BICT EAI galois

# BICT 2019

## 11th EAI International Conference on Bio-Inspired Information and Communications Technologies

**MARCH 13–14, 2019 | PITTSBURGH, PENNSYLVANIA, UNITED STATES**

## Conference Program

Carnegie Mellon University
Software Engineering Institute

# Welcome Message

**Welcome to BICT 2019**

Welcome to the Eleventh International Conference on Bio-inspired Information and Communications Technologies (BICT 2019) held March 13th and 14th 2019 at Carnegie Mellon University in Pittsburgh, Pennsylvania, U.S.A. Our conference attracts researchers and practitioners in diverse disciplines that seek the understanding of key principles, processes, and mechanisms in biological systems and leverage those understandings in design, engineering, and technological applications. Past iterations of the conference have attracted significant contributions in Direct Bioinspiration (physical biological materials and systems used within technology) as well as Indirect Bioinspiration (biological principles, processes and mechanisms used within the design and application of technology). This year, the scope expands to include a third thrust: Foundational Bioinspiration (bioinspired aspects of game theory, evolution, information theory, and philosophy of science). Through Foundational Bioinspiration, we gain scientific and philosophical perspectives into the role of emergent bioinspired and biomimicry technologies and their wider implications.

This year's keynote speakers are Sheri M. Markose (Professor of Economics at the University of Essex), Brian Skyrms (Distinguished Professor of Logic and Philosophy of Science, Economics, and Philosophy at University of California Irvine, and Professor of Philosophy at Stanford University), Michael Lotze (Department of Surgery, Immunology, and Bio-engineering, University of Pittsburgh School of Medicine) and William E. Novak (Carnegie Mellon University Software Engineering Institute). The program also contains fourteen accepted papers and four special sessions: Human Machine Teaming (chaired by Ryan D. McKendrick, Northrup Grumman), Ethics in AI Applications in Industry (chaired by Thomson Nguyen, Kleiner-Perkins), and Re-Engineering Philosophy of Nature, Multiple Realisation, and Natural Kinds (chaired by Paola Hernández-Chávez, University of Pittsburgh), and Nature and Games celebrating Bud Mishra's 60th birthday (chaired by Steven Massey, University of Puerto Rico). Additionally, the banquet will feature an interactive music composition by Jakub Polaczyk (New York Conservatory) titled *"Around the B-E-ES"!*

Biology offers an empirical and profound glimpse of dynamic stability, robustness, control, resilience, and survival. Accordingly, the application of biological research to systems and technology holds immense potential and reveals many technical challenges. We look forward to a full two-day program featuring many fruitful discussions and presentations charting the current and future advances in bioinspired technologies.

**General Chair**

Bud Mishra, Courant Institute of Mathematical Sciences

**Technical Program Committee**

William Casey, Carnegie Mellon University Software Engineering Institute

Yang Cai, Carnegie Mellon University

Jun Suzuki, University of Massachusetts

Eric Hatleback, Carnegie Mellon University Software Engineering Institute

# Table of Contents

Conference Technical Program 2

Keynote Speakers 4

Presented Papers and Abstracts 8

Panels and Sessions 17

Conference Committees 23

General Information 26

Jared L. Cohon University Center Floor Plan 27

Conference Online 28

EAI Summits 28

Become an EAI Member 29

About EAI 29

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# Conference Technical Program

## Day 1 (March 13)

| | | |
|---|---|---|
| 7:45 | Opening Remarks | Bud Mishra |
| | **Indirect Bio-Inspiration** | |
| 8:00 | The Digital Origins of Intelligence: How We Became Smart and Protean | Sheri Markose |
| 9:00 | Break | |
| | **Robotics and Artificial Intelligence** | |
| 9:15 | Field Coverage for Weed Mapping Toward Experiments with a UAV Swarm | Dario Albani, Tiziano Manoni, Arikhan Arik, Daniele Nardi, and Vito Trianni |
| 9:45 | Evolutionary Multi-Objective Optimization for Evolving Soft Robots in Different Environments | Jun Ogawa |
| 10:15 | Self-Assembly from a Single-Molecule Perspective | Kevin Richard Pilkiewicz, Pratip Rana, Michael Mayo, and Preetam Ghosh |
| | **Bio-Inspired Approaches to Cyber Systems** | |
| 10:45 | Break | |
| 11:00 | Cyber Regulatory Networks: Towards A Bio-Inspired Auto-Resilient Framework for Cyber Defense | Usman Rauf, Mujahid Mohsin, and Wojciech Mazurczyk |
| 11:30 | Bio-Inspired Approach to Thwart Against Insider Threats: An Access Control Policy Regulation Framework | Usman Rauf, Mohamed Shehab, Nafees Qamar, and Sheema Sameen |
| 12:00 | Bio-Inspired System Identification Attacks in Noisy Networked Control Systems | Alan Oliveira de Sa, António Casimiro, Raphael C. S. Machado, and Luiz F. R. da C. Carmo |
| 12:30 | Lunch | |
| | **Foundational Bio-Inspiration** | |
| | **Bio-Inspired and Brain-Inspired Computing** | |
| 1:30 | Classification of Permutation Distance Metrics for Fitness Landscape Analysis | Vincent A Cicirello |
| 2:00 | Blinded by Biology: Bio-Inspired Tech-Ontologies in Cognitive Brain Sciences | Paola Hernández-Chávez |
| 2:30 | A Distribution Control of Weight Vector Set for Multi-Objective Evolutionary Algorithms | Tomoaki Takagi, Keiki Takadama, and Hiroyuki Sato |
| 3:00 | Break | |
| 3:30 | From Democritus to Signaling Networks | Brian Skyrms |
| 4:30 | Break | |
| 6:30 | Galois Music Event “Around the B-E-ES” at Wyndham Pittsburgh University Center<br>Reception and Dinner at Wyndham Pittsburgh University Center | Jakub Polaczyk (composer/pianist/teacher) |

## Day 2 (March 14)

| | | |
|---|---|---|
| | **Direct Bio-Inspiration** | |
| 8:00 | Know Yourself: Evaluating the Full Adaptome in TIL, PBMC, and Lymph Nodes in Solid Tumor Patients | Michael Lotze |
| 9:00 | Break | |
| | **Nano Medicine and Medical Informatics** | |
| 9:15 | Medical Diagnostics Based on Encrypted Medical Data | Kelsey Horan, Delaram Kahrobaei, Kayvan Najarian, Jonathan Gryak, Vladimir Shpilrain, Reza Soroushmehr, and Alexey Gribov |
| 9:45 | Membrane Computing Aggregation (MCA): An upgraded Framework for Transition P-Systems | Alberto Arteta, Luis Fernando Mingo, Nuria Gomez, and Yanjun Zhao |
| 10:15 | Cheating the Beta Cells to Delay the Beginning of Type-2 Diabetes Through Artificial Segregation of Insulin | Huber Nieto-Chaupis |
| 10:45 | Break | |
| | **Artificial Chemsitry and Biology** | |
| 11:15 | A Scalable Parallel Framework for Multicellular Communication in Bacterial Quorum Sensing | Satyaki Roy, Mohammad Aminul Islam, Dipak Barua, and Sajal Das |
| 11:45 | Physics-Based Nanomedicine to Alleviate Anomalous Events in the Human Kidney | Huber Nieto-Chaupis |
| 12:15 | Space Partitioning and Maze Solving by Bacteria | Ayyappasamy Sudalaiyadum Perumal, Monalisha Nayak, Viola Tokárová, Ondřej Kašpar, and Dan V. Nicolau |
| 12:45 | Lunch | |
| 1:45 | Human Machine Teaming | Ryan D. McKendrick |
| | The Evolution of Vigilance | William Helton |
| | Human Traits Embedded in Labels for Supervised Learners | Ryan McKendrick, Brian Falcone, Amanda Harwood, and Bradley Feest |
| 2:30 | Ethics in AI Applications in Industry and Startups | Thomson Nguyen |
| 3:15 | Break | |
| 3:30 | Inherent Moral Hazards in Acquisition: Improving Contractor Cooperation | William E. Novak |
| 4:30 | Re-Engineering Philosophy of Nature, Multiple Realisation and Natural Kinds | Paola Hernández-Chávez |
| | What is "Biological" About Biologically-Inspired Computational Models in Cognitive Science? Implications for the Multiple Realisation Debate | Mahi C. Hardalupas |
| | Fundamental Design Principles in Engineering and in the Architecture of Nature | William C. Wimsatt |
| 5:30 | Nature and Games and Closing Panel, Celebrating Bud Mishra's 60th Birthday | Steven E. Massey |

# Keynote Speakers

## Professor Sheri M. Markose

Professor of Economics at The University of Essex, U.K.

Sheri Markose has a PhD from the London School of Economics and has been a professor of Economics at the University of Essex, U.K., since 2006. As founder director (2002–2009) of the Centre For Computational Finance and Economic Agents (CCFEA), Sheri pioneered a multidisciplinary curricula covering agent based computational economics (ACE) and complexity sciences. She is well known for data driven network based ACE models developed for projects on managing systemic risk when she was a researcher for the IMF, Academic Advisor to G20 OTC Derivatives Reforms, and a Senior Consultant for the Reserve Bank of India (2011-2015). Her long standing interest in Gödel logic was prompted by the Austrian economist, F.A Hayek, in the context of his work on complex phenomena, and by Ken Binmore who pointed out in 1987 that extant game theory was flawed in failing to deal with the Gödel archetype of the Liar who negates what can be computed. Culminating in her 2017 paper in Journal of Dynamics and Games (AIMS), Sheri laid the groundwork for a Genomic Nash Equilibrium as one where the Gödel sentence, often regarded to be a funky and esoteric construction, is shown to be ubiquitous in code based genomic systems as it permits a code to self-report that it is under attack. In the absence of this, 'thinking outside the box', strategic innovation, and an arms race in novelty production are not possible. Subsequently, Sheri was invited to be an Associate Editor of Frontiers of AI and Robotics: Computational Intelligence.

**The Digital Origins of Intelligence: How We Became Smart and Protean**
In the spirit of the 'dynamic' genome of Barbara McClintock, I use a new notion of a Genomic Nash Equilibrium (GNE), to show how the Gödel-Turing-Post conditions of computational universality, acquired at critical points of genomic evolution, make us smart and protean. The key aspect of a GNE is that the genomic system encodes the famous self referential Gödel sentence as one where a code self-reports it is under attack or negated by, what is effectively, a hacker/virus (aka 'Liar'). If the latter cannot be eliminated, such code based digital systems embark on an arms race of novelty production with syntactic objects or phenotypes not previously there. It is widely known that viral software of genomic transposons provides scope for reuse and replication as in routine digital operations of 'scissor-paste' and 'copy-paste'.

However, few recognize that the workings of the adaptive immune system (AIS in tissues like the thymus medulla, as also the mirror neuron system for complex social cognition, are text book cases of information processing in a formal recursive Gödel meta-mathematics. This is typically organized in a tuple of a code centred self and the 'other' in an offline domain of recordings and simulations that have a bijective relationship with online machine executions of the same codes. The thymus medulla remarkably makes 'copies', in an offline environment, of ~85% of the genome that involves codes of programs that halt, viz. are 'theorems' in the system of ribosomal machine executions of 3-D prints of the morphology and regulation of the organism. Application of negation on these halting codes generates a digitally listable set of codes of self-antigens analogous to refutable propositions formalized in the Emil Post theory of creative and productive sets. GNE implies exciting new hypotheses on AIS and social cognition, and on the high incidence of repeat sequences in the human genome due to the model of regulatory networks as a distributed ledger.

## Professor Brian Skyrms

Distinguished Professor of Logic and Philosophy of Science, Economics, and Philosophy at U.C. Irvine, and Professor of Philosophy at Stanford University

### From Democritus to Signaling Networks

Professor Brian Skyrms is a fellow of the American Academy of Arts and Sciences and of the National Academy of Sciences of the U.S.A. His books include:

- Evolution of the Social Contract
- The Stag Hunt and the Evolution of Social Structure
- Signals: Evolution Learning and Information, and most recently
- Ten Great Ideas About Chance (co-authored with Persi Diaconis).

## Michael Lotze

Professor of Surgery, Immunology, and Bio-engineering, University of Pittsburgh School of Medicine

### Know Yourself: Evaluating the Full Adaptome in Til, Pbmc, and Lymph Nodes in Solid Tumor Patients

> “If you know the enemy and know yourself, you need not fear the result of a hundred battles. If you know yourself but not the enemy, for every victory gained you will also suffer a defeat. If you know neither the enemy nor yourself, you will succumb in every battle.”
>
> —*Sun Tzu, The Art of War*

The adaptive immune system is the 'best doctor' in wartime for both diagnosing and treating diseases, integrating five elemental, highly networked lymphoid cells that both support and counter-regulate each other: NK cells, NKT cells, αβ T-cells, γδ T-cells, and B cells expressing an IgH and κ or λ light chains. It carries out these tasks with unmatched precision, with the help of rearranged T and B cell receptors, our most diverse set of expressed and rearranged genes, fundamentally distinguishing one individual from another. Even identical twins only share ~6% of their repertoire. This autologous receptor diversity, ranging from 1015 to 1025 for each chain of the rearranged receptors, contains only two chains expressed in each cell. By combining dimer avoidance multiplex PCR and next generation sequencing (NGS), we have developed, in partnership with iRepertoire, Inc., high-throughput methods to study adaptive immunity. The adaptome is the sum-total of expressed T and B cell receptor genes in a sample, composed of seven chains, including the αβ and δ chains for T cells, and IgH heavy chains and κ or λ light chains for B cells. The immune repertoire is the sum-total of the individual clonotypes within one chain, including individual CDR3 sequences. In order to reflect the breadth and depth of the adaptome, the following criteria assessing any method needs to be ascertained AFTER validation:

1. Does it demonstrate inclusive and quantitative methods that are reproducible between sites (Huntsville/iRepertoire and Hillman/UPMC Adaptome Center);
2. Can analysis comprising bulk sequencing provide robust identification of high frequency clones (and enable subsequent assessment of underlying 'important' biology);
3. Do measures of clonal diversity enable understanding of the underlying structure and providence of the repertoire, integrating with neoepitope and common antigen/metabolite expression; and
4. Is there evidence of convergent evolution that could allow homologous or identical CDR3's to be associated with individual disease entities, creating hope for novel diagnostics and/or disease burden assessments?

Integrating studies of the peripheral blood, lymph nodes, and tumor allows for dynamic interrogation of the immune alterations occurring with age, treatment, and response to emergent and established immunotherapies. Confirming that this analysis can also be conducted on archival tissues increases its value.

## William E. Novak

Principal Member of the Technical Staff at the Carnegie Mellon University Software Engineering Institute

Bill Novak is a researcher, consultant, and instructor in the acquisition and development of software-intensive systems. Mr. Novak has over thirty-five years of experience with government acquisition, real-time embedded software and electronics product development, and business management. He has held positions with GE Corporate Research and Development, GE Aerospace, Texas Instruments, Tartan Laboratories, and GTE Automatic Electric Laboratories. Mr. Novak received his M.S. in Computer Engineering from Rensselaer Polytechnic Institute, and B.S. in Computer Science from the University of Illinois at Urbana-Champaign.

### Inherent Moral Hazards in Acquisition: Improving Contractor Cooperation

In the Government As The Integrator (GATI) model of acquisition, prime contractors no longer hand-select the members of the acquisition team or consortium, as they often did in the Lead System Integrator (LSI) model. One drawback of GATI acquisitions, thus, is that independent contractors may have little incentive to cooperate by sharing data and supporting other contractors, potentially resulting in delays, overruns, and poor performance. These problems are considered in this work to be both breakdowns in cooperation and expressions of moral hazards. Since the need for cooperation among contractors is still critical to success, finding ways to motivate that cooperation to improve program performance and outcomes is key to effective GATI acquisition. In this research, potential incentive mechanisms were analyzed for their ability to promote cooperation by applying game theory framing and analysis to this GATI acquisition context, and using system dynamics and agent-based modeling to study the results for their ability to promote cooperation and improve program outcomes.

**MUSIC EVENT**

## “Around the B-E-ES”!

### Jakub Polaczyk

A Carnegie Mellon University alumni (2013), Jakub is a polish composer and pianist currently living in NYC. Since 2015 he has been teaching at the New York Conservatory of Music and in 2018 was appointed a Music Director of the Chopin and Friends Festival in NYC. In his installation “Around the B-E-ES,” prepared for the BICT 2019 conference, in response to the general extinction of bees which is caused by the use of cellular phones, he creates an illusion of a bee hive.

By his piano improvisation based on the notes B-E-Eb, together with audience participation, he creates an interaction. Brushing objects in the room with electric toothbrushes, used in connection with a video display of Wi-Fi disorder and piano improvisation, he generates a soundscape of the buzzing and gradually disappearing hive.

# Presented Papers and Abstracts

## A Distribution Control of Weight Vector Set for Multi-Objective Evolutionary Algorithms

**Tomoaki Takagi, Keiki Takadama, and Hiroyuki Sato**

**Corresponding Author: Tomoaki Takagi** tomtkg@uec.ac.jp

For solving multi-objective optimization problems with evolutionary algorithms, the decomposing the Pareto front by using a set of weight vectors is a promising approach. Although an appropriate distribution of weight vectors depends on the Pareto front shape, the uniformly distributed weight vector set is generally employed since the shape is unknown before the search. This work proposes a simple way to control the weight vector distribution appropriate for several Pareto front shapes. The proposed approach changes the distribution of the weight vector set based on the intermediate objective vector in the objective space. A user-defined parameter determines the intermediate objective vector in the static method, and the objective values of the obtained solutions dynamically determine the intermediate objective vector in the dynamic method. In this work, we focus on MOEA/D as a representative decomposition-based multi-objective evolutionary algorithm and apply the proposed static and dynamic methods for it. The experimental results on WFG test problems with different Pareto front shapes show that the proposed static and dynamic methods improve the uniformity of the obtained solutions for several Pareto front shapes and the dynamic method can find an appropriate intermediate objective vector for each Pareto front shape.

## A Scalable Parallel Framework for Multicellular Communication in Bacterial Quorum Sensing

**Satyaki Roy, Mohammad Aminul Islam, Dipak Barua, and Sajal Das**

**Corresponding Author: Satyaki Roy** sr3k2@mst.edu

Certain species of bacteria are capable of communicating through a mechanism called Quorum Sensing (QS) wherein they release and sense signaling molecules, called autoinducers, to and from the environment. Despite stochastic fluctuations, bacteria gradually achieve coordinated gene expression through QS, which in turn, help them better adapt to environmental adversities. Existing sequential approaches for modeling information exchange via QS for large cell populations are time and computational resource intensive, because the advancement in simulation time becomes significantly slower with the increase in molecular concentration. This paper presents a scalable parallel framework for modeling multicellular communication. Simulations show that our framework accurately models the molecular concentration dynamics of QS system, yielding better speed-up and CPU utilization than the existing sequential model that uses the exact Gillespie algorithm. We also discuss how our framework accommodates evolving population due to cell birth, death

and heterogeneity due to noise. Furthermore, we analyze the performance of our framework vis-a-vis the effects of its data sampling interval and Gillespie computation time. Finally, we validate the scalability of the proposed framework by modeling population size up to 2000 bacterial cells.

## Bio-Inspired Approach to Thwart Against Insider Threats: An Access Control Policy Regulation Framework

**Usman Rauf, Mohamed Shehab, Nafees Qamar, and Sheema Sameen**

**Corresponding Author: Usman Rauf uraufuncc.edu**

With the ever increasing number of insider attacks (data breaches) and security incidents it is evident that the traditional manual and standalone access control models for cyber-security are unable to defend complex and large organizations. The new access control models must focus on auto-resiliency, integration and fast response-time to timely react against insider attacks. To meet these objectives, even after decades of development of cyber security systems, there still exist inherent limitations (i.e., understanding of behavioral anomalies) in current cyber-security architecture that allow adversaries to not only plan and launch attacks effectively but also learn and evade detection easily. In this research we propose a bio-inspired integrated access control policy regulation framework which not only allows us to understand anomalous behavior of an insider but also provides theoretical background to link behavioral anomalies to the access control regulation. To demonstrate the effectiveness of our proposed framework we use real-life threat dataset for the evaluation purposes.

## Bio-Inspired System Identification Attacks in Noisy Networked Control Systems

**Alan Oliveira de Sa, António Casimiro, Raphael C. S. Machado, and Luiz F. R. da C. Carmo**

**Corresponding Author: Alan Oliveira de Sa** alan.oliveira.sa@gmail.com

The possibility of cyberattacks in Networked Control Systems (NCS), along with the growing use of networked controllers in industry and critical infrastructures, is motivating studies about the cybersecurity of these systems. The literature on cybersecurity of NCSs indicates that accurate and covert model-based attacks require high level of knowledge about the models of the attacked system. In this sense, recent works recognize that Bio-inspired System Identification (BiSI) attacks can be considered an effective tool to provide the attacker with the required system models. However, while BiSI attacks have obtained sufficiently accurate models to support the design of model-based attacks, they have demonstrated loss of accuracy in the presence of noisy signals. In this work, a noise processing technique is proposed to improve the accuracy of BiSI attacks in noisy NCSs. The technique is implemented along with a bio-inspired metaheuristic that was previously used in other BiSI attacks: the Backtracking Search Optimization Algorithm (BSA). The results indicate that, with the proposed approach, the accuracy of the estimated models improves. With the proposed noise processing technique, the attacker is able to obtain the model of an NCS by exploiting the noise as a useful information, instead of having it as a negative factor for the performance of the identification process.

## Classification of Permutation Distance Metrics for Fitness Landscape Analysis

**Vincent A Cicirello**

**Corresponding Author: Vincent A Cicirello** vincent.cicirello@stockton.edu

Commonly used computational and analytical tools for fitness landscape analysis of optimization problems require identifying a distance metric that characterizes the similarity of different solutions to the problem. For example, fitness distance correlation is Pearson correlation between solution fitness and distance to the nearest optimal solution. In this paper, we survey the available distance metrics for permutations, and use principal component analysis to classify the metrics. The result is aligned with existing classifications of permutation problem types produced through less formal means, including the A-permutation, R-permutation, and P-permutation types, and has also identified subtypes. The classification can assist in identifying appropriate metrics based on optimization problem feature for use in fitness landscape analysis. Implementations of all of the permutation metrics, and the code for our analysis, are available as open source.

# Cyber Regulatory Networks: Towards a Bio-Inspired Auto-Resilient Framework for Cyber-Defense

**Usman Rauf, Mujahid Mohsin, and Wojciech Mazurczyk**

**Corresponding Author: Usman Rauf** **urauf@uncc.edu**

After decades of deploying cyber-security systems, it has become a well-known fact that the existing cyber-security architecture has numerous inherent limitations that make the maintenance of the current network security devices unscalable and provide the adversary with asymmetric advantages. These limitations include: (1) difficulty in obtaining the global network picture due to lack of mutual interactions among heterogeneous network devices, (2) poor device self-awareness in current architectures, (3) error-prone and time consuming manual configuration which is not effective in real-time attack mitigation, (4) inability to diagnose misconfiguration and conflict resolution due to multi-party management of security infrastructure. In this paper, as an initial step to deal with these issues, we present a novel bio-inspired auto-resilient\emph{security} architecture. The main contribution of this paper includes: (1) investigation of laws governing the dynamics of correct feedback control in Biological Regulatory Networks (BRNs), (2) studying their applicability for synthesizing correct models for bio-inspired communication networks, i.e. Firewall Regulatory Networks (FRNs), (3) verification of the formal models of real network scenarios, to prove the correctness of the proposed approach through model checking techniques.

## Evolutionary Multi-Objective Optimization for Evolving Soft Robots in Different Environments

**Jun Ogawa**

**Corresponding Author: Jun Ogawa** ogawa@u-aizu.ac.jp

Conventional evolutionary robotics assigns a task and an evaluation to a virtual robot and acquires an optimal control system. In many cases, however, the robot is composed of a few rigid primitives and the morphology imitates that of real animals, insects, and artifacts. This paper proposes a novel approach to evolutionary robotics combining morphological evolution and soft robotics to optimize the control system of a soft robot. Our method calculates the relational dynamics among morphological changes and autonomous behavior for neuro-evolution (NE) with the development of a complex soft-bodied robot and the accomplishment of multiple tasks. We develop a soft-bodied robot composed of heterogeneous materials in two stages: a development stage and a locomotion stage, and we optimize these robotic structures by combining an artificial neural network (ANN) and age-fitness pareto optimization (AFP). In terms of our experimental results, our approach enabled us to develop some adaptive structural robots that simultaneously acquire behavior for crawling both on the ground and underwater. Subsequently, we discovered an unintentional morphology and behavior (e.g., walking, swimming, and crawling) of the soft robot through the evolutionary process. Some of the robots have high generalization ability with the ability to crawl to any target in any direction by only learning a one-directional crawling task.

## Field Coverage for Weed Mapping Toward Experiments with a UAV Swarm

**Authors: Dario Albani, Tiziano Manoni, Arikhan Arik, Daniele Nardi, Vito Trianni**

**Corresponding Author: Dario Albani** dario.albani@istc.cnr.it

Precision agriculture represents a very promising domain for swarm robotics, as it deals with expansive fields and tasks that can be parallelised and executed with a collaborative approach. Weed monitoring and mapping is one such problem, and solutions have been proposed that exploit swarms of unmanned aerial vehicles (UAVs). With this paper, we move one step forward towards the deployment of UAV swarms in the field. We present the implementation of a collective behaviour for weed monitoring and mapping, which takes into account all the processes to be run onboard, including machine vision and collision avoidance. We present simulation results to evaluate the efficiency of the proposed system once that such processes are considered, and we also run hardware-in-the-loop simulations which provide a precise profiling of all the system components, a necessary step before final deployment in the field.

## Medical Diagnostics Based on Encrypted Medical Data

**Kelsey Horan, Delaram Kahrobaei, Kayvan Najarian, Jonathan Gryak, Vladimir Shpilrain, Reza Soroushmehr, and Alexey Gribov**

**Corresponding Author: Kelsey Horan khoran@gradcenter.cuny.edu**

We utilize a type of encryption scheme known as a Fully Homomorphic Encryption (FHE) scheme which allows for computation over encrypted data. Our encryption scheme is more efficient than other publicly available FHE schemes, making it more feasible. We conduct simulations based on common scenarios in which this ability is useful. In the first simulation we conduct time series analysis via Recursive Least Squares on both encrypted and unencrypted data and compare the results. In simulation one, it is shown that the error from computing over plaintext data is the same as the error for computing over encrypted data. In the second simulation, we compute two known diagnostic functions over publicly available data in order to calculate computational benchmarks. In simulation two, we see that computation over encrypted data using our method incurs relatively lower costs as compared to a majority of other publicly available methods. By successfully computing over encrypted data we have shown that our FHE scheme permits the use of machine learning algorithms that utilize polynomial kernel functions.

## Membrane Computing Aggregation (MCA): An Upgraded Framework for Transition P-Systems

**Authors: Alberto Arteta, LuisFernando Mingo, Nuria Gomez, and Yanjun Zhao**

**Corresponding Author: Alberto Arteta aarteta@troy.edu**

MCA (Membrane computing aggregation) is an experimental computational frame. It is inspired by the inner properties of membrane cells (Bioinspired system). It is capable of problem solving activities by maintaining a special, "meaningful" relationship with the internal/external environment, integrating its self-reproduction processes within the information flow of incoming and outgoing signals. Because these problem solving capabilities, MCA admits a crucial evolutionary tuning by mutations and recombination of theoretical genetic “bridges” in a so called “aggregation” process ruled by a hierarchical factor that enclosed those capabilities. Throughout the epigenetic capabilities and the cytoskeleton and cell adhesion functionalities, MCA model gain a complex population dynamics specifics and high scalability. Along its developmental process, it can differentiate into meaningful computational tissues and organs that respond to the conditions of the environment and therefore "solve" the morphogenetic/configurational problem. MCA, above all, represents the potential for a new computational paradigm inspired in the higher level processes of membrane cells, endowed with quasi universal processing capabilities beyond the possibilities of cellular automata of and agent processing models.

## Self-Assembly from a Single-Molecule Perspective

**Authors: Kevin Richard Pilkiewicz, Pratip Rana, Michael Mayo, and Preetam Ghosh**

**Corresponding Author: Kevin Richard Pilkiewicz**
**kevin.r.pilkiewicz@usace.army.mil**

As manipulating the self-assembly of supramolecular and nanoscale constructs at the single-molecule level increasingly becomes the norm, new theoretical scaffolds must be erected to replace the thermodynamic and kinetics based models used to describe traditional bulk phase active syntheses. Like the statistical mechanics underpinning these latter theories, the framework we propose uses state probabilities as its fundamental objects; but, contrary to the Gibbsian paradigm, our theory directly models the transition probabilities between the initial and final states of a trajectory, foregoing the need to assume ergodicity. We leverage these probabilities in the context of molecular self-assembly to compute the overall likelihood that a specified experimental condition leads to a desired structural outcome. We demonstrate the application of this framework to a simple toy model in which three identical molecules can assemble in one of two ways and conclude with a discussion of how the high computational cost of such a fine-grained model can be overcome through approximation when extending it to larger, more complex systems.

## Blinded by Biology: Bio-Inspired Tech-Ontologies in Cognitive Brain Sciences

**Paola Hernández-Chávez**

**Corresponding Author: Paola Hernández-Chávez** **hcpaola@gmail.com**

In his pioneering paper on neuromorphic systems, Carver Mead conveyed that: “Biological information-processing systems operate on completely different principles from those with which most engineers are familiar” (Mead 1990: 1629). 1 This paper challenges his assertion. While honoring Mead’s exceptional contributions, specific purposes, and correct conclusions, I will use a different line of argumentation. I will make use of a debate on the classification and ordering of natural phenomena to illustrate how background notions of causality permeate particular theories in science, as in the case of cognitive brain sciences. This debate shows that failures in accounting for concrete scientific phenomena more often than not arise from (1) characterizations of the architecture of nature, (2) singular conceptions of causality, or (3) particular scientific theories — and not rather from (4) technology limitations per se. I aim to track the basic bio-inspiration and show how it spreads bottom-up throughout (1) to (4), in order to identify where bioinspiration started going wrong, as well as to point out where to intervene for improving technological implementations based on those bio-inspired assumptions.

# Physics-Based Nanomedicine to Alleviate Anomalous Events in the Human Kidney

**Huber Nieto-Chaupis**

**Corresponding Author: Huber Nieto-Chaupis** huber.nieto@gmail.com

One of the irreversible complications of type-2 diabetes is known as diabetic nephropathy by which is characterized by the abundance of giant proteins in the urine. In most cases nephropathy might be identified in late stages of disease. In this paper we present a multidisciplinary methodology that combines physiology and physics that targets to identify in the very early phase the diabetic nephropathy through the deployment of a nano device that has capabilities to detect anomalous flux of albumin and others proteins along the area belonging to the renal glomerulus. From the fact that most of the proteins contain negative charge this turns out to be advantageous to deploy a nanodevice with a dual superficial charge density: positive and negative, in the sense that its electric interaction with proteins gives a result of either attraction or repulsive displacement, a fact that is seen as indirect measurement of the Rate Albumin Excretion, an indicator to evaluate the degradation of the kidney in time. We propose in a coherent and sustainable manner all these ideas through simulations where the prospective capability of a nanodevice as to measure the pass of electric charges inside the renal glomerulus is analyzed. We use electromagnetic pulses in order to carry out tasks of surveillance with respect to the transition of proteins of albumin from the microvascularity systems to the zone of urine formation. The results of this paper would support the prospective implementation.

## Cheating the Beta Cells To Delay the Beginning of Type-2 Diabetes Through Artificial Segregation of Insulin

**Huber Nieto-Chaupis**

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In this paper we focus in artificial mechanisms to detain the beginning of the type-2 diabetes. We propose a nanosensor whose central role is that of emitting and receiving signals. From purely electrical interactions between the nanosensor and Calcium 2+ ions through artifical entrance of Calcium ions inside the beta-cells allowing them to segregate insulin. The permanent segregation of insulin is seen from the angle of advanced networks in the sense that the segregation of insulin granules can be done to distance. In order to guarantee the permanent segregation of insulin granules by avoiding the intake of pharmacology for large periods. The electrical interactions inside the beta cells is the main assumption of this paper. We propose a full Internet of Bio-Nano Things network (IOBNT) aimed to regulate the continuous segregation of insulin in prediabetes patients through a prospective nanosensor that would play a double role as to acquire signals derived from the electromagnetic interaction between the Calcium ions and the nanosensor. Our scheme proposes the concept by which the nanosensor is permanently under communication with a bio-cyber interface fact that enables to upload data to the cloud in an unstoppable manner. It is expected that IOBNT runs in circuit of unstoppable communication involving also clouds, servers and endocrinologists in a sustainable manner for a continuous surveillance that guarantee the regulate segregation of insulin by the beta cells.

## Space Partitioning and Maze Solving by Bacteria

**Ayyappasamy Sudalaiyadum Perumal, Monalisha Nayak, Viola Tokárová, Ondřej Kašpar, and Dan V. Nicolau**

**Corresponding Author: Dan V. Nicolau** dan.nicolau@mcgill.ca

Many bacteria dwell in micro-habitats, e.g., animal or plant tissues, waste matter, and soil. Consequently, bacterial space searching and partitioning is critical to their survival. However, the vast majority of studies regarding the motility of bacteria have been performed in open environments. To fill this gap in knowledge, we studied the behaviour of E. coli K12-wt in microfluidic channels with sub-10 μm dimensions, which present two types of geometries, namely a diamond-like network and a maze. The velocity, average time spent and distance required to exit the networks, have been calculated to assess the intelligent-like behaviour of bacteria.

# Panels and Sessions

## Human Machine Teaming (Cybernetics)

**Chair: Ryan McKendrick**

### The Evolution of Vigilance

**William Helton**

**Author: William Helton** whelton@gmu.edu

Psychologists have proposed cognitive resource theories of human and other animal behavior. An example of where such theories have utility is understanding the increased lapses of attention with time-on-task. Vigilance, awareness of external critical stimuli, over time typically declines. Animals often become less responsive to environmentally important stimuli. An example in people would be failing to detect a car parked ahead on the road while driving for an extended trip. Behavioral lapses can occur because of either reallocation of cognitive resources to some other task, including internal thoughts—processing streams, or because of depletion of necessary cognitive resources. Since processing ability increases after a rest break of sufficient duration cognitive resources are renewable. The exact underlying mechanisms of depletion and renewal remain uncertain, but comparative research may elucidate the critical role rest and recuperation of cognitive resources has in understanding behavior.

### Human Traits Embedded in Labels for Supervised Learners

**Ryan McKendrick, Brian Falcone, Amanda Harwood, and Bradley Feest**

**Corresponding Author: Ryan McKendrick** rmckz8@gmail.com

There are a number of key data-centric questions that must be answered when developing classifiers for operator functional states. Here we focus exclusively on the labeling of cognitive load data for supervised learning. We explored three methods of labeling cognitive states for three-state classification. The first method labeled states as either high, adequate or low cognitive load. This labeling was derived from a tertiary split of the amount of information an individual had to hold on each trial of a spatial memory task. The second method was more adaptive, it employed a mixed effects stress-strain curves and estimated individual's performance asymptotes with respect to the same spatial task. The final method was similar to the second approach, yet it employed using mixed effects Rasch modeling to estimate individual capacity limits within the spatial task within the context of item response theory. To assess the strength of each of these labeling approaches we compared area under the curve (AUC) for receiver operating curves (ROC) as well the AUC of precision-recall ROCs (PR-ROC) from elastic net and random forest classifiers. We also transferred these classifiers to a synthetic intelligence, surveillance, and reconnaissance (ISR) task.

# Human-Machine Teaming

**David Burke**

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Our work on human-machine teaming is based on two design principles. The first is that a successful science of human-machine teaming requires a practical theory of group rationality. Game theory is often described as the science of strategic rationality, but it is fundamentally built on the concept of individual rationality. Likewise, social choice theory studies group decision-making, but only through the aggregation of individual preferences. We claim that there needs to be an explicit conception of a group, including its beliefs and preferences, in order to accurately model human-machine teaming dynamics.

The second design principle is captured in the following dynamic: for all agents, attention is a finite and precious resource. Being embedded in a high-tempo, complex environment containing both human and machine partners places severe cognitive demands on that agent. The key challenge here is for the agent to update its mental models, including its model of other agent's mental models. This is accomplished by minimizing expected information-theoretic surprisal over a characteristic time scale. If the surprisal rate is too high, agents aren't able to learn and cope with change effectively. Adaptation is demonstrated when agents are able to take actions that are congruent with their mental models and the current stream of sensory inputs.

# Philosophy of Science Session: “Re-Engineering Philosophy of Nature, Multiple Realisation and Natural Kinds”

**Chair: Paola Hernández-Chávez**

## What is “Biological” About Biologically-Inspired Computational Models in Cognitive Science?: Implications for the Multiple Realisation Debate

**Author: Mahi C. Hardalupas**
PhD student, Department of History and Philosophy of Science, University of Pittsburgh
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In this talk, I investigate the use of biologically-inspired computational models in cognitive science and their implications for the multiple realisation debate in philosophy of mind. Multiple realisation is when the same state or process can be realised in different ways. For example, flight is a potential multiply realised process. Birds, planes and helicopters all fly relying on the same aerodynamic principles but their mechanisms for flying differ substantially: birds have two wings which they flap in order to achieve flight, planes also have two wings, but they are static rather than flapping and helicopters use rotors on the top to produce enough lift for flight. If these “ways” of flying are considered sufficiently different, then we can conclude that flight is a multiply realised process. Philosophers of mind (such as Putnam (1967) and Fodor (1974) but more recently Polger & Shapiro (2016)) have frequently taken multiple realisation to be significant for metaphysical debates about whether mental processes can be reduced to neural processes. The idea being that if mental processes such as pain are multiple realised, then pain does not reduce to a neural process since it can be instantiated in other ways.

The current literature on multiple realisation (for example, Polger and Shapiro (2016) and Aizawa (2018a; 2018b)) doesn’t consider how artificial and engineered systems such as biologically-inspired computational models fit into this debate. I argue that the use of these models in cognitive science motivates the need for a new kind of multiple realisation, which I call ‘engineered multiple realisation’ (or EMR). By this, I mean that scientists aim to create multiple realisations of cognitive capacities (such as object recognition) through engineering systems. I describe various examples of this in cognitive science and explain how these models incorporate biological elements in different ways. Given this, I claim that EMR cannot bear on metaphysical debates about the nature of mental processes. Instead, I argue that, when building computational models as EMRs, there are different payoffs for incorporating biology into the models. For example, one approach is that researchers are often motivated to incorporate biological elements into their models in the hope that doing so will lead to better performance of their models (Baldassarre et al (2017); George (2017); Laszlo &

Armstrong, (2013)) Another approach incorporates biological elements into models as a way to test hypotheses about the mechanisms underlying human vision (Tarr & Aminoff, 2016). I emphasize that these payoffs depend on the goals of different modelling approaches and what the approaches take to be biologically relevant for these goals. By sketching out different approaches and their notions of biological relevance, I show that there are many important roles that EMR can play instead of informing traditional metaphysical debates about the reduction of mental to neural processes.

## Fundamental Design Principles in Engineering and in the Architecture of Nature

**Author: William C. Wimsatt**
Senior Fellow, Center for Philosophy of Science, University of Pittsburgh, 2018–2019
Universities of Chicago and Universities of Minnesota, emeritus.

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I consider, illustrate, and argue for the fundamentality of several design principles that emerge in all evolving systems, in their design and in their analysis. These include robustness or the use of multiple means using less reliable elements to secure more reliable outcomes, near decomposability, which can arise by different paths both top-down (securing context dependent quasi-independence, to facilitate evolution as first noted by Lewontin), and bottom up (through aggregation of relatively context-independent stable sub-assemblies, as first noted by Simon), and differential generative entrenchment as noted and used in different ways by several different writers including Riedl, Wallace Arthur, Brian Arthur, Wimsatt to explain and to predict patterns of differential evolutionary conservation and change, and inference patterns in evolutionary developmental biology including Bauplans, and combinatorial recombinations and entrenchments, generating adaptive radiations, families of technologies, and the importance of history.

# AI Applications and Ethics in Industry

**Chair: Thomson Nguyen**

## Distributed Autonomy for Robotics

**James Edmondson**

The majority of robots and cyber-physical systems developed and deployed today are stand-alone systems, and they are often controlled remotely by a human operator or even two or more operators. The useful options available for general development of multi-agent systems and swarms with collaborative intelligence and mission-focused autonomy for controlled experiments is limited. Researchers have even fewer tool and development options for pushing the state-of-the-art in trustworthy, predictable, and scalable distributed artificial intelligence for real-world, outdoor environments. In this talk, I will discuss my efforts over the past decade to bring large-scale, multi-agent systems into reality via my work in extensible middleware and algorithm development in the Group Autonomy for Mobile Systems project (GAMS: http://gams.ai) and in Unreal Engine simulation options for AR/VR integration. I will present videos of simulated systems and real world, outdoor multi-agent robotics. I will also outline the process of creating beneficial emergent good behaviors in distributed agents with techniques inspired by Dijkstra self-stabilizing system concepts in finite state machines, implemented in GAMS and another middleware I have been maintaining called the Multi-Agent Distributed Adaptive Resource Allocation project (MADARA: http://madara.ai). Finally, I will discuss determinism in distributed artificial intelligence and my work applying software model checking and statistical model checking to the autonomy development process.

## Machine Ethics

**David Burke**

Most existing attempts to formalize machine ethics have focused on two of the three main schools of thought of ethics: deontological approaches, which are rules-based and often involving concepts of obligation and permission, or utilitarian/consequentialist approaches, which attempt to calculate in some manner the greatest good for the greatest number. We have instead been pursuing an approach based on the computationally instantiating the five principles described by Haidt in his “Moral Foundations Theory”: harm, reciprocity, authority, loyalty, and disgust. These design primitives allow us to express moral constraints, objectives, and outcomes for machine ethics.

We measure our success in specifying and expressing ethical machine behaviors by the amount of congruence achieved between humans and machines, measured along the following dimensions:

1. Congruence in Identification — does the machine have similar abilities to a human when it comes to perceiving the salient characteristics of the scenario? That is, can the machine identify what ethical violations or moral challenges are involved in the scenario?
2. Congruence in Assessment — is the machine able to articulate the stakes involved for both the human and the machine in resolving the potential ethical violation? An additional question we are investigating is how to characterize and build the necessary trust between the human and the machine so that they are able and willing to share these assessments.
3. Congruence in Action — Given the machine’s decisions and/or recommendations, how do we resolve residual conflicts? For instance, say the machine makes a decision or recommendation, and the human disagrees — does there exist an effective resolution procedure?

# Nature and Games Session, Celebrating Bud Mishra's 60th birthday and Closing Panel

**Chair: Steven Massey**

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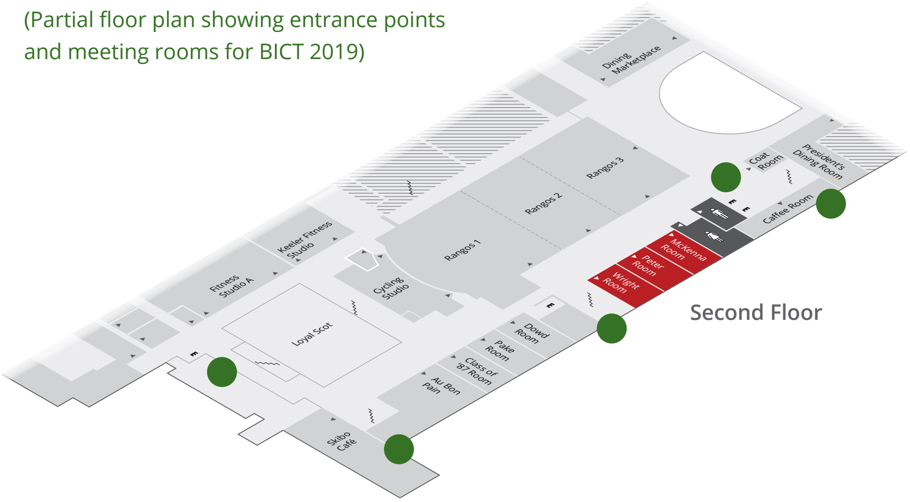
(Partial floor plan showing entrance points and meeting rooms for BICT 2019)



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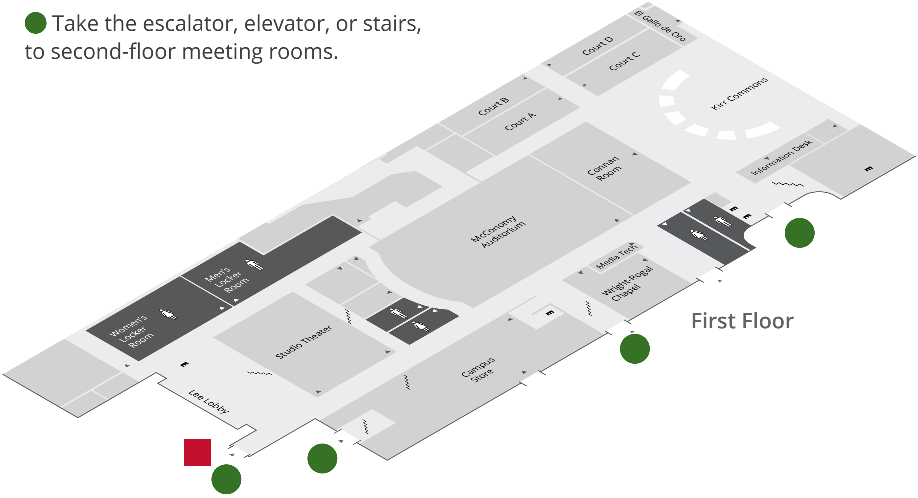

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