

ADVANCE Award Symposium
Poster Presenters
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Title: Bayesian sequential approach to monitor COVID-19 variants through positivity rate from wastewater

Authors: Maria L. Daza-Torres* J. Cricelio Montesinos-López, Yury E. Garcia, Heather N. Bischel, Miriam Nuño

Abstract: Trends in COVID-19 infection have changed throughout the pandemic due to myriad factors, including changes in transmission driven by social behavior, vaccine development and uptake, mutations in the virus genome, and public health policies. Mass testing was an essential control measure for curtailing the burden of COVID-19 and monitoring the magnitude of the pandemic during its multiple phases. However, as the pandemic progressed, new preventive and surveillance mechanisms emerged. Implementing vaccine programs, wastewater (WW) surveillance, and at-home COVID-19 tests reduced the demand for mass severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing. We propose a sequential Bayesian approach to estimate the COVID-19 positivity rate (PR) using SARS-CoV-2 RNA concentrations measured in WW through an adaptive scheme incorporating changes in virus dynamics. PR estimates are used to compute thresholds for WW data using the CDC thresholds for low, substantial, and high transmission. The effective reproductive number estimates are calculated using PR estimates from the WW data. This approach provides insights into the dynamics of the virus evolution and an analytical framework to continue monitoring the COVID-19 trends. The proposed modeling framework was applied to the City of Davis and the campus of the University of California Davis.

Title: Robust Scattering Feature Extraction from Acoustic Dolphin Wavefields for Sonar Object Classification

Authors: Wai Ho CHAK*, Naoki Saito

Abstract: Obstacle avoidance technology is crucial for the US Navy to conduct shallow water and very shallow water mine counter-measure (MCM). Mine or underground object detection depends on beamforming of sonar waveforms and interpretation of images generated from those waveforms. To address the problem of underground object detection, the dolphin-based marine mammal systems (MMS) are adopted as a solution in the US Navy. The monogenic wavelet scattering network (MWSN), which is similar to a convolutional neural network with interpretability, was used to further process the sonar data in our experiment. Our result shows that sonar object classification using dolphin signal as a source in synthetic aperture sonar (SAS) can be significantly improved by the MWSN at a higher layer.

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Authors: Maria L. Daza-Torres*, J. Cricelio Montesinos-López, Cesar Herrera, Yury E. García, C. Winston Bess, Heather N. Bischel, and Miriam Nuño

Abstract: Trends in COVID-19 infection have changed throughout the pandemic due to myriad factors, including changes in transmission driven by social behavior, vaccine development and uptake, mutations in the virus genome, and public health policies. Mass testing was an essential control measure for curtailing the burden of COVID-19 and monitoring the magnitude of the pandemic during its multiple phases. However, as the pandemic progressed, new preventive and surveillance mechanisms emerged. Implementing vaccine programs, wastewater (WW) surveillance, and at-home COVID-19 tests reduced the demand for mass severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing. We propose a sequential Bayesian approach to estimate the COVID-19 positivity rate (PR) using SARS-CoV-2 RNA concentrations measured in WW through an adaptive scheme incorporating changes in virus dynamics. PR estimates are used to compute thresholds for WW data using the CDC thresholds for low, substantial, and high transmission. The effective reproductive number estimates are calculated using PR estimates from the WW data. This approach provides insights into the dynamics of the virus evolution and an analytical framework to continue monitoring the COVID-19 trends. The proposed modeling framework was applied to the City of Davis and the campus of the University of California Davis.

Title: Elucidating the structural features of viral proteins using Cryo-EM and protein folding software

Authors: Michael Keith*, Tamara Christiani

Abstract: Structural biology has been critical in explaining mechanistic unknowns of viruses. Modern technical advances are allowing researchers to generate atomic models using only a protein sequence. Here, we present our structural biology methods and preliminary results for two viral proteins. For bacteriophage P4, we were able to construct its connector – a portal protein that joins the DNA-filled capsid with several tail proteins to generate an infectious virus – using Google Collab AlphaFold2 and HSYMDOCK. We found that the structure is strongly correlated to our initial cryo-electron microscopy (cryo-EM) map of phage connector. Additionally, we describe charged zones within the central channel which have varying diameters. We also present the cryo-EM density map for the SARS-CoV-2 S protein, resulting from over-expression in Chinese Hamster Ovary cells. The 3.95 Å resolution structure is of the prototypic spike ectodomain in its closed conformation. Our results are comparable to existing S protein maps with notable similarity to the Wuhan S protein. We will continue to analyze these viral structures via molecular dynamic simulations to generate energy-minimized models and explore the interactions of these structures with double-stranded DNA and human ACE2, respectively.

Title: Gröbner bases and Markov Chains on graphs with degree and colored balance conditions

Authors: Felix Almendra Hernandez*, Jesus De Loera, Sonja Petrovic

Abstract: We present a quadratic Markov and Gröbner basis for the degree-corrected variant of the stochastic blockmodel for random graphs. The basis generalizes the 1993 result of De Loera, Sturmfels and Thomas. This is current work in collaboration with Jesús De Loera and Sonja Petrović.

Title: Finding Minimal Step Conformations of Biological Two-Component Links

Authors: Jonathan Chang, Jacob Lusk, Mariel Vazquez, Gabriel Freund, Shawn

Abstract: The structure of links is present in biology such as in DNA replication and polymers. The finding of links in biology draws a connection to the mathematical field of topology. When studying and developing a proper model for these objects, it is fruitless to take projections or images of them as there are numerous projections for a singular object and formalizing the topology will be incredibly challenging. Thus, we discretize the amount of projections through modeling and representing them in the simple cubic lattice. An object in the simple cubic lattice must have vertices at integer coordinates, the edges must be a unit length and can only form angles of 90 or 180 degrees, and all vertices must be connected and self-avoiding. A two-component link is when there are two parts that are intertwined such that you cannot separate them without cutting. We utilize a computer-assisted approximation for the minimal step confirmations using a markov chain, Monte-Carlo sampling method, the BFACF algorithm. This will perform equivalent moves on a knot configuration while preserving its unique topology with the intention to reduce the amount of edges. Understanding the lattice model for links is crucial in order for other biological applications.

Title: The Monogenic Image on the 2-Torus

Authors: Brian Knight*, Naoki Saito

Abstract: By viewing a 1D signal as the boundary value of a function on the unit disc in \mathbb{C} , one can obtain a useful factorization by supplementing its conjugate counterpart so that this boundary function the boundary of an analytic function on the disc, and using the so called Blaschke products to compute a useful notion of instantaneous phase and amplitude. This is done by the Poisson/Cauchy integral formula or the Hilbert transform. The monogenic signal is the higher dimensional analog of this boundary function for 2D signals, and in the current literature it is treated as the boundary of a monogenic function on the upper half plane. We show a representation of the monogenic signal as the boundary value of a monogenic function on the half-cylinder and explore its use in computing an instantaneous phase and amplitude of 2D signals.

Title: Novel Resolution of Singularities within Point Cloud Data using TDA

Authors: *Greg DePaul and Erik Carlsson

Abstract: We set out to develop a technique for resolving singularities present in point cloud data in the hopes of recognizing intrinsic dimensionality of a dataset. This is done in the hopes of generalizing the technique in higher dimensions as a way of avoiding over confident modeling issues.

Title: Toward orbit recovery for cryo-electron microscopy: over-complete tensor decomposition for projected multi-reference alignment

Authors: Tait Weicht*, Albert Fannjiang, Alex Wein

Abstract: Cryo-electron microscopy (cry-EM) is a technique that seeks determine the structure of a molecule by freezing and imaging in vitreous ice. Individual molecules assume arbitrary orientations and imaging them projects their 3D structure into two dimensions. The conditions of the ice often results in a low signal-to-noise ratio (SNR) making recovery of the 3D structure from images quite a challenging problem. Simpler models seek to understand how to recover signals in similar circumstances i.e., observations affected by a set of unknown group actions and lots of noise. Multi-reference alignment (MRA) is one such model where entries of an unknown vector are cyclically shifted and corrupted with some additive noise. Success has been found in solving MRA by decomposing the third moment (a third order tensor) of the sample distribution. Tensor decomposition is a challenging task in its own right but a useful tool as it generalizes matrix operations like the singular value decomposition to multi-way arrays. We examine why adding a projection step to the original MRA model significantly increases the difficulty of recovering the signal via tensor decomposition.

Title: Determining Immune response profile from RNA-seq data

Authors: *Inglis tucker, Elizabeth Hammond

Abstract: Using GSEA as support for FACS sorting of differentiated immune cells.

Title: High knotting probability in helical DNA liquid crystal filaments

Authors: Zhijie Wang*, Tamara Christiani, Pei Liu, M. Carme Calderer, Mariel Vazquez, Javier Arsuaga

Abstract: The folding of DNA within bacteriophages is important for understanding how these viruses infect bacteria. Research has shown that DNA in bacteriophage P4 is often knotted, and models based on liquid crystals and other theories have been developed to explain this phenomenon. The authors of this paper hypothesize that the knotting probability observed in bacteriophage capsids is dependent on the ratio between the bending and twist moduli that describe the liquid crystalline state of the DNA inside phage capsids. They have developed a model of perturbed DNA in a cylindrical capsid based on cryo-EM images of bacteriophages and found that the knotting probability is high under a small ratio between the bending and twist modulus, and that the probability decays exponentially as the value of alpha is increased. The next step is to obtain the knot distributions of different classes of alpha and compare them with experimental data.

Title: Dynamic Wireless Resource Management and Transceiver Adaptation for Efficient Spectrum Utilization and Coexistence

Authors: Yu-Chien Lin*, Prof. Zhi Ding

Abstract: MIMO technology and massive MIMO play a vital role in enhancing the spectrum and energy efficiency of 5G and future wireless systems. For massive MIMO to succeed, accurate downlink (DL) channel state information (CSI) at the gNodeB is crucial. While time-division duplexing (TDD) systems have the advantage of uplink/downlink channel reciprocity, frequency-division duplexing (FDD) systems rely on user equipment (UE) feedback to acquire DL CSI. However, in FDD systems, the increasing number of DL antennas expected in millimeter wave or terahertz bands puts a significant feedback burden on uplink (UL) resources. As the number of antennas grows, the number of required DL pilots also increases, leading to reduced spectrum efficiency. Therefore, reducing CSI feedback and pilot resources is critical for deploying massive MIMO in FDD systems. The project demonstrates several deep learning-based and model-driven CSI feedback frameworks that reduce UL feedback overhead and pilot resources by introducing wave propagation physics. Additionally, we propose lightweight and low-complexity CSI feedback methods to address the limited computational and storage resources of low-cost UEs while delivering comparable DL CSI recovery performance to state-of-the-art methods.