing, graphic applications, animated simulations, simulation of traveling electrical waves in excitable tissue.

Implemented parallel version of my simulation code on supercomputers of the TeraGrid, a facility funded by the National Science Foundation (NSF). Through this exercise, I became familiar with the operation of large computing servers. In 2004 I was awarded an NIH instrumentation grant for HPC equipment that included a multiprocessor UNIX server. I set up the facility similarly to NSF HPC equipment. I followed several system administration courses offered by SUN Microsystems and acquired the competences necessary to support the facility. I eventually trained system administrators to insure the day to day operation of the facility.

I leveraged this expertise in my company by offering HPC services, set-up, repair, and support LINUX servers. The repair service is slowly taking off because it meets an academic need. I expect the set-up and support services to take-off when I will sell integrated computer systems running my applications.

Refs: Arkady Pertsov, department of pharmacology SUNY Upstate Medical University, Email: pertsova@upstate.edu, phone: 315-464-7986, Andrzej Krol, department of radiology SUNY upstate medical university, Email: krola@upstate.edu, phone: 315-464-7029

Professional experience

Funded academic research program, 1999-

My research deals with the modeling & simulation of bioelectric phenomena with an emphasis on the cardiovascular system. The ultimate goal is to advance diagnostic and therapeutic options for diseases related to impaired bioelectric functions, e.g. cardiac arrhythmias, motor control, Bowel movement, to name a few. Software support I put in place over the years encompass tools to:

(i) Analyze protein kinetics: Process bioelectric signals generated by isolated cells subjected to external electrical stimulation in a manner to deduce the components of models (ordinary differential equations) dictating the kinetics of proteins mediating the passage of ions across cell membranes. I owe 2 patents on this technology.

Refs (from a total of 4 papers, see CV): Raba et al. Bull. Math Biol. 2013;75(5):752-773

(ii) Model the electrical activity of excitable cells: Includes an editor and an ODE array solver. With the editor one defines a cell, i.e., cell compartments, the membrane surrounding them, proteins controlling the passage of ions across cell membranes, and electrochemical reactions taking place within compartments. Proteins and chemical agents change dynamically with changes in compartments ionic composition. The editor output the ODE array in a structured repository the solver can interpret to integrate the equations. This one is optimized to solve stiff ODE arrays encountered in this field.

Refs: Could provide user manual under non-disclosure agreement.

(iii) Build geometric models: From medical images reconstruct a geometric model of physiologic structures. The geometric model in question is a collection of surfaces defined with parametric B-Splines that are constrained at their joints. It covers the interpretation of computerized tomography (CT), magnetic resonance (MR), and laser scanning confocal microscopy (LSCM) images. Processes include: contrast enhancement, surface extraction, vector fields delineation, and the morphing of geometric frontiers with parametric B-Splines.

Refs (from a total of 4 papers, see CV): Bayer et al. Hindawi, Computational and Mathematical methods in biology. Special issue on: image-based computational cardiology, 2014:1-16

(iv) Mesh geometric models: Two important constraints for simulations in biology. In general we are interested to simulate electrical activity on tissue based on cell dynamics. Cells are of the order of few micrometers, and tissue of several centimeters. Thus physiologic structure meshes are typically composed of few million nodes. Consequently the PDE solver should be able to handle very large sparse matrix systems. Due to their size, as of to date, they are solved with iterative methods. For an iterative matrix solver to converge in a reasonable time, the mesh should be of high quality. This means: not include nearly degenerate elements, and have elements size, surfaces, as well as edge angles that are smoothly graded in space.

The other constraint is the nature of the geometries. The surfaces bounding the physiologic structures have a high degree of curvature with multiple intrusions and protrusions. Generating quality meshes for such geometries is far from being a trivial task.

I contributed to advance technology for this task. First with a new method to generate the initial mesh. Second, with a variational method to regularize the mesh for various attributes, i.e. elements: volume, surface, face angles, and edge angles.

Refs (from CV): Multiscale modeling of cardiac arrhythmias in mice. SIAM meeting on life sciences held in Portland Oregon July 11-14,2004, Realistic modeling of the mouse heart. A tool for genomic. The 74^{th} congress of the ACFAS held at University McGill Montreal, May 15-19 2006. Role played by tissue microstructure .... World congress on Mathematical modeling held in Richmond Virginia, May 31 to June 3^{rd} 2011.

(v) Solve PDE array with the FEM: Suite of applications to build the matrix system resulting from the discretization of partial differential equations (PDEs) defined in physiologic structure. The PDEs are solved with the finite element method (FEM) and that solver is coupled with the cell model solver, such that the electrical activity of any tissues the cells of which been previously characterized with the above mentioned cell model can be simulated. The system permit to vary spatial distribution of various attributes, e.g.: protein expression, conductivity, cardiac fiber orientation.

Refs (from CV): Iterative methods for the solution of the cardiac bidomain equations. Eastern sectional meeting of the American Society. Held in Rochester NY, Sept. 22-23, 2012.

(vi) Scale PDE solvers on massively parallel computers: The parallel version of my PDE solver been implemented on massively parallel supercomputers in operation at the NSF TeraGrid, Buffalo computational center, and on my server. Such resources are necessary to simulate bioelectric activity at tissue and organ scales. My MPI parallel code displays superlinear scaling on multiprocessors servers. Indeed I received a high mark review from NSF funding committees for my parallel implementation. That permitted me to secure NIH funding to acquire HPC equipment and create a computer modeling core at SUNY Upstate Medical.

That code is undergoing further development to take advantage of multiprocessors, multicores servers. The programming model combines thread programming for core communication and the message passing interface (MPI) library for processor (across mother board) communication. No need to say, data sharing and communication synchronization is much more elaborate in this model. In this regard my multiblock approach to meshing greatly facilitates domain decomposition and load balancing. Specifically, I have applications to decompose a geometric model into portions and to map each of them to blocks of a multiblock structure. The multiblock is composed exclusively of parallepipeds and is therefore easy to mesh and partition for load balancing. The mapping, multiblock-to-geometry, provides mesh nodes coordinate transformations permitting to: write elementary equations, build the FEM matrix system, and more easily apply boundary conditions. At this stage some of the steps are published, but not all.

Refs (see CV): NSF funding for computational resources from 2006-2013. NIH shared instrumentation grant, funding to purchase HPC equipment. My computational approach been evaluated by scientific review committees for each grant.

(vii) Support traveling electrical wave analysis: Carry several measurements on traveling electrical waves and on tissue state, e.g. isopotentials, traveling velocity, upstroke velocity, amplitude, curvature, rays, current lines, delineation of various loci on a traveling waves, tracking of their trajectory, visualization of tissue state over loci trajectories, to name a few. All of which are important to elucidate traveling wave dynamics that is at the basis of cardiac arrhythmia diagnostic as well as the prediction of drug efficacy.

Ref (see CV): The paper that best exemplify the tools I developed for traveling wave analysis is: Bull. Math. Biol. 2019;81(7):2649-2690.

Medical imaging. 2013-

(i) Optimize a PET image reconstruction pipeline for radiation dose and image contrast

Work done for the radiology department of the SUNY Upstate Medical University. Determine whether the image reconstruction pipeline could be tuned to operate with lower radioactive tracer dose while preserving image contrast. This is important for cancer treatment in children. Through a research agreement with Siemens, the radiology department has access to images and processes of the reconstruction pipeline. Based on these and other applications we designed, we analyzed filtering prior to back projection and conditions for convergence in the OSEM algorithm.

Our 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.

(ii) Simulate gamma-camera receptors for design purposes

Work done for the radiology department of the SUNY Upstate Medical University. Developed an application to simulate gamma-photons interaction with LSO, LYSO, BGO or BSO crystals. This include: gamma-photons absorption by the crystal, their conversion to optic photons, and the optic photons transport in crystals. The application was developed with the C++ programming language, the Geant4 Library `http://geant4.cern.ch/`, and one of our product that is still undergoingdevelopment, xScheme, for scientific visualization.

We subsequently used this simulator to prototype receptors. This includes (i) finding the mechanical work that need to be done on the crystal surface to optimize light transport, (ii) the type of surface reflectors that is most effective, (iii) finding the best distribution of silicon photomultipliers (1 end, 2 ends, side, strips ... etc.), (iv) quantify the distribution of photons arrival time (V) and precise the matching characteristics required by the photomultipler, e.g., acceptance of jitter time, threshold, power, gain. This work is still ongoing.

Ref for medical imaging: Prof. Andrzej Krol. Department of Radiology SUNY Upstate Medical University. Email: Krola@upstate.edu, Phone: 315-464-7029

(iii) Implement a novel image reconstruction algorithm in a portable MRI scanner, initial phase

Work done for Brain Biosciences (`http://www.brain-bio.com`) and in collaboration with prof. Krol from SUNY Upstate medical. Beside being appealing for field imaging (combat zones, disaster sites) the Brain Bioscience portable MRI scanner has the potential to reduce brain and limb imaging costs. However this technology's sensitivity to motion negatively impact its resolution. We initiated work to assess whether a more performant reconstruction algorithm conceived in Krol's laboratory could improve resolution. At this stage we generated sinograms form list files gathered from the scanner. Prototype reconstructions with C/C++ programming language will follow. This work is still ongoing.

Ref for medical imaging: Prof. Andrzej Krol. Department of Radiology SUNY Upstate Medical University. Email: Krola@upstate.edu, Phone: 315-464-7029

Instrumentation

(i) High precision oxymeter, 2013-2015

For Complex Biosystems Inc. The specimen, either: finger tip, ear lobe, tip toe, fore front, is stimulated with light at two different wavelengths, each displaying different absorption to oxygenated/non-oxygenated blood. Following stimulation light radiating from the specimen is collected with a lens fixed it. The source, 2 small lasers emitting in the IR and UV range, and the receptors, photodiodes with sensitivity in the wavelength range of the light radiated by the specimen, are in a shielded enclosure at a distance from the specimen. The signal is transmitted a low noise without significant loss through optical fibers. The photodiodes are attached to a high gain low noise custom designed amplifier. The amplifier outputs feed the ADC of an instrumentation microprocessor, the propellor^{TM} from parallax inc. We initiated this project after we researched light absorption by biological tissue. We developed instrumentation for this project and were able to better characterize light absorption & transmission by biological tissue. Our signal processing based on this research is innovative and greatly improve the precision of blood oxygenation measurements.

Professional experience

The instrumentation microprocessor is sufficiently powerful to handle All signal processing and generate a meaningful output a health professional can read. Signal acquisition and processing been developed independently. We showed we could achieve unprecedented precision, and consistency. We are waiting the right business opportunity to build a fully functional unit.

Ref (from CV): Costantino et al. Journal of Biomedical Optics, 2017;22(7);076009, 1-11

(ii) Time of flight mass spectrometer, Master's thesis

Built a time of flight (TOF) mass spectrometer in a research setting. Conceived the ion source. Formulated a mathematical model for ion transport in electrostatic deflectors. Used it to optimize the electrostatic deflectors configuration, i.e.: plates arrangement, their shape, as well as potential distribution. Designed an amplifier to apply high voltage on the electrostatic deflector plates. Finally elaborated the control system.

Other applications development & professional services, prior to 1993

(i) Clinical R&D Engineer

For the clinical research institute of Montreal. Developed an application to manage pneumological sounds with the objective to train clinicians. The application included a back end data base, a front end to query the DB, graphic user interface, drivers to listen to the sounds, and signal processing tools to extract features permitting to better characterize pneumological diseases.

(ii) Software engineer

For DMR a software consultation firm in Quebec city that was purchased by Fujitsu. Member of the team supporting an infrastructure service that included: a software development methodology, consultation in development planning, and software tools to support the development methodology.

Specific skills

Programming languages & libraries: C 20 years, C^{++} 2 years, OpenGL 4 years, MPI 12 years, Thread programming, 4 years, OpenMP 2 years, Cuda 3 years, FFmpeg 1 year.

Scripting language: Perl 3 years

Performance analysis: gprof, PAPI, and TAU, 2 years.

Software development method & tools: Waterfall 4 years, Agile beginner, subversion 6 years, CVS 2 years.

Management Writing specifications for programmers, 4 years.

Operating systems LINUX system administration, 12 years.

high performance computing (HPC) hardware Intell/AMD chips & compilers workstation & server integration, set up & support of high performance computing platform, Infiniband interconnect, 12 years.

HPC software MPI library, Thread programming, Job scheduling, data migration across various type of storage, I/O's across different platforms/OS, efficient use of memory, 12 years.

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

Honors, awards, and solicitations for service

Funding (i) Research Foundation of SUNY (PI) 2007-2009, (ii) Hendrix Funds (PI) 2006-2007, (iii) Whitaker Foundation (PI) 1999-2002, (iv) NIH (program director) 1995-2005, (v) NIH (PI) 2004.

Computation NSF (PI) Resources for high performance computing 2008-2013

Competition Gordon K Moe, Young investigator award, American Heart Association 1994

Reviewer *Funding agencies:* (i) American Heart Association 2008-present, (ii) National Institute of Health 2009-2010, (iii) National Science Foundation 2001-2006, (iv) National Academy of Sciences 2003, (v) Health Research Council of New Zeland 2005.
Journals: (i) Annals of Biomed. Engn, (ii) Proceedings of the National Academy of Sciences, (iii) Biophysical J., (iv) IEEE Trans. on Biomed. Engn, (v) IEEE Trans. on Medical Imaging.

Invited talks 18 invited presentations, several of them renumerated