2023 Postdoctoral Research Symposium

Abstract book
A message from the PSA Board

The 2022/2023 PSA Board would like to thank you for your attendance and participation in the 8th annual UC Davis Postdoctoral Research Symposium. Without the support and participation of UC Davis postdocs, this event and the PSA couldn’t exist. We hope that you have an enjoyable and productive time during the symposium and that this event inspires you to become more engaged with the postdoc community at UC Davis. We would also like to take this opportunity to mention additional social events for postdocs, including the monthly Postdoc Meet & Greet gatherings and the annual Postdoctoral Appreciation Dinner, both organized by Graduate Studies. You can find more information about these events on their website.

We are wholly indebted to the various UC Davis schools and colleges for their collective financial support for the 2023 PRS. Without their contributions, we would be unable to provide this conference to the UC Davis postdoc community without a cover charge. Thank you for keeping this event free for attendees and therefore equitable for all postdocs, not just those with sufficient income!

This year the PSA board attempted to build on a successful 2022 PRS by emphasizing full-length talks and poster presentations to highlight the breadth and depth of the excellent research being conducted at UC Davis by postdocs. We are also extremely proud to have recruited the UC Davis Chinese Orchestra and Olympic opener Ms. Wu, to serenade us during dinner.

We would like to thank our plenary Speaker Prof. Diane Beckles for agreeing to share her story regarding diversity, equity, and inclusion in STEM with us. Additionally, we would like to thank the Chancellor of UC Davis Gary May, who will be announcing the winners of the much-coveted Postdoctoral Excellence Awards before Dinner. This engagement reiterates that the UC Davis leadership is interested and engaged with the work that we do.

The PSA board would also like to extend their heartfelt thanks to several key members of the Graduate Studies academic staff, including Executive Director Nicole Rabaud, Dean Jean-Pierre Delplanque, Associate Dean Ellen Hartigan-O’Connor, and Associate Dean Duncan Temple Lang. We would also like to thank the Graduate Studies support staff, including Rosemary Martin Ocampo, Trina Giardino, Olga Garzón-López, Jacqueline Dosick, and Sara Camara.

Finally, the PSA board would like to thank the many volunteers who’ve helped ensure the symposium is run without a hitch. The enormous response from the postdoc community to our volunteer calls has been overwhelming and is a timely reminder that the postdoc community of UC Davis is alive and well.
Dr. Nathalie Aoun - Chair

Dr. Aoun is a postdoc in the Lowe-Power lab at the Plant Pathology (PLP) department. She obtained her Ph.D. in plant-microorganisms interactions in 2019 from the French National Institute of Agricultural Research (INRAE – Toulouse) in France. During her Ph.D. She investigated the natural variation of Arabidopsis response to *Ralstonia pseudosolanacearum* in a global warming context using molecular genetics approaches. Currently, in her postdoc, she is investigating genetic factors that benefit plant pathogenic *Ralstonia* growth across plant species using functional genomics approaches. Besides research, Nathalie is leading efforts within the PLP department to join postdocs over scientific and social gatherings. She is also a volunteer in organizing research seminar series and reviewing resumes for undergraduate and graduate students (monthly on LinkedIn).

Outside of lab life, she likes to hike, travel, and discover new cuisines.

Dr. Charlotte Smith - Treasurer

Dr. Smith is a postdoc in the Ripplinger and Grandi labs in the Department of Pharmacology. She is originally from the UK and completed her Ph.D. and first postdoc position at the University of Manchester prior to moving to Davis in Nov 2021. Her background is in cardiac physiology, focusing on the structure and function of the upper chambers of the heart, the atria. Since moving to Davis she has shifted from working on isolated cells to performing whole heart dual optical mapping and she uses this technique to study abnormal atrial rhythms in diseases like atrial fibrillation.

Outside of the lab she enjoys going out for dinner with friends, traveling, exploring new places and watching soccer.

Dr. Christopher Hart – Vice Chair

Dr. Hart, is an Australian postdoc in the Dawson Lab, in Microbiology and Molecular genetics. He started his postdoc in Feb 2020 after his Ph.D. in drug discovery against the protistan parasite *Giardia duodenalis*, at the Griffith Institute for Drug Discovery. His research now focuses on gene expression changes through the cell’s lifecycle with a particular interest in transcription factors unique to *G. duodenalis*, as well as genetic tool development for neglected pathogens more broadly.

Outside of the lab, he is usually found playing or watching soccer, or out with the family enjoying the sun/surf!
Dr. Bharti Singal - Secretary

Dr. Singal is a Postdoctoral Scholar at Al-Bassam's lab in the department of Molecular and Cellular Biology. She is a first-generation Ph.D. from Nanyang Technological University, Singapore, a gold medalist in M.Sc. Bioinformatics and a passionate STEM mentor at multiple international NGOs. Through her research aided with CryoEM, she is unraveling the mysteries behind neurodevelopmental disorders and congenital defects related to the brain and heart. She utilizes an interdisciplinary approach with her experience in structural biology, biochemistry, and computational biology to investigate biological questions related to human diseases. She has prior experience in working with infectious diseases. She advocates for women in STEM and has voluntarily developed an award-winning program Kalpana: She for STEM, with an NGO in India to promote women in higher STEM careers globally. To promote interdisciplinary learning, she founded BioXspace-Synergizing STEM. Outside lab and voluntary work, she enjoys traveling and exploring various cultures, food, dance, music, and architecture.

Dr. Leticia Cavole – Relations Officer

Leticia obtained her PhD in Marine Biology at the Scripps Institution of Oceanography, University of California San Diego. During her doctorate, she studied how to travel back in time using fish otoliths and fishermen's local ecological knowledge. She is passionate about fish ecology and conservation, and for her postdoc at UC Davis, she is using a similar otolith approach to reconstruct the life history and habitat use of critically endangered fish species in the San Francisco Estuary. In her spare time, she like to paint, swim and play the guitar.

Dr. Felix Ogunmokun – Career and Development Officer

Dr. Ogunmokun completed his Ph.D. in Soil and Water Sciences (soil physics/hydrology) from the Hebrew University of Jerusalem, Israel. After his PhD, he started a postdoc at UC Davis. His research interest is in irrigation science and contaminant transport in the vadose zone. I also hold the title of project manager for a USDA NIFA-funded project here at UC Davis. For fun he loves to play volleyball and chess.
2023 PRS Volunteers

Abstract Evaluation Committee
Coordinator: Rushika Kayshap
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Brianna Hunter
Connie Rojas
Amita Rawat
Malathy Palayam
Ana Santos
Claire P Prowse-Wilkins
Sreenivasan Meyyappan
Afef Margouzi
Orly Tonkykh
George Eusebio Kuodza
Uzma Ashraf
Ahmed El-Moghazy
Tina Lynn Rylee
Michael Onyedika Eze
Juliette Di Francesco
Juliya Abbasi
Sarah Shaffer
Diogo Manzano Galdeano

Presentations Committee
Coordinator: Malathy Palayam
Chao Huang
Orly Tonkykh
Tina Lynn Rylee
Michael Onyedika Eze
Juliya Abbasi
Sumi Nechat
Ulrika Beittner

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Ahmed El-Moghazy
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Orly Tonkykh
Sai Veena Sunkara
Ulrika Beittner
Rukmangada Maratikyathanahalli
Spikanta
Daniela Soto

Food and Beverage Committee
Coordinator: Charlotte Smith
Erica Nielsen
Dante Rojas
Flore Marie Herve
Rukmangada Maratikyathanahalli
Spikanta
Frank Assiamah

Registration Committee
Coordinator: Upasana Thirupadhiripuliyur Sridharan
Yi-Chang Sung
Connie Rojas
Rukmangada Maratikyathanahalli
Spikanta

Social Media Committee
Jennifer Claire Bullen
Juliya Abbasi
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<tr>
<td>8:00 - 9:00</td>
<td>Registration, breakfast, and poster set up</td>
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<td>9:00 - 9:30</td>
<td>Welcome session in Ballroom A</td>
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<td>9:00 - 9:10</td>
<td>Opening Remarks</td>
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<td>9:10 - 9:20</td>
<td>PSA Chair: Nathalie Aoun</td>
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<td>Opening Remarks by the Vice Provost and</td>
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<td>Dean of Graduate Studies</td>
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<td>9:20 - 9:30</td>
<td>PRS 2023 announcements</td>
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<td>9:30 - 10:15</td>
<td>Diversity, Equity, and Inclusion in STEM</td>
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<td>Invited speaker: Prof. Diane Beckles</td>
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<td>10:15 - 11:15</td>
<td>Capabilities and Limitations of Youth</td>
<td>Investigation on Tandem Kinase Protein, a</td>
<td>A generative adversarial network to speed up</td>
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<td>All-Terrain Vehicle Operators</td>
<td>New Class of Disease Resistance Protein</td>
<td>optical Monte Carlo simulation</td>
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<td>Guillerme De Moura Araujo</td>
<td>Yi-Chang Sung</td>
<td>Carlotta Trigila</td>
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<td>10:35 - 10:55</td>
<td>Habitual sleep duration and health-related</td>
<td>Single-cell profiling of complex plant</td>
<td>Multigenerational impacts on DNA methylation</td>
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<td>quality of life among family caregivers in</td>
<td>responses to bacterial infection</td>
<td>signatures in autism spectrum disorder</td>
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<td>the United States (US)</td>
<td>Jie Zhu</td>
<td>George Eusebio Kuodra</td>
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<td>10:55 - 11:15</td>
<td>Should I stay, or should I go? Fitness</td>
<td>Resting mitochondrial complex I from</td>
<td>Sustainable, Reusable yet Compostable</td>
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<td>tradeoffs for migratory and resident Delta</td>
<td>Drosophila melanogaster adopts a helix-</td>
<td>Microbial-Resistant</td>
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<td>Smelt</td>
<td>locked state.</td>
<td>Stational Cooling Media, “Jelly Ice Cubes”</td>
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<td>Leticia Maria Cavole</td>
<td>Abhilash Padavannil</td>
<td>Jiahuan Zou</td>
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<td>11:15 - 11:45</td>
<td>Morning Break</td>
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<td>11:45 - 12:15</td>
<td>Elucidation of a dynamic interplay between</td>
<td>Seed germination responses of branched</td>
<td>Accurate Oxygen Abundance of Interstellar</td>
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<td>a heterotrimeric G protein and different</td>
<td>broumrape (Phealipanche ramosa) to various</td>
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<td>beta-adrenergic Yanxiao Han</td>
<td>ammonium compound</td>
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<td>12:05 - 12:25</td>
<td>Brucella abortus replication in the</td>
<td>Compost application reduces N2O production</td>
<td>A 3D Radiative Transfer-based Plant</td>
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<td>placenta takes place primarily in the</td>
<td>in California</td>
<td>Multispectral Image Synthesis Framework</td>
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<td>extracellular space and requires the ability</td>
<td>olive orchards</td>
<td>Tong Lei</td>
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<td>12:25 - 12:45</td>
<td>High availability rumen-protected choline</td>
<td>A proactive approach to prepare for the</td>
<td>A Coding Basis and Three-in-One Integrated</td>
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<td>alters ureterine microbiome in dairy cows</td>
<td>invasion of Tuta absoluta into California</td>
<td>Data Visualization Method ‘Ana’ for the Rapid</td>
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<td>Thaisa Campos Marques</td>
<td>Benjamin Lee</td>
<td>Analysis of Hefei Zhao</td>
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<td>Lunch Break</td>
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<td>Ballroom A: Poster Session</td>
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<td>Ochratoxin A contamination of California</td>
<td>Homologous recombination occurs frequently</td>
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<td>pistachios and their causal agents</td>
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<td>Pummi Singh</td>
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<td>15:05 - 15:25</td>
<td>Qualifying the fruiting characteristic of</td>
<td>The adaptive mechanisms of plant</td>
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<td>Chandler walnut trees</td>
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<td>Use of a non-GMO based method for</td>
<td>Leveraging quantitative genetic mapping</td>
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<td>provitamin A biofortification in</td>
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<td>tetraploid wheat grains</td>
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<td>15:45 - 16:15</td>
<td>Afternoon Break</td>
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<td>16:15 - 16:17</td>
<td>The neuropathological landscape of</td>
<td>Accelerating detection of bacteria in</td>
<td>Wildfire-Urban Interface: Emissions from</td>
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<td>Hispanic and Non-Hispanic White Dedicents</td>
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<td>with Alzheimer’s disease</td>
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<td>Prakash Singh Badal</td>
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<td>16:35 - 16:55</td>
<td>Specific Patterns of GABergic Interneuron</td>
<td>Less saturated fat, healthier lipid</td>
<td>Continuous re-optimization of reservoir</td>
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<td>Pathology in the Autistic Prefrontal</td>
<td>intake: the design of oleogels with</td>
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<td>Cortex are Associated with</td>
<td>small molecular weight surfactant for food</td>
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<td>16:55 - 17:15</td>
<td>Fixel based analysis to investigate white</td>
<td>Effects of using a reduced protein Nordic</td>
<td>Phylogeography of the California trapdoor</td>
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<td>matter alterations in individuals with</td>
<td>diet as complementary feeding on infant</td>
<td>spider genus (Hebestasis: Halonoprotidae)</td>
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<td>Mild cognitive impairment and</td>
<td>serum metabolomes</td>
<td>Lisa Chamberland</td>
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<td>Anjan Bhattarai</td>
<td>Zhichao Zhang</td>
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<td>17:30 - 19:30</td>
<td>Closing ceremony in Ballroom A</td>
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<td>PSA awards for best talks and posters</td>
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<td>Postdoctoral Excellence Awards</td>
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<td>Chancellor Gary May</td>
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<td>Traditional Chinese music concert</td>
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<td>Ms. Wenying Wu and the Davis Chinese</td>
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Upcoming events/workshops

The UC Davis Ombuds Office is a confidential, independent, impartial, and informal problem-solving and conflict-management resource. They offer individual meetings, mediation, and training to facilitate conflict resolution and invite for all postdocs with university-related issues and concerns to visit their office. The Ombuds can assist by listening to concerns, clarifying issues, identifying policies and resources, and providing coaching and communication strategies.
Postdocs are invited to register for their upcoming session “Complete Conflict Competence Training for Graduate Students and Postdocs” that will take place on Tuesday April 25 9am - 2pm in 1230 Walker Hall (West Conference Room).
Please visit the Ombuds Office stand during the morning break and https://ombuds.ucdavis.edu/ to find out more.

OMBUDS office will be giving a workshop on the “Conflict Competence Basics and Ombuds Office Services” that will be hosted by PSA on May 5th, 2023.

UC Davis Graduate Studies

Graduate studies is an important resource for Postdoctoral Scholars at UC Davis. Support staff in Graduate studies are equipped to handle your questions related to being a postdoc here at UC Davis. If you have any inquiries related to your employment contract, benefits, conflicts management, etc. please reach out to Graduate Studies.

Additionally, Graduate studies hosts several social events just for postdocs. Join us at Meet & Greet events to meet over coffee and breakfast with UC Davis postdocs, PSA, and graduate studies staff! Event dates are announced by email every month and can also be found on the Graduate Studies website. In addition to the monthly Meet & Greets, Graduate studies organizes an annual Postdoc Appreciation Dinner, once the weather is more amenable. Keep an eye on your emails for the 2023 edition!
Resting mitochondrial complex I from Drosophila melanogaster adopts a helix-locked state.

Abhilash Padavannil¹, Anjaneyulu Murari², Shauna-Kay Rhooms², Edward Owusu-Ansah²,³ and James A. Letts¹*

¹Department of Molecular and Cellular Biology, University of California, Davis, CA 95616, USA
²Department of Physiology and Cellular Biophysics, Columbia University Irving Medical Center, New York, NY 10032, USA.
³The Robert N. Butler Columbia Aging Center, Columbia University Irving Medical Center, New York, NY 10032, USA.

Respiratory complex I is a proton-pumping oxidoreductase key to bioenergetic metabolism. Biochemical studies have found a divide in the behavior of complex I in metazoans that aligns with the evolutionary split between Protostomia and Deuterostomia. Complex I from Deuterostomia including mammals can adopt an off-pathway “deactive” state, whereas complex I from Protostomia cannot. The presence of off-pathway states complicates the interpretation of structural results and has led to considerable mechanistic debate. Here we report the structure of mitochondrial complex I from the thoracic muscles of the model protostomian Drosophila melanogaster. We show that, although D. melanogaster complex I (Dm-CI) does not deactivate the resting state of Dm-CI adopts multiple conformations. We identify a new helix-locked open state in which an N-terminal α-helix on the NDUF54 subunit wedges between the peripheral and membrane arms. Comparison of the Dm-CI structure and conformational states to those observed in bacteria, yeast and mammals provides insight into the roles of subunits across organisms, explains why Dm-CI does not deactivate and reveals incompatibilities with current mechanistic models of complex I turnover. Additionally, the Dm-CI structure and novel regulatory mechanism will allow for the development of more selective pesticides for agriculture and human disease.

Compost application reduces N2O production in California olive orchards

Andrew J. Curtright*ᵃ, Savannah Haas ᵃ, William R. Horwath ᵃ, Xia Zhu Barker ᵃ,ᵇ

ᵃ Department of Land, Air and Water Resources, University of California, Davis
ᵇ Department of Soil Science, University of Wisconsin—Madison
*Correspondence: acurtrigg@ucdavis.edu

Overapplication of nitrogen (N) within agriculture can cause nitrate leaching and nitrous oxide emissions. The prevent this, the application of compost with a high C:N ratio promotes soil N retention. The California olive industry has grown rapidly in the past decade, but growers lack nutrient guidelines developed for California production systems. To address this, we conducted a multi-year trial to determine the effects of N application rate and compost on olive production and soil N cycling. We supplied N at three application rates, with or without compost. Throughout the growing season we monitored greenhouse gas production and concentrations of soil N, and we measured olive yield and olive oil quality during harvest. We found that reduced application of N did not affect olive yield or olive oil quality. Higher rates of N application tended to increase N₂O emissions throughout the growing season. Compost application mitigated these effects by reducing concentrations of inorganic N and decreasing flux of N₂O, particularly in plots receiving the highest amount of N. After the first year of this study, we show that lower rates of N application can reduce N loss without affecting olive yield and that compost also reduces the potential for N loss.
Talk abstracts

Fixel based analysis to investigate white matter alterations in individuals with Mild cognitive impairment and Alzheimer’s disease

Anjan Bhattarai 1,2, *, Pauline Maillard 1, Charles DeCarli 1, Audrey Fan 1,2

1 Department of Neurology, University of California Davis, Davis, CA, USA
2 Department of Biomedical Engineering, University of California Davis, Davis, CA, USA
*Correspondence: anbhattarai@ucdavis.edu

Alzheimer’s disease (AD) is the leading cause of dementia, and is associated with altered white matter (WM) microstructures in the brain. Diffusion Magnetic Resonance Imaging (dMRI) is a non-invasive method of examining white matter alterations in AD and Mild cognitive Impairment (MCI). dMRI based Fixel-based analysis (FBA) is a novel method that enables the investigation of fibre specific WM alterations at the microscopic level.

We investigated fibre tract-specific changes in the whole-brain WM in individuals with MCI and AD using dMRI based FBA.

N= 102 participants were included in this study, including 34 individuals with AD, 34 with MCI, and 34 control subjects. dMRI data were obtained on a 3T MRI scanner. dMRI data were processed to generate FBA maps.

The whole-brain FBA showed significant reduction in Fibre Density (FD) in individuals with AD compared to MCI, in regions including splenium of corpus callosum, fornix, and the left uncinate fasciculus. Furthermore, AD showed significant reduction in FD in the left uncinate fasciculus compared to controls. FBA-derived measures demonstrated sensitivity in detecting microstructural white matter alterations in AD. These findings highlight the utility of FBA as a potential biological marker for providing valuable insights into pathophysiologic changes in AD.

Figure1: Fixel based analysis (FBA) of white matter alterations in Mild cognitive impairment and Alzheimer’s Disease. (A) General overview of the FBA processing steps in this study. (B) White matter regions showing significant reductions (p<0.05) in Fibre Density (FD) are superimposed onto the population template.
Talk abstracts

A proactive approach to prepare for the invasion of Tuta absoluta into California

Benjamin Lee*, Kris Godfrey, and Ian Grettenberger

Department of Entomology and Nematology, University of California - Davis

*Correspondence: bwalee@ucdavis.edu

The South American tomato leafminer, *Tuta absoluta*, is a devastating pest of tomatoes globally and poses a significant threat to tomato production in the United States. Broad-spectrum insecticides and endemic natural enemies have had some success in controlling *T. absoluta* in invaded regions, however insecticide resistance is widespread, variation in natural enemy communities across regions makes reliance on biological control difficult, and resistant tomato varieties have not yet been developed. To improve the U.S. tomato industry’s response to *T. absoluta* invasion into the US, our studies will i) identify parasitoids that may attack *T. absoluta* and the potential role of parasitoid control in California, and ii) evaluate resistance characteristics of wild tomato relatives from *T. absoluta*’s native range. Using a related moth, *Keiferia lycopersicella*, we infested tomato plants to survey parasitoid communities in the Sacramento and San Joaquin Valleys and identified several candidates for biological control of *T. absoluta*. Additionally, we conducted resistance assays on 12 accessions of wild tomato (*Solanum habrochaites*) collected throughout *T. absoluta*’s native range. Further testing of insecticide and biological control efficacy, alongside identification of resistance traits for future breeding programs, will help to enable a rapid response to invasion by *T. absoluta* into the US.

A generative adversarial network to speed up optical Monte Carlo simulation

Carlotta Trigila*, Anirudh Srikanth, Emilie Roncali

1Department of Biomedical Engineering, University of California, Davis, Davis, CA, United States

2Department of Radiology, University of California, Davis, Davis, CA, United States

*Correspondence: ctrigila@ucdavis.edu

Optical Monte Carlo simulations are widely used to design and optimize scintillator-based gamma detectors in nuclear medicine and high-energy physics. In such detectors, detailed light transport and collection are needed to optimize their performance. However, the time and memory burden caused by the track-wise approach to particle transport in commonly used Monte Carlo codes make optical simulation prohibitive at a system level, where thousands of scintillators must be modeled. Generative Adversarial Networks (GANs) are explored as a tool to accelerate optical simulations of scintillator-based detectors. GANs learn representations of a training dataset by modeling high-dimensional distributions. Once trained, the GAN produces distributions following the probability distribution of the training data. We will present the architecture and training set of the first GAN version. The training set comprises a large dataset of phase space generated by Monte Carlo simulation. We compare the spatial distributions obtained with the GAN with the ones of the training and show similarities higher than 94%. The GAN generates hundreds of realistic optical photon spatial distributions in a few milliseconds compared to the few seconds needed for a complete transport simulation. We show how GANs enable high-fidelity optical simulation of nuclear medicine systems, mitigating their computational complexity.
Talk abstracts

Specific Patterns of GABAergic Interneuron Pathology in the Autistic Prefrontal Cortex are Associated with Intellectual Impairment and Restricted Repetitive Behavior Symptomology

Brett D. DuFour*, Erin L. McBride, Trevor Bartley, Pablo Juarez, & Verónica Martínez-Cerdeño

1. Department of Psychiatry & Behavioral Sciences, UC Davis School of Medicine
2. Institute for Pediatric Regenerative Medicine (IPRM), Shriner’s Hospital for Children
3. Department of Pathology & Laboratory Medicine, UC Davis School of Medicine
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Autism Spectrum Disorder (ASD) is a neurodevelopmental condition characterized by deficits in social communication and repetitive behaviors. It remains largely uncharacterized how specific neurobiological alterations underlie the clinical profile of ASD. We have previously shown that parvalbumin-positive Chandelier cells (ChC), a specific type of GABAergic interneuron, are reduced in number in the ASD prefrontal cortex. Here we assessed the relationship between interneuron pathology with ASD symptom severity and comorbidity, using clinical records from ASD (n=20) and neurotypical control (n=19) brain donors. Total GABAergic interneuron number was significantly reduced in ASD subjects with intellectual disability (208.5 ± 37.1 INs/bin) in the PFC - by 36.6% relative to ASD without intellectual disability (329.0±31.5 INs/bin, p=0.024) and by 38.7% relative to neurotypical controls (340.1±25.7 INs/bin, p=0.009). ASD motor stereotypy severity was correlated with ChC loss severity in BA47, as indicated by reductions in PV+ interneurons (r=-0.722, p=.043) and GAT1+ Cartridges (r=-0.710, p=0.049). For the first time, we have identified a link between circuit level pathology in human Autism (ChC loss) with a specific core symptom domain (Restricted Repetitive Behavior). Additionally, we identified that intellectual impairment in ASD reflects a more severe form of a common underlying neuropathology, cortical GABAergic interneuron loss.

Multigenerational impacts on DNA methylation signatures in autism spectrum disorder

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The prevalence of Autism Spectrum Disorder (ASD) has been on the rise in recent years, and the underlying causes are not fully understood. However, recent research suggests that genetics and environmental factors may play a role in the development of ASD. In order to investigate the potential impact of multigenerational epigenetic inheritance on the development of ASD, our study recruited 349 participants from the CHARGE (Child Autism Risks from Genetics and the Environment), including grandparents, parents, and children. We hypothesize that DNA methylation patterns associated with ASD may be detectable across generations and associated with grandparental environmental exposures. A questionnaire was used to gather information about the participants’ exposure to environmental factors, and biospecimens, including saliva samples and dried blood spots, were collected. DNA was extracted from the biospecimens and subjected to whole genome bisulfite sequencing (WGBS) to analyze DNA methylation. We are currently awaiting sequencing results. In the bioinformatics analysis, we will use DMRichR to examine differences in methylation among subjects and Comethyl to compare correlation patterns between methylation marks and selected variables, including grandparental exposures. This research will provide new insights into the underlying etiology of ASD and pave the way for future research in the field.
Talk abstracts

**Homologous recombination occurs frequently in co-infected cells and is significantly influenced by multiplicity of infection**

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Coronaviruses (CoVs) are positive-sense RNA viruses that are broadly distributed in nature and routinely spillover into new species, which can result in mortality and economic losses in humans and domesticated animals. For this reason, it is important to understand the mechanisms that may be associated with CoV host switching. One such mechanism, recombination, is the process by which two viruses exchange part of their genetic material to create novel strains that are distinct from either parental virus. Though recombination is widely accepted to play a role in CoV spillover and has been shown to have occurred throughout the evolutionary history of most human CoVs, there is little known about the mechanism or genetic limitations. To address these gaps, we conducted coinfection experiments with canine and feline CoV, at different multiplicities of infection (MOI) at 24 and 48 hours post infection (hpi) and characterize the recombinant genomes produced using nanopore long-read sequencing. Recombination was not influenced by hpi and was observed consistently across replicates. However, MOI had a significant impact on the probability of recombination, with low MOI experiments producing fewer recombinants. These studies utilize a novel sequencing approach to show that recombination occurs readily in the absence of selection pressure.

**Leveraging quantitative genetic mapping data for discovery of novel genetic variants underlying root architecture in tomato**

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Tomato (*Solanum lycopersicum*) is a model system for fleshy fruit development and findings in this system can be used for genetic improvement of all solanaceous crops, including potato, pepper, and eggplant. In addition to decades of well-documented breeding data, a high-quality genome sequence is available along with a growing molecular and genomic toolbox. One of these resources is a well-characterized panel of over 150 accessions wild and domesticated accessions (Varitome panel). While fruit and flower traits are exceedingly well-characterized for the Varitome panel, no published studies have explored root-related traits. Roots are responsible for absorption of water and all non-photosynthetic nutrients. Furthermore, root development is highly plastic and responsive to environmental perturbations. We therefore hypothesized that we could use the Varitome panel to map genetic variants underlying early seedling root traits. Here, we use high throughput image analysis of early seedling root architecture to map potential causal variants using a genome wide association study. In doing so, we observed measurable heritability across our 12 root traits. When we performed our genome wide association study, we found 47 unique significant loci across six traits. Currently, we are testing these significant loci and their nearby variants for gene regulatory activity.
Talk abstracts

Habitual sleep duration and health-related quality of life among family caregivers in the United States (US)

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Purpose: This study examined the association between habitual sleep duration and health-related quality of life (HRQOL) measures in family caregivers.

Methods: Cross-sectional data of 23,321 family caregivers in the 2016 Behavioral Risk Factor Surveillance System was used. Logistic regression models tested association between sleep duration (<7 [short], 7 - 9 [normal, reference], >9 hours [long]) and general health (fair or poor, good to excellent [reference]). Zero-inflated negative binomial models were used to analyze association of sleep duration with poor mental health days and poor physical health days.

Results: Short sleep duration was associated with fair or poor health (odds ratio [OR], 1.40; 95% CI: 1.12, 1.74). Caregivers with long sleep duration were twice more likely to report fair or poor health (OR, 2.07; 95% CI: 1.34, 3.21). Short sleep duration was associated with higher number of poor mental days (RR [risk ratio], 1.17; 95% CI: 1.04, 1.31) and poor physical health days (RR, 1.26; 95% CI: 1.10, 1.45) while long sleep duration was associated with higher number of poor mental health days (RR, 1.31; 95% CI: 1.08, 1.60).

Conclusion: The association between sleep duration and HRQOL point to a potential role of adequate sleep in promoting caregivers’ health and wellbeing.

Sustainable, Reusable yet Compostable Microbial-Resistant Stational Cooling Media, “Jelly Ice Cubes”

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Serious economic losses of foods could be caused by temperature abuses, quality loss and microbial cross-contamination. Ice and ice packs are commonly used as heat storage material in the cold chain of food and pharmaceutical industries. The use of water in making traditional ice and the utilization of plastics in manufacturing reusable ice packs have both imposed significant environmental burdens on the planet. We aimed to solve the above challenges via multidisciplinary approaches. A novel stationary cooling media, “Jelly Ice Cubes (JICs)”, was proposed, and the concept was experimentally proved. JICs were proven to be microbial resistant (self-cleanable), compostable, and customizable with comparable cooling efficacy with traditional ice while generating no meltwater at its unfrozen status. It is anticipated that the research can impact the global cold chain by reducing water and plastic use while preventing product quality loss and contamination caused by temperature abuses and melting water while promoting the sustainability and health of humans and the planet.
Talk abstracts

A Coding Basis and Three-in-One Integrated Data Visualization Method ‘Ana’ for the Rapid Analysis of Multidimensional Omics Dataset

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With innovations and advancements in analytical instruments and computer technology, omics studies based on statistical analysis, such as phytochemical omics, oilomics/lipidomics, proteomics, metabolomics, and glycomics, are increasingly popular in the areas of food chemistry and nutrition science. However, a remaining hurdle is the labor-intensive data process because learning coding skills and software operations are usually time-consuming for researchers without coding backgrounds. A MATLAB® coding basis and three-in-one integrated method, ‘Ana’, was created for data visualizations and statistical analysis in this work. The program loaded and analyzed an omics dataset from an Excel® file with 7 samples * 22 compounds as an example, and output six figures for three types of data visualization, including a 3D heatmap, heatmap hierarchical clustering analysis, and principal component analysis (PCA), in 18 s on a personal computer (PC) with a Windows 10 system and in 20 s on a Mac with a MacOS Monterey system. The code is rapid and efficient to print out high-quality figures up to 150 or 300 dpi. The output figures provide enough contrast to differentiate the omics dataset by both color code and bar size adjustments per their higher or lower values, allowing the figures to be qualified for publication and presentation purposes. It provides a rapid analysis method that would liberate researchers from labor-intensive and time-consuming manual or coding basis data analysis. A coding example with proper code annotations and completed user guidance is provided for undergraduate and postgraduate students to learn coding basis statistical data analysis and to help them utilize such techniques for their future research.

Wildfire-Urban Interface: Emissions from Buildings

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The increasing intensity of wildfire, especially in California, has placed more than 25% of communities in the wildfire-urban interface (WUI). Although wood is an environmental-friendly and often local material of construction, it can quickly become a source of emissions from wildfire in case of a large fire penetrating a community. This study presents a framework to estimate wildfire emissions in terms of CO₂, greenhouse gases, and particulate matter. For this purpose, we consider a typical single-family light-frame wooden house with an area of 1816 sqft located in Paradise, California. This building is one of many which are being used for reconstruction after the devastating 2018 Camp Fire. We also discuss the effects of construction choices on wildfire emissions. The study considers combustion conditions, the environment, and material type. Finally, the behavior of an innovative alternative construction material made of compressed and stabilized earth block masonry is discussed. The results show that the earth block building contributes significantly reduced levels of wildfire emissions compared to the traditional wooden house.
Talk abstracts

Capabilities and Limitations of Youth All-Terrain Vehicle Operators

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All-terrain vehicles (ATVs) are widely used in both occupational and recreational settings, particularly among youth on farms. However, the increase in ATV power and size presents a risk for youth. A recent study revealed that riders younger than 16 years old accounted for 25% of ATV-related injuries on American farms. This study aimed to understand the limitations youth face when operating ATVs and the impacts on incidents.

We evaluated youth strength, anthropometry, and field of vision. Firstly, we measured the forces required to activate the controls of 10 ATVs and compared it to the strength of youth from various ages. Secondly, we used an ergonomics software (SAMMIECAD) to verify youth’s ability to reach the ATV’s controls. Lastly, we used SAMMIECAD to quantify the youth’s field of vision and compare it to an adult’s.

Results showed that ATV control forces exceeded youth strength, particularly with the foot brake. Anthropometric simulations indicated that most youth could not reach some controls. Youth also had a limited field of vision compared to adults, which makes it difficult to see potential hazards. This study highlights the need for parents to consider youth’s physical capabilities when selecting ATVs for occupational settings to improve safety for youth.

Single-cell profiling of complex plant responses to bacterial infection

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Cell response to pathogen infection varies within a plant leaf, yet this heterogeneity is not well resolved. We exposed Arabidopsis to Pseudomonas syringae or mock treatment and profiled transcriptomes of >11,000 individual cells using single-cell RNA sequencing. Integrative analysis of cell populations from both treatments identified distinct pathogen responsive cell clusters exhibiting transcriptional responses ranging from immunity to susceptibility. Pseudotime analyses through pathogen infection revealed a continuum of disease progression from an immune to susceptible state. Confocal imaging of promoter reporter lines for transcripts enriched in immune cell clusters expressed surrounding substomatal cavities colonized or in close proximity to bacterial colonies, suggesting cells within immune clusters represent sites of early pathogen invasion. Genes enriched in susceptibility clusters were highly induced at later stages of infection and exhibited more general localization. Overall, our work uncovers cellular heterogeneity within an infected leaf and provides unique insight into plant differential response to infection at a single-cell level.
Talk abstracts

Phylogeography of the California trapdoor spider genus (*Hebestatis*: Halonoproctidae)

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Spanning from Oregon to Baja Mexico, the California Floristic Province (CAFP) hosts a wide range of diverse ecosystems and is a well-known ‘hotspot’ of animal and plant diversity. The Central Valley ecoregion in California divides coastal and inland foothills and mountain ranges and serves as a genetic barrier for species with low vagility. Trapdoor spiders are common throughout the CAFP and are known for their low vagility and high endemism. The trapdoor spider, *Hebestatis*, comprises a single described species *H. theveneti*, can be found in the Sierran and Coastal foothills surrounding the Central Valley. This research aimed to examine the intraspecific relationships and phylogeography within *H. theveneti*. We collected *Hebestatis* from 46 localities, including the northern and southernmost record of the genus. Ultraconserved element (UCE) data were used to generate maximum likelihood and coalescent-based tree inferences. Using SNP data, we ran variational autoencoder (VAE) clustering analyses to assess patterns of gene flow across populations. We found 11 phylogenetic and geographically structured populations, which showed admixing between geographically proximate populations. We also found sympatric populations and evidence for trans-valley ‘leaks’ across the Central Valley. This research infers both ancient vicariance and recent gene flow across this geologically complex landscape.

*Brucella abortus* replication in the placenta takes place primarily in the extracellular space and requires the ability to acquire glucose

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*Brucella abortus* is a zoonotic pathogen whose natural reservoir is cattle. During chronic infection, *B. abortus* persists in alternatively activated macrophages (AAM). We know that *B. abortus* needs glucose to sustain chronic infection. However, in pregnant cattle *Brucella* targets the placenta, causing abortion and infertility. There, *B. abortus* invades trophoblasts, macrophages and neutrophils, and the extracellular space. Little is known about the metabolic pathways enabling *B. abortus* to exploit the placental niche. We hypothesized that glucose utilization within AAM would also be important during *B. abortus* placental infection.

To test this hypothesis, we used a pregnant mouse model conditionally deficient for PPARγ in macrophages (*Ppargfl/fl LysMcre/−*), wild type pregnant mice and BeWo cells. We showed that *B. abortus* needs glucose to establish infection in the placenta, but AAM were not the main niche for *B. abortus* replication. Moreover, glucose was not required for replication in trophoblast. However, *B. abortus* needed to acquire glucose to replicate within an extracellular niche of the placenta, since, mice infected with a mutant defective for glucose uptake (*gluP*) had markedly increased fetal viability. Our results demonstrate that extracellular replication of *B. abortus* is important to induce pathology associated with abortion and transmission of infection.
Talk abstracts

**Less saturated fat, healthier lipid intake: the design of oleogels with small molecular weight surfactant for food applications**

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Oleogels have raised great interest among food scientists, as they have large potential in replacing solid/saturated fat with comparable physical properties but healthier lipid intake. These solid fat alternatives were designed using functional oleogelator such as surfactants, waxes, and carbohydrate polymers. Ethylcellulose (EC) has shown promise as a directly dispersible polymer oleogelator, but these oleogels generally display limited plasticity due to poor solvent/polymer interactions, which restricted food applications. This work seeks to expand the scope of EC as a functional oleogelator by characterizing the impact of incorporating various amphiphilic small molecule surfactants in canola oil. Seven surfactants were selected to understand the effect of chemical structure with respect of head and tail groups on EC-based oleogel properties. Monoacylglycerol (MAG) and stearic acid (StAc) both enhanced gel strength to the largest degree (by ~18-fold), while sodium stearoyl lactylate (SSL) and citric acid esters of monoglycerides (CIRTEM) produced the greatest improvement in shear recovery (higher gel elasticity). In contrast, diacetyl tartaric acid esters of monoglycerides (DATEM) diminished gel strength. The physicochemical and microstructural nature of these surfactants in modifying gel properties and their molecular mechanisms will be discussed in relation to developing functional polymer-based oleogel as fat mimetics for different industrial applications.

![Fig.1 Schematic presentation of designed ethylcellulose-based oleogel with added surfactants: gel microstructure and potential food applications.](image-url)
Should I stay, or should I go? Fitness tradeoffs for migratory and resident Delta Smelt

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Abstract: Migratory fish may display a variety of life history strategies (i.e., phenotypes) to persist in dynamic ecosystems. However, it remains unknown how these phenotypes influence the fitness of small fish in estuaries. Delta Smelt (Hypomesus transpacificus) is at imminent risk of extinction but exhibits a complex life history, with semi-anadromous migrant (SA), brackish-water resident (BWR), and freshwater resident (FWR) phenotypes inferred through otolith strontium isotope analysis. Here we used Generalized Additive Models to examine how Delta Smelt fitness metrics, including body and gonad weight, fecundity, and egg area, vary in relation to hydrology and phenotype in the San Francisco Estuary. Body weight reduced during a drought period (e.g., 2013-2016) and recovered during a wet year (2017) for all phenotypes, exemplifying the importance of freshwater outflow for the species. The FWR had lower body weight, gonads, and fecundity than BWR and SA. Nonetheless, FWR had larger eggs than other phenotypes, potentially due to hydration at lower salinity. Larger body sizes and fecundity in SA appears to support selection for adopting the migratory strategy. For the tiny Delta Smelt, where SA groups are the bulk of the population (~80-85%), having greater bodies and fecundity might ensure energy for upstream movement and reproduction.
Talk abstracts

The adaptive mechanisms of plant pathogenic Ralstonia host range

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Pathogen host range impacts epidemiology and pathology. Pathogens have evolved adaptive mechanisms that create high genetic diversity. This genetic diversity allows generalist pathogens populations to cross species barriers and infect different host species. However, adaptive mechanisms of generalist pathogens that co-evolve with plant species remain poorly understood. Here we investigate Ralstonia’s adaptations that affect host physiology and defenses in the plant pathogenic Ralstonia. To identify Ralstonia’s adaptation genes, we used high-throughput forward genetic screening based on a random barcode transposon mutant sequencing approach to quantify the fitness of thousands of bacterial mutants in planta. We inoculated eight tomato cultivars with the library of barcoded mutants. Using Illumina sequencing, we quantified the relative abundance of bacterial mutants before and after growth in tomato cultivars. This quantification allows us to identify genetic factors that are required or detrimental to in planta bacterial growth in the selective environment. Our analysis revealed that Ralstonia spp. use common and unique genes in plants with varying levels of plant defenses. Our results show that type-3 effectors RipP2 and RipAC are detrimental to Ralstonia’s growth in specific tomato cultivars. Ongoing studies will help us understand the function of these genes under the pressure of plant defenses.
Accelerating detection of bacteria in food using Artificial Intelligence and optical imaging

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In assessing food microbial safety, the presence of *E. coli* is a critical indicator of fecal contamination. However, conventional detection methods require the isolation of bacterial macro-colonies for biochemical or genetic characterization, which takes a few days and is labor-intensive. In this study, we show that the real-time object detection and classification algorithm YOLOv4 (You Only Look Once version 4) can accurately identify the presence of *E. coli* at the microcolony stage after 3-h cultivation. Integrating with phase-contrast microscopic imaging, YOLOv4 discriminated *E. coli* from seven other common foodborne bacterial species with an average precision of 94%. This approach also enabled rapid quantification of *E. coli* concentrations over three orders of magnitude with the $R^2$ of 0.995. For romaine lettuce spiked with *E. coli* (10 - 10$^3$ CFU/g), the trained YOLOv4 detector had a false-negative rate of less than 10%. This approach accelerates analysis and avoids manual result determination, which has the potential to be applied as a rapid and user-friendly bacterial sensing approach in food industries.

Figure. Schematic illustration of artificial intelligence-based rapid bacterial detection
Talk abstracts

Seed germination responses of branched broomrape (Phelipanche ramosa) to various ammonium compound

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Branched broomrape is a parasitic weed that recently re-emerged in California tomato fields. It is currently classified as an "A" pest and subjected to state-enforced quarantine action. This weed can produce thousands of tiny seeds and is easily spread by farm machinery and equipment. To prevent branched broomrape seed dispersal, disinfestation of farm machinery should occur before entering uninfested fields. Therefore, we tested the effectiveness of various ammonium compounds, including DDAC, ADBC, DDAB, AB, and AC, on the prevention of branched broomrape seed germination in different exposure duration. We tested seven concentrations: 0, 0.05, 0.1, 0.2, 0.5, 1, and 2.5 %. The exposure times tested were 1, 3, 5, and 10 minutes. Dose-response analysis showed that ADAC, DDAB, and DDAC, effectively prevented broomrape germination. The effective dose for 50% reduction in germination varied significantly across the above three chemistries, and ED50 ranged from 0.00002 in DDAC at 1 minute to 0.402 (w/v) in ADAC at 10 minutes. The viability decrease in response to DDAB and DDAC occurred sharply, and complete prevention was achieved below 0.5 concentration at only a 1 minute exposure duration. The declining response to ADAC was slower and AC and AB had no sanitation effect on broomrape seed.

Ochratoxin A contamination of California pistachios and their causal agents

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Ochratoxin A (OTA) is an IARC Class 2b carcinogen produced by Aspergillus and Penicillium spp. that contaminates many crops, including pistachios. Pistachios are economically significant to United States in terms of production and export and California (CA) produces over 50% of the global production. OTA contamination of pistachios is a potential barrier to export due to border rejections. We examined the prevalence of OTA in CA produced pistachios and investigated its causal agents. We detected >5 µg/kg OTA, the European Union maximum regulatory limit, in 18% of the 809 field samples collected during 2018-21. OTA levels exceeded 100 µg/kg in 3% samples. Fungi responsible for OTA contamination were isolated from leaves, nuts, and soil collected from 14 pistachio orchards. Pathogenicity assays and DNA sequences suggest that A. westerdijkiae, A. ochraceus and A. melleus are the causal fungi of OTA contamination of pistachios in CA. While these fungi produced >1000 µg/kg OTA in inoculated pistachios at 25ºC, representative isolates contaminated pistachios with >25,000 µg/kg OTA at temperatures ranging from 15-30ºC. Results suggest frequent contamination of pistachios in CA with variable levels of OTA produced by distinct species. The current study helps CA pistachio industry implement effective management of OTA in pistachios.
Talk abstracts

The status of digital pathology and associated infrastructure within Alzheimer's Disease Centers

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Talk abstracts

In the area of Alzheimer disease and related disorders, digital pathology (DP) has transformative potential. However, infrastructure barriers may limit adoption. To provide insights into implementation barriers, in 2019 a survey was conducted within National Institutes of Health’s Alzheimer’s Disease Centers (ADCs). Questions covered funding sources, infrastructure, and data management related to DP. Of the 35 ADCs to which the survey was sent, 33 responded. Most respondents (81%) stated their ADC had access to a digital slide scanner, the most frequent brand being Aperio/Leica (62.9%). Approximately a third of respondents stated there were fees to utilize the scanner. For DP and machine learning (ML) resources, 41% of respondents stated none was supported by their ADC. For scanner purchasing and operations, 50% of respondents stated they received institutional support. Some were unsure of the file size of scanned digital images (37%) and total amount of storage space files occupied (50%). Most (76%) were aware of other departments at their institution working with ML; a similar (76%) percentage were unaware of multi-university or industry partnerships. These results demonstrate many ADCs have access to a digital slide scanner; further investigations are warranted to understand hurdles to implement DP and ML workflows.

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Continuous re-optimization of reservoir policies as an adaptation to climate change

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With changing climate and extremes in occurrences of floods and droughts, there is necessity for reservoirs operations to adapt to climate change to efficiently manage existing infrastructure. We develop a continuous re-optimization approach in which parameters of rule curve are adapted with a fixed frequency (f) using a recent window (w) of observations. The approach is demonstrated for the multi-reservoir system in the Sacramento-San Joaquin River basin, California using climate models ensemble as forcing scenarios. For each reservoir, we test a range of frequencies from 1-20 years and window sizes from 5-50 years to find the best combination for re-optimization. Through this experiment, we find how the reservoir operating curve parameters change over time, and how this modifies typical storage trajectories in wet and dry scenarios. We also compare the results of re-optimization with the simulation of the calibrated historical policy, and with a perfect foresight optimization. Demand shortage cost of water supply for re-optimization scenario is found be lower than that of traditional optimization. The proposed methodology enables reservoir operators to develop a strategy for regularly adapting control policies based on nonstationary hydrology by choosing the frequency of optimization and maximizing the performance of the system.
Vitamin A cannot be synthesized \textit{de novo} in human body. Due to the insufficient intake of vitamin A and/or provitamin A from diets, vitamin A deficiency (VAD) has been recognized as a public-health issue in developing countries. Provitamin A carotenoids (especially β-carotene, the most efficient provitamin A carotenoid) can be converted to vitamin A. Generating staple crops with a high accumulation of β-carotene provides long term alleviation to VAD. Wheat is one of the most important dietary sources of carbohydrates and proteins while it doesn’t naturally accumulate β-carotene. Provitamin A biofortification in wheat is particularly challenging due to the lack of natural variations and polyploid genetic backgrounds. In this study, Targeting Induced Local Lesions in Genomes (TILLING) mutants were identified and characterized to genetically dissect the roles of β-hydroxylases (HYD, key enzymes in carotenoid metabolism) in tetraploid wheat. By blocking the activities of lycopene ε-cyclase (LCYe) and HYD to divert carbons from competing branch of β-carotene biosynthesis and reduce the turnover of β-carotene using the non-GMO based TILLING mutants, up to six fold of increase in β-carotene accumulation was achieved in tetraploid wheat grains. Our results on molecular, biochemical, and physiological characterization of the mutant combinations will be presented.
**Talk abstracts**

**High availability rumen-protected choline alters uterine microbiome in dairy cows**

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Abstract Body: Rumen-protected choline (RPC) promotes benefits in milk production, immunity, and health during the transition period and early lactation in dairy cows. Metritis is an inflammatory uterine disease present in ~20% of dairy cows after parturition caused by bacterial infection. Albeit the impact of nutrition on the immune system in improving health has received emphasis in RPC studies, the interplay between the uterine microbiome and the immune system remains unclear. Our objective was to characterize the role of RPC in the uterine microbiome as a proxy for uterine immune competence. Holstein cows were enrolled in Control or RPC group (CholiGEM™, 15 g/d from 21 days prepartum and 30 g/d from calving to 21 days postpartum). Vaginal discharge samples were collected at the calving and seven days postpartum for 16S gene sequencing. The diversity of the species assessed by the Shannon index was reduced in cows receiving RPC compared to the Control at calving. RPC altered the uterine microbiome composition at Phylum at seven days postpartum, decreasing the relative abundance of the major bacteria genera associated with the metritis development, Fusobacterium. High bioavailability RPC impacted uterine microbiome signature and may impact overall uterine health in dairy cows.

**Investigation on Tandem Kinase Protein, a New Class of Disease Resistance Protein**

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Wheat blast, caused by Magnaporthe grisea, poses a threat to global wheat production. The breeding of resistant wheat variants is an effective and environmentally friendly approach for disease control. A recent class of disease resistance proteins include proteins with two fused kinase domains, termed tandem kinase proteins (TKPs). Recently, the RWT4 TKP, with kinase-pseudokinase protein architecture, was identified that provides resistance to Magnaporthe grisea pathotypes containing the PWT4 effector. To understand immune responses mediated by RWT4, a rice protoplast expression system was used in this study. RWT4 induced cell death, a hallmark of plant defense, when co-expressed with the recognized PWT4 effector. In contrast, a TKP (WTK3) with 93% amino acid sequence identity to RWT4 was unable to trigger cell death when co-expressed with PWT4. Sequence and structure analysis of RWT4 and WTK3 revealed a unique C-terminus extension region within RWT4’s pseudokinase domain, suggesting the potential role of this domain in effector perception. Data will be reported on the importance of each domain in effector recognition and the use of TKP modular structure to engineer novel recognition capabilities. Collectively, these data provide insight into how TKPs are activated and their potential for generating novel immune recognition capabilities in monocots.
High-throughput phenotyping methods based on deep learning and remote sensing have been widely used to predict crop traits. However, many popular deep learning models are supervised, which means that reference datasets obtained through time-consuming and labor-intensive experiments are needed for annotating images. Therefore, in order to reduce the cost of obtaining datasets for model training, we proposed a framework for plant multispectral image synthesis in the present paper, which is an extension of the Helios 3D plant modelling software. This framework can simulate real target multispectral cameras and generate corresponding plant images with fully resolved reference labels such as plant structures and leaf chemical contents. Specifically, the Helios provides a simulated environment that enables placement of the 3D geometric models of plants and soil and specify their unique optical, biophysical, and chemical properties at a small scale. The main part of the synthesis framework contains three sub-models: camera calibration model, ray-tracing model, and leaf optics model. Overall, this framework can produce high-quality and fully labelled synthetic multispectral images of plants under the specified lighting environment. We hope that it can reduce the need for datasets in deep learning training and promote the development of plant high-throughput phenotyping.
Talk abstracts

Elucidation of a dynamic interplay between a heterotrimeric G protein and different beta-adrenergic receptors

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Heterotrimeric G proteins are molecular switches which can be regulated to either turn on or turn off based on their binding to transmembrane G-protein-coupled receptors (GPCRs) and guanine nucleotides, GTP or GDP. What are the molecular determinants for the activation and dissociation of G proteins? In this study we focused on interactions of GTP and GDP with stimulatory G protein (Gs), which is coupled with prototypical GPCRs, the beta1-adrenergic receptor (β1AR) and β2AR using Rosetta modeling and all-atom molecular dynamics simulations. We found that GTP/GDP binding indirectly alters Gsα conformation by causing inter-domain rearrangement while directly causing α5 helix tilting, thus favoring Gsα dissociation. GTP/GDP binding also enhances correlations between Gsα inter-domain arrangement and Gsα conformational changes. Specifically, we found negative correlation between α5 tilting angle and α1 – α5 stacking which was different from the apo Gs protein case we observed previously. In summary, we analyzed conformational specificities of Gs protein -guanine nucleotide interactions and found correlations between Gs dissociation and its internal domain rearrangement. This provides intrinsic molecular insights into the understanding of G protein activation and may be beneficial for the design of safe and efficacious pharmaceuticals in precisely controlling the signaling properties of beta-ARs.

Qualifying the fruiting characteristic of Chandler walnut trees

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Crop load is usually associated with shoot morphology and canopy position, but this relationship has not been well quantified in walnut. In this study, fruit number variation in relation to shoot length and within-canopy distribution was investigated for mature walnut trees cv. ‘Chandler’ using manually measured and LiDAR (light detection and ranging) scanned data. Manual shoot measurement was used to describe the development of current year floral shoots arising from previous year parent shoots, while LiDAR data was used to describe the spatial distribution of fruits (nuts). Our results showed that parent shoot length had a positive relationship with the number of fruits which were born on floral shoots that developed mainly from the terminal bud of the parent shoot. However, long parent shoots were far less frequent than short parent shoots at the whole tree level, so the majority of fruit on the tree came from short parent shoots (<=10 cm). About half of the fruits were located near the outer canopy, within 10 cm from the canopy edge, and the rest were evenly distributed inside the canopy to a depth of about 90 cm, particularly at mid-canopy height.
Accurate Oxygen Abundance of Interstellar Gas in Mrk 71 from Optical and Infrared Spectra

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The heavy element content ("metallicity") of the Universe is a record of the total star formation history. Gas-phase metallicity in galaxies, as well as its evolution with time, is of particular interest as a tracer of accretion and outflow processes. However, metallicities from the widely-used electron temperature (Te) method are typically ~2x lower than the values based on the recombination line method. This "abundance discrepancy factor" (ADF) is well known and is commonly ascribed to bias due to temperature fluctuations. We present a measurement of oxygen abundance in the nearby (3.4 Mpc) system, Mrk 71, using a combination of optical and far-IR emission lines to measure and correct for temperature fluctuation effects. Our far-IR result is inconsistent (>2σ) with the metallicity from recombination lines and instead indicates little to no bias in the standard Te method, ruling out the long-standing hypothesis that the ADF is explained by temperature fluctuations for this object. Our results provide a framework to accurately measure metallicity across cosmic history, including with recent data reaching within the first billion years with JWST and the Atacama Large Millimeter Array (ALMA).
Effects of using a reduced protein Nordic diet as complementary feeding on infant serum metabolomes

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Introduction:
The Nordic diet has shown to reduce adult weight, blood triglyceride levels, and blood pressure as well as improve blood HDL in randomized control trials. High protein intake during the complementary feeding period in children has been associated with higher weight gain and later onset of obesity. In this study, we compared the effect of feeding a protein-reduced complementary Nordic diet vs a non-Nordic complementary (control) diet on infant plasma metabolomes.

Methods:
In this randomized controlled trial, infants were randomly assigned to a reduced protein Nordic diet or a regular diet at 4- to 5-months of age (n=125 per group). Infant plasma at 12 and 18 months were sampled and subjected to NMR-based metabolomics analysis.

Results:
There were significant differences when comparing the plasma metabolomes of infants in the Nordic diet group compared to the control diet group at both 12 and 18 months. Some of the differences included essential and non-essential amino acid concentrations, urea, and energy metabolite concentrations.

Significance:
Our data overall suggest that diet during the complementary feeding period has a profound impact on the serum metabolome. Long-term impacts remain to be assessed.
Next-generation nanotheranostics for cancer therapy

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Cancer is a devastating disease and one of the leading causes of death worldwide. Conventional treatments, chemotherapy, and radiotherapy have limited efficacy. However, recent advances in nanotechnology have paved the way for creating next-generation nanotheranostics as smart multifunctional ‘all-in-one’ nanoparticles that combine diagnostic, therapeutic, and targeting agents into a single biocompatible and biodegradable carrier. Our work aims to harness the potential of Human Serum Albumin (HSA) as a next-generation nanotheranostics platform. HSA plays a critical role in transporting various drugs. Its established biocompatibility and lack of toxicity make it as a promising platform for delivering therapeutic agents for cancer therapy. Herein, our work involves the identification of cancer biomarkers through computational analysis of RNA seq and microarray that could be targeted by our nanotheranotics. Moreover, drug screening will be conducted on cancer cell lines to test their potency. Additionally, we prepared several targeting ligands to conjugate HSA with the most effective drug and ligand- based on their potency and effectiveness. In conclusion, our work provides new avenues for breakthroughs in the early detection, diagnosis, and treatment of cancer by utilizing the HSA as a next-generation nanotheranostics platform. The success of this approach has the potential to greatly contribute significantly to the advancement of cancer therapy.

Determine the optimal interaction of insecticide concentration and canopy coverage for cotton aphid and whitefly management

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Cotton pests such as cotton aphids and whiteflies pose a major threat in California, where chemical insecticides are commonly used to control them. The coverage of insecticides varies between ground and aerial applications with a greater coverage but diluted insecticide and aerial applications having a concentrated but low coverage because per acre insecticide rates are similar irrespective of application types. However, the optimal interaction of insecticide coverage and concentrations against these pests is yet to be determined. Thus, this study aimed to determine the efficacy of insecticide concentration and coverage against cotton aphids and whiteflies. By using a tracker sprayer, we simulated different levels of insecticide coverage for both ground (such as 4, 8, 15, 21, 30, and 40%) and aerial (2, 4, and 7%) applications. We also assessed cotton aphid mortality 4 days after insecticide application. The preliminary results showed that a ground application spray coverage of 15% or more was effective in killing 70% or more aphids, while an aerial application spray coverage of 7% killed 76% of aphids. This project will help determine the optimal interaction between insecticide concentration and coverage to effectively control these cotton pest’s pressure.
CFDose V2.0: Towards a patient-specific computational modeling approach to treatment planning for Y-90 radioembolization

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Y-90 radioembolization, a form of targeted radiation therapy, is done by creating a millimeter-size incision in the patient’s leg to access the femoral artery and guiding a catheter to the liver artery. Once nearby the liver arterial system, tumors can be locally targeted by delivering small glass beads that emit radiation, ensuring other parts of the body are spared. However, variations between patients and challenging treatment planning protocols can lead to inaccurate targeting of microspheres to the tumor, causing detrimental patient outcomes. To help address this problem, we have developed a modeling framework, CFDose (figure 1), that incorporates clinical patient cone-beam Computed Tomography (CBCT) images to predict microsphere transport in the patient liver vasculature using computational fluid dynamics (CFD). In this work, we focus on improving the accuracy of the CFD modeling by incorporating microsphere transport modeling with an increased model fidelity. We have improved our model by including more detailed description of the catheter site and varying the microsphere injection parameters (e.g., particle velocity, catheter curvature). These improvements to the model accuracy could help reduce the uncertainty in patient-specific predictions of the microsphere distribution between liver segments thereby showing improved tumor targeting through high-precision dosimetry.

Duopoly Business Competition in Cross-Silo Federated Learning

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In cross-silo federated learning, clients (e.g., organizations) collaboratively train a global model using private local data. In practice, clients may be not only collaborators but also business competitors. This paper studies the overlooked but practically important problem of business competition in cross-silo FL. We formulate the clients’ market competition as a three-stage game, where the clients decide their FL training strategies in Stage I and the pricing strategies in Stage II, and then heterogeneous customers decide purchasing strategies in Stage III. The game analysis is highly challenging, as clients’ collaborations and competitions are complexly coupled. We manage to characterize the equilibrium properties and find that market competition always reduces the clients’ profits and can further lead to a worse global model when clients’ costs are high. To mitigate this issue, we propose a general framework that enables proper revenue (profit plus cost) sharing among clients. Both theoretical analysis and numerical results with MNIST show that revenue sharing significantly improves the global model accuracy and clients’ profits. Counter-intuitively, even if market competition limits clients’ profits, it can lead to a better global model when clients’ costs are low, as clients strive to survive in the market by contributing more training resources.
Poster abstracts

Environmental and economic assessment in the production of Winegrape by the integration of regenerative practices in the Sonoma County area (CA)

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The climate change emergency requires us to take quick action to make our agro-productive systems more resilient, sustainable and less impactful in using resources within our ecosystems. Regenerative agriculture (RA) has emerged as a toolkit of principles and practices that can help to restore and preserve biodiversity and soil health by creating a functioning ecosystem that can reduce inputs by giving better resource management among the different processes within the ecosystem. Life cycle assessment (LCA) has become an essential tool not only for describing the environmental impacts along a production system but also a way to design potential scenarios in terms of environmental impacts, to identify hotspots to improve production processes and further reduce environmental impact. Associated with life cycle analysis, it is essential to quantify in economic terms to understand the benefits and costs linked to the insertion of new practices to support any decision-making investment further. This work aims to produce an environmental and economic assessment of four Winegrape growing scenarios in the Sonoma County area (CA) by integrating different regenerative practices (i.e. use of compost, no-tillage, cover crops and sheep grazing).

Protist Transcription Factors

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Specific Transcription Factors (TFs) are the most abundant and direct mechanism cells use to manipulate gene expression, a process that is critical to the survival of all living organisms. The identity and structure of TFs in model eukaryotes have been thoroughly examined, however TFs are understudied in other eukaryotic species, particularly early branching lineages such as the metamonads. TFs generally consist of at least two domains. DNA binding domains bind specific DNA sequences, and effector domains cause a shift in gene expression. While effector domains are not well conserved, DNA binding domains show remarkable homology, a few structural motif families are responsible for most known DNA-protein interactions. This homology can be exploited to find motifs in proteins using statistical algorithms, particularly Hidden Markov Models. This project aimed to computationally find and compare TFs throughout early branching eukaryotes, with particular focus on metamonads. Emphasis was placed on comparing the complements of TFs in free-living protists (e.g., *Kipferlia bialata*), to those found parasitic organisms (e.g., *Giardia duodenalis*). We expect to find additional TFs by using a curated reduced-cutoff approach, and to be able to better determine whether a parasitic organism has an intrinsically smaller TF repertoire, as has been suggested previously.
Pistachio (Pistacia vera L., 2n = 2x = 30) is one of the most economically important long-lived crops. Although dioecious pistachio trees are highly resilient to abiotic stresses, they require a certain amount of winter rest period to exit bud dormancy and to flower synchronically between male and female trees. Although the reference-quality genome is essential to understand genetic diversity, which is a major source of crop improvement and breeding, genomic diversity for a species cannot be captured from a single reference genome. In the present study, we report chromosome-scale haplotype-resolved reference genomes of six genetically diverse pistachio cultivars. The genome assemblies ranged from 568.55 to 608.21 Mb in size with contig N50 of 28 - 37 Mb. More than 98% of conserved orthologs (BUSCO) were represented for all genome assemblies. The genome annotation using Iso-seq data from five different tissues and developing stages revealed dynamics of transposable elements and gene content variation in pistachio genomes. The two haplotypes showed substantial sequence variation and pan-genome construction characterized remarkable presence-absence variation of structure and gene content. The reference genomes with fully annotated genes and pan-genome construction serve as rich resources for genomic breeding and improvement and comparative genomics of pistachio.
Poster abstracts

A genoscape approach for fingerprinting floodplain food subsidies in the Central Valley: Using genomics to track zooplankton connectivity

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Floodplain and tidal wetlands in California’s Central Valley (CCV) has been reduced by 95% in the last 15 years. In contemporary floodplain habitats, zooplankton reach densities over 100 times greater than the main river channel. *Daphnia pulex* is a ubiquitous and abundant zooplankton in these habitats and has been shown to be an important food resource for native fish communities. During seasonal winter flooding in northern California floodplains it remains unclear where these important indicator species originate and how far they move through the Central Valley rivers and the Delta complex. We will use whole genome sequencing for genomic fingerprinting to track floodplain subsidies in the CCV. By characterizing the genetic variation of *D. pulex* populations in CCV floodplains, we can construct a genoscape of source populations and their connectivity across the landscape. We will sample individual *D. pulex* across a variety of floodplains at early, mid, and late winter, during flooding events of the habitats that drain into the Sacramento River and Delta, including the Sutter and Yolo Bypass and the Cosumnes River floodplain. Identifying *D. pulex* source populations and the structure and connectivity of *D. pulex* across a highly managed landscape, will provide a better understanding of how seasonal zooplankton subsidies are synchronized with migratory salmonid phenology.

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Sex-Specific cAMP Signaling Domains in Vascular Smooth Muscle

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The ubiquitous second messenger 3’,5’ monophosphate (cAMP) is essential for regulating vascular smooth muscle (VSM) function. While the effects of cAMP have been traditionally linked to VSM relaxation, recent work from our group challenged this long-held view by identifying a previously unappreciated Gs-protein coupled receptors (GsPCRs)/adenylyl cyclase (AC) pathway that triggers cAMP and promotes VSM contraction in response to elevations in extracellular glucose. These results indicate that GsPCRs/AC/cAMP versatility to regulate VSM contractility to diverse stimuli depends on their spatially confined properties within the cell, of which little is known. Moreover, no studies have examined how biological sex regulates discrete cAMP pools and the functional implications in VSM. We hypothesize that the production of discrete cAMP pools is essential for integrating receptor-dependent cAMP signaling to control VSM function. To test our hypothesis, we are using VSM cells expressing cAMP biosensors targeted to the cytosol (cyt), plasma membrane (PM), and sarcoplasmic reticulum (SR) and measuring. We uncovered a sex-specific distribution of cAMP signaling domains where cAMP pools are constrained in the SR of male but not in female mice. Our study highlights a sex-dependent regulation of cAMP signaling in VSM that could contribute to the sex-specific regulation of vascular function.
Habitual sleep duration and health-related quality of life among family caregivers in the United States (US)

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This study examined the association between habitual sleep duration and health-related quality of life (HRQOL) measures in family caregivers. Cross-sectional data of 23,321 family caregivers in the 2016 Behavioral Risk Factor Surveillance System was used. Logistic regression models tested association between sleep duration (<7 [short], 7-9 [normal, reference], >9 hours [long]) and general health (fair or poor, good to excellent [reference]). Zero-inflated negative binomial models were used to analyze association of sleep duration with poor mental health days and poor physical health days. Short sleep duration was associated with fair or poor health (odds ratio [OR], 1.40; 95% CI: 1.12, 1.74). Caregivers with long sleep duration were twice more likely to report fair or poor health (OR, 2.07; 95% CI: 1.34, 3.21). Short sleep duration was associated with higher number of poor mental days (RR [risk ratio], 1.17; 95% CI: 1.04, 1.31) and poor physical health days (RR, 1.26; 95% CI: 1.10, 1.45) while long sleep duration was associated with higher number of poor mental health days (RR, 1.31; 95% CI: 1.08, 1.60). The association between sleep duration and HRQOL point to a potential role of adequate sleep in promoting caregivers’ health and wellbeing.

Structure of maize BZR1-type β-amylase BAM8 provides new insights into its noncatalytic adaptation

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Plant β-Amylase (BAM) proteins play an essential role in growth, development, stress response, and hormone regulation. Despite their typical (β/α) 8 barrel structure as active catalysts in starch breakdown, catalytically inactive BAMs are implicated in diverse yet elusive functions in plants. The noncatalytic BAM7/8 contain N-terminal BZR1 domains and were shown to be involved in the regulation of brassinosteroid signaling and possibly serve as sensors of yet an uncharacterized metabolic signal. While the structures of several catalytically active BAMs have been reported, structural characterization of the catalytically inactive BZR1-type BAMs remain unknown. Here, we determine the crystal structure of Zea mays BZR1-type BAM8 and provide comprehensive insights into its noncatalytic adaptation. Using structural-guided comparison combined with biochemical analysis and molecular dynamics simulations, we revealed conformational changes in multiple distinct highly conserved regions resulting in rearrangement of the binding pocket. Altogether, this study adds a new layer of understanding to starch breakdown mechanism and elucidates the acquired adjustments of noncatalytic BZR1-type BAMs as putative regulatory domains and/or metabolic sensors in plants.
Experiences in the production of aquaponic food on a small scale

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Aquaponics is a technique that combines the production of fish (aquaculture) and plants (hydroponics) in a sustainable method. It is widely used on a small scale, often for self-consumption purposes. The objective of this study was to identify the food production in small-scale aquaponic systems (SAS) managed by 1) a family and 2) small producers. For case 1), two SAS were self-built in Polígono Sur, one of the poorest neighborhoods in Spain. These SAS produced a total of 62 kg of tilapia and 352 kg of produce in one year, resulting in sufficient food for a single family’s subsistence. For case 2), an online survey was conducted to small aquaponic producers in Spain and Latin America. It was determined that the production of healthy and high-quality food was a more important motivation for producers than economics, for this reason the producers often did not pay much attention to expenses and production yields. The SAS yielded polycultures consisting of leafy vegetables, fruits, and aromatics herbs. Tilapia was the most frequently used fish species. Because farmers generally lack knowledge of SAS pest and disease management, and water quality, it is necessary to develop training programs for producers focused on these knowledge gaps.

A computational model to reveal mechanisms of sex-based differences in vascular smooth muscle cells


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Smooth muscle cells regulate the diameter of small resistance arteries and arterioles to control blood flow and blood pressure. Here, we describe a computational model of the vascular smooth muscle myocyte based on new electrophysiological and Ca \textsuperscript{2+} data from resistance arteries indicating key sex-specific differences in male and female arterial myocytes. We use the model to reveal mechanisms underlying membrane potential and intracellular Ca \textsuperscript{2+} allowing us to understand novel concepts in vascular smooth muscle physiology and pathophysiology. While electrophysiology data indicate similar amplitude and time course of K \textsuperscript{V} 1.5 current in male and female myocytes, whole cell simulations suggest that K \textsuperscript{V} 1.5 current is the dominant current regulating membrane potential in male myocytes. In female cells, K \textsuperscript{V} 2.1 currents are larger than male myocytes. Predictions from simulated female myocytes suggest that K \textsuperscript{V} 2.1 plays a primary role in the control of membrane potential. Over the physiological range of membrane potentials, the gating of a small number of voltage-gated K + channels and L-type Ca \textsuperscript{2+} channels are predicted to drive sex-specific differences in intracellular Ca \textsuperscript{2+} and excitability. Finally, the model predicts that female arterial smooth muscle is more sensitive to clinically used Ca \textsuperscript{2+} channel blockers than male myocytes, providing a new framework to investigate the potential sex-specific impact of anti-hypertensive drugs.
Leveraging quantitative genetic mapping data for discovery of novel genetic variants underlying root architecture in tomato

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Tomato (Solanum lycopersicum) is a model system for fleshy fruit development and findings in this system can be used for genetic improvement of all solanaceous crops, including potato, pepper, and eggplant. In addition to decades of well-documented breeding data, a high-quality genome sequence is available along with a growing molecular and genomic toolbox. One of these resources is a well-characterized panel of over 150 accessions wild and domesticated accessions (Varitome panel). While fruit and flower traits are exceedingly well-characterized for the Varitome panel, no published studies have explored root-related traits. Roots are responsible for absorption of water and all non-photosynthetic nutrients. Furthermore, root development is highly plastic and responsive to environmental perturbations. We therefore hypothesized that we could use the Varitome panel to map genetic variants underlying early seedling root traits. Here, we use high throughput image analysis of early seedling root architecture to map potential causal variants using a genome wide association study. In doing so, we observed measurable heritability across our 12 root traits. When we performed our genome wide association study, we found 47 unique significant loci across six traits. Currently, we are testing these significant loci and their nearby variants for gene regulatory activity.

Fate of foodborne pathogens on lemons after lab- and pilot-scale finishing wax application

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To determine the bactericidal effects of applying finishing wax to lemons followed by a drying step, lemons were inoculated with rifampin-resistant cocktails of Listeria monocytogenes (LM), Salmonella, or Enterococcus faecium NRRL 2354 (EF) at 6.0 log CFU/lemon. Inoculated lemons were waxed, and then held at 22 or 60°C for 4 min. For each pilot-scale trial, 30 EF- inoculated lemons and 120 uninoculated lemons were waxed (87 L/h) and dried at ~50°C. The post-waxing survival and transfer of inoculated bacteria was determined for a subset of 40 uninoculated lemons. Application of finishing waxes led to reductions of 2.0 to 3.1 and 2.8 to 4.4 log CFU/lemon for LM and 0.5 to 2.6 and 1.7 to 3.7 log CFU/lemon for Salmonella after holding at 22 and 60°C, respectively. Reductions of EF were lower by 0.2 to 0.8 log CFU/lemon compared to Salmonella depending on treatment. EF reductions of 1.6 to 2.7 log CFU/lemon of were observed during the pilot-scale trials. EF was recovered from 72.5% of uninoculated lemons by whole-fruit enrichment but not plating (&lt;1.3 log CFU/lemon). Application of finishing wax followed by heated drying may reduce pathogens on lemons but may also lead to low-level cross contamination when initial contamination is high.
Sustained effects of small-quantity lipid-based nutrient supplements provided during the first 1000 days on child growth at 9-11 years in a randomized controlled trial in Ghana

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Background and Objective: There is limited research on the impact of nutritional supplementation in the first 1000 days on long-term child growth. We aimed to investigate the effects of pre- and postnatal small-quantity lipid-based nutrient supplements (SQ-LNS) on child growth at age 9-11 years.

Methods: The International Lipid-Based Nutrient Supplements (iLiNS) DYAD-Ghana trial was a randomized controlled trial conducted in 2009-2014. 1320 pregnant women ≤ 20 weeks gestation were randomly assigned to receive daily (1) iron and folic acid during pregnancy and placebo during 6 months postpartum, (2) multiple micronutrients (18) during pregnancy and 6 months postpartum, or (3) SQ-LNS (20 g/d) for pregnant women during pregnancy and 6 months postpartum and SQ-LNS for children from 6 to 18 months of age. In 2021, we assessed child growth at age 9-11 years using height-for-age z-score (HAZ), BMI-for-age, waist-to-height ratio, triceps skinfold and mid-upper arm circumference. Models were adjusted for child’s age at measurement. Results: We re-enrolled and assessed outcomes in 966 children. LNS children had a marginally higher HAZ (p=0.060) than non-LNS children [mean (SD) of −0.04 (0.96) vs −0.16 (0.99)]. There were no other group differences. For child HAZ, there was an interaction with child sex (p interaction=0.075) and maternal pre-pregnancy BMI (kg/m²) (p interaction=0.002). Among females, HAZ was higher in the LNS [0.08 (0.07)] than non-LNS [-0.16 (0.05)] group (p=0.010); among males, the LNS [-0.16 (0.08)] and non-LNS, [-0.16 (0.06)] groups did not differ (p=0.974). Among women with BMI<25, HAZ was higher in the LNS [-0.04 (1.00)] than non-LNS [-0.30 (0.94)] group (p=0.003); among women with BMI≥25, the LNS (-0.03 (0.90 SD)) and non-LNS, (0.07 (1.02 SD)) groups did not differ (p=0.321). Conclusions: Children who received pre- and post-natal SQ-LNS tended to have higher HAZ overall than non-LNS children. In exploratory effect modification testing, SQ-LNS positively affected HAZ among female children and children of non-overweight/obese women. LNS did not increase BMI-for-age. This sustained impact of LNS suggests it may be a useful tool for improving long-term child growth.
Poster abstracts

The gastrointestinal microbiome of dairy cows outweighs genetics in determining dairy cow’s efficiency to produce milk: A holistic multi-omics study

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Feedstuffs are the major expenses in livestock production, meaning reductions in feed costs have a profound effect on dairy farm profitability. Therefore, there has been an increasing interest in breeding animals based on their efficiency in utilizing dietary nutrients. Given the low heritability of milk production efficiency in dairy cows (RFI, h = 0.15), attention has turned to other factors that could modulate this trait. Therefore, we hypothesized the rumen microbiome of dairy cows that digest most of their dietary nutrients plays a greater role in modulating this trait than host genetics. We found in a large cohort of dairy cows that the rumen microbiome contributed to about 87% of the total variation of this trait, while host genetics contributed to only 13%. Further analyses indicated greater protozoa activity in the rumen of more efficient cows. A link between protozoa activity and greater ruminal ornithine abundance was also observed in these animals. Once into circulation, ruminal ornithine can stimulate the release of growth hormone in the pituitary gland, potentially improving the milk production efficiency of dairy cows. These findings show the incorporation of microbiome genetic information into genomic predictions is pivotal to supporting more efficient and sustainable livestock production.

Sustainable, Reusable yet Compostable Microbial-Resistant Stational Cooling Media, “Jelly Ice Cubes”

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Serious economic losses of foods could be caused by temperature abuses, quality loss and microbial cross-contamination. Ice and ice packs are commonly used as heat storage material in the cold chain of food and pharmaceutical industries. The use of water in making traditional ice and the utilization of plastics in manufacturing reusable ice packs have both imposed significant environmental burdens on the planet. We aimed to solve the above challenges via multidisciplinary approaches. A novel stationary cooling media, “Jelly Ice Cubes (JICs)”, was proposed, and the concept was experimentally proved. JICs were proven to be microbial resistant (self-cleanable), compostable, and customizable with comparable cooling efficacy with traditional ice while generating no meltwater at its unfrozen status. It is anticipated that the research can impact the global cold chain by reducing water and plastic use while preventing product quality loss and contamination caused by temperature abuses and melting water while promoting the sustainability and health of humans and the planet.
Characterization of the novel neuronal peptide NHIP

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Autism spectrum disorder (ASD) is a neurodevelopmental disorder with a complex etiology involving genetic, environment, and gene-environment interactions. Whole genome bisulfite sequencing (WGBS) of placental samples from newborns later diagnosed with ASD revealed a hypomethylated block in the 22q13.33 region. This led to the identification of the novel gene NHIP (neuronal hypoxia inducible, placenta), which has decreased expression in ASD placenta and brain. Assessing NHIP transcript levels in the neuronal LUHMES cell line revealed that its expression increases following differentiation and exposure of differentiated neurons to hypoxia. Immunofluorescent staining revealed that NHIP also encodes a small peptide that localizes to the nucleus. We hypothesize that NHIP plays a protective role during oxidative stress through its interaction with other proteins involved in gene regulation. To explore this hypothesis, we sought to identify NHIP-binding proteins that may contribute to its function. Using affinity purification mass spectrometry, we identified 121 putative proteins from brain extracts that bind to NHIP, many of which are involved in transcription, translation, and neurodevelopmental disorders. Based on the predicted 3D structure of NHIP, it is possible that NHIP may be interacting with these proteins by mimicking a common transcriptional activation domain motif (9aaTAD). We have also begun developing NHIP-knockout cell lines, which we will use to further investigate the role of NHIP in transcription, translation, and oxidative stress. Characterization of NHIP will allow for evaluation of its potential use as a neuroprotective therapeutic in neurodevelopmental disorders such as ASD.

AI-powered cloud-based diagnosis of battery systems for electric vehicles

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Over the past decade, there have been sold more than 20 million electric vehicles (EVs) worldwide which include multi-billion batteries. Despite continuous progress in battery analysis, predicting the degradation and possible failure of battery systems in vehicle applications has faced severe challenges. In this project, we have considered this challenge by developing two specialized machine learning techniques based on the recorded data from EVs in operation that are uploaded to the cloud: (i) a well-integrated technique consisting of physics-informed supervised learning, high-dimensional unsupervised learning, and semi-supervised learning developed for the fault diagnosis of battery systems. (ii) a stacking ensemble machine learning designed for the estimation and prediction of battery health. The project aims to provide an accurate prediction of battery states and early diagnosis of battery failure with a focus on real-life situations across long-term spatio-temporal scales. The data-driven cloud-based framework integrating longitudinal electronic health records with real-world data enables continuous battery performance evaluation for EVs. Applications of specialized machine learning architectures stemming from observational, statistical, and physical understanding of batteries from both materials, cell and pack levels not only have the potential to produce new insight, but also contribute to more accurate predictions of the evolution of electrochemical systems.
Poster abstracts

**Computationally Efficient AI frameworks for Neuropathology Image Analysis**

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Patients suffering from neurodegenerative and neurological disease are increasing; more than 120,000 deaths due to Alzheimer’s disease were reported in 2018, and the number of patients is predicted to rise to 13 million in the U.S by 2050. Brain infarcts are amongst the most common cerebrovascular pathology of aging and are closely associated with future risk of stroke and cognitive impairment. It is very important to carefully inspect the brain tissues and understand the disease progression and pathophysiology. The digital pathology, a dynamic, image-based environment that enables the acquisition, management and interpretation of pathology information generated from a digitized glass slide, is rapidly gaining momentum as a proven and essential technology. With the help of digital slide scanners, the physical tissue slides can be scanned into digital whole slide images (WSIs). In addition, deep neural networks have recently gained popularity in digital pathology for image analysis tasks including segmentation, tissue classification, detection and counting. The gigapixel WSIs with AI are used for the neuropathology image analyses to aid deeper phenotyping of neurodegenerative diseases. Moreover, the aim is to build a generalized, effective, and computationally efficient artificial intelligence based framework that can somehow reduce the labelling costs and data collection efforts.

**Pilot study of acceptability of high-arabinose commercially available products and their impact on the fecal microbiome of low-, middle-, and high-income families in the U.S.**

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Dietary fiber is a non-digestible carbohydrate for which their fermentation in the gut results in the production of different bioactive compounds. Fiber consumption during early stages of life is relevant because their benefits extend into adulthood. Arabinose is one of the most abundant monosaccharides in cereals, legumes, nuts, and fruits. It is poorly absorbed in the upper GI tract, and thus considered to play an important role in shaping the gut microbiome. No studies have investigated the acceptability, and effect on the fecal microbiome of high-arabinose (HA) products in children. The purpose of this work is to present the study design of a pilot study to evaluate the acceptability, of 20 HA commercially available products and their impact on the fecal microbiome in children as a part of a regular diet. This pilot study will be a longitudinal trial that will target children and their parents from low- (n=20), middle-, and high-income (n=10) families in the U.S. who are at-risk for gut dysbiosis. This 5-week study will include 3 home visits to test the acceptability of HA products by parents and children, followed by 3 weeks of daily intake at home of 2-3 HA products by children. The primary outcome of acceptability will be assessed using validated sensory scales and daily intake questionnaires. The secondary outcome of modifications on the fecal microbiome will be evaluated by using validated questionnaires of GI function and by quantifying fecal short chain fatty acids and glycans, as well as shotgun metagenomics sequencing in stool samples that parents will collect before and after the daily intake of HA products.
Effects of coupled diffusion and surface-mediated redox chemistry in the generation of hexavalent chromium from chromium-iron-manganese mixed mineral systems

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Hexavalent chromium[(Cr(VI)] is a carcinogen that is widely found in groundwater across California and derives from both geogenic and anthropogenic sources. A major geochemical mechanism for Cr(VI) generation is the oxidation of Cr(III) oxyhydroxide minerals by redox-active manganese (Mn) oxides (e.g. MnO₂). While previous studies have focused on the oxidative mobilization of Cr(VI) by Mn oxides, the potential for re-adsorption of Cr(VI) onto other soil minerals (e.g. iron(Fe) oxyhydroxides) has received less attention. Knowledge of Cr dynamics in mixed mineral systems, however, is needed to predict Cr(VI) concentrations in soils and groundwater. In this study, we examined Cr(VI) generation and mobilization to solution in Cr(OH)₃, δ-MnO₂ and 2-line ferrihydrite mixed-mineral systems at pH 7.0. Without 2-line ferrihydrite, the oxidative mobilization of Cr(VI) from Cr(OH)₃ by δ-MnO₂ increased with increasing Cr(OH)₃ concentration and decreasing ionic strength. These results suggests that the oxidative mobilization of Cr(VI) is regulated by particle-particle interactions between the two oppositely charged minerals in addition to the solubility of Cr(OH)₃. In the presence of 2-line ferrihydrite, Cr(VI) mobilization to solution was suppressed, but the effect decreased with increasing ionic strength which increases the charge repulsion between negatively charged Cr(VI) (i.e., CrO₄²⁻) and 2-line ferrihydrite. Our results elucidate the mechanism of Cr(VI) release in mixed mineral systems, which can be used to model Cr(VI) dynamics in soil systems.

Development of an enzyme-based surrogate to assess the antimicrobial effectiveness of fresh produce washing

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Adding sanitizers in wash water is critical for preventing bacterial cross-contamination during fresh produce washing. However, antimicrobial effectiveness is complicated by various parameters including sanitizer concentrations and organic loads of wash water. To validate the antimicrobial effectiveness of produce washing, non-pathogenic surrogate bacteria are commonly used as indicators, but this requires time-consuming and labor-intensive microbiological testing. This study aimed to develop a non-living surrogate for rapid and visual assessment of antimicrobial effectiveness during fresh produce washing. Catalase was selected as the enzyme-based surrogate because it is one of the key antioxidant enzymes that mitigate bacterial oxidative stress during sanitation. To quantify changes in catalase activity upon antimicrobial treatments, a visual assay based on foam height measurement was developed. A linear regression model was established between catalase concentrations and foam height. Sanitizers inactivated catalase as a function of sanitizer concentrations. Sanitizer concentrations could be predicted by the foam height of catalase using an exponential decay regression model. Besides, catalase inactivation with sanitizers showed an exponential growth regression to Escherichia coli reduction in the presence of organic loads. This enzyme-based surrogate provides a fast and visual approach for assessing wash water sanitation during fresh produce washing.
Poster abstracts

Characterization of amino acids profile on ‘Bordeaux grape varieties’ from California, USA and Tuscany, Italy
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Understanding the amino acid composition is useful because these compounds are a source of nitrogen for yeast which have significant biological effects during the alcoholic fermentation process and are precursors of aroma compounds in wine. Grape must amino acid profile has been correlated to the maturity of the grapes, and its source is linked to soil fertility, enzymatic degradation of the grape proteins during fermentation, yeast, and lactic bacteria metabolism. Twenty-three amino acids and glutathione were profiled in thirty-three juices of ‘Bordeaux grape varieties’ grown in Bolgheri, Tuscany, Italy and Napa Valley, California, USA. The method was carried out by pre-column derivatization followed by UHPLC-FLD; relative standard deviation values for repeatability (n= 20) were < 5%. The differences between grape juices related to their geographic and varietal origins were made with principal component analysis. Most of the amino acids quantified had similar correlations in Cabernet franc juices and, to a lesser degree, Cabernet sauvignon juices, from Bolgheri and Napa Valley vineyards. Amino acids in Merlot juices from both regions presented correlations different from Cabernet sauvignon and Cabernet franc. The most abundant amino acids in ‘Bordeaux grape varieties’ were PRO, GABA and ARG, varied by 2, 2 and 3-fold, respectively.

Molecular signaling pathways that drive changes in brain structure in health and schizophrenia
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Connections between neurons in the brain, also known as synapses, are often found on microscopic protrusions from neuronal dendrites called dendritic spines. These spines are dynamic structures that change in shape and size in response to activation of neuronal inputs during learning, in a process known as synaptic plasticity. Importantly, an abnormal regulation of dendritic spine plasticity has been observed in several psychiatric disorders, including schizophrenia, which is associated with a decreased spine density. NMDA-type glutamate receptors are key regulators of synaptic plasticity, and their dysfunction has been linked to the pathogenesis of schizophrenia. Traditionally, the mechanisms by which NMDA receptors regulate dendritic spine plasticity were thought to occur downstream of ion flux through the receptor. Notably, we recently made the surprising discovery that ion-flux independent NMDA receptor signaling can drive dendritic spine shrinkage and elimination in a mouse model of schizophrenia. We showed that NMDAR hypofunction brought on by lack of D-serine, contributes to schizophrenia associated spine loss in serine-racemase knock-out mouse model of schizophrenia. Here, I will present our current understanding of the role ion-flux independent NMDA receptor signaling has in the regulation of spine shrinkage and elimination in health and mouse model of schizophrenia.
**Poster abstracts**

**Bayesian sequential approach to monitor COVID-19 variants through positivity rate from wastewater**

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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.

**Interstitial Space Properties of 18 F-fluorodeoxyglucose in Nonalcoholic Fatty Liver Disease**

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Interstitial space is the fluid space surrounding tissue cells. Transport and uptake properties of the radiotracer 18 F-fluorodeoxyglucose (FDG) in this space may be distinct in healthy subjects and nonalcoholic fatty liver disease (NAFLD) patients. The three-tissue (3T) model, which explicitly separates the free-FDG compartment into the interstitial space and the intracellular space, provided a better fit quality than the conventional two-tissue (2T) model (A), as further demonstrated by the negative Akaike information criteria (AIC) difference (B). (rate of FDG transport from plasma to the interstitial space) (C), and (distribution volume of FDG in the interstitial space) (D) differentiated nonalcoholic steatohepatitis (NASH), which was histologically-proven by NAFLD activity score (NAS) greater than 4 (NAS > 4), from non-NASH subjects (NAFLD with NAS 4 and healthy subjects). This study indicates that FDG characterization of the interstitial space has the strong potential to derive multiparametric PET imaging biomarkers to assess NASH in NAFLD.
Poster abstracts

Rapid and Widespread Interferon Stimulated Response in Olfactory Sensory Neurons Upon SARS-CoV-2 infection

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Olfactory loss is one of the clinical manifestations of COVID-19. SARS-CoV-2 (CoV2) is demonstrated to infect sustentacular cells in the olfactory epithelium (OE). The molecular mechanism of CoV2 induced olfactory loss is still unclear. Humanized transgenic mouse, K18-hACE2, provided a genetic model to study CoV2-olfactory mucosa interactions. Consistent with the hACE2 expression pattern, we observed CoV2 infections specifically in sustentacular cells after nasal inoculation. Infection of different CoV2 strains, including Wildtype (UCD4), Alpha (B.1.1.7), Beta (B.1.351), Delta (B.617.2) and Omicron (B.1.1.529), are examined. CoV2 infection sites in the mouse OE are sparsely distributed. Overall infection patterns are comparable between strains with Alpha strain gives the most robust infection. Rapid transcriptional responses are observed at 24hr post infection in the OE by whole tissue RNA-seq. The most prominent pathways identified are interferon signaling and cytokine-receptor interactions. Further spatial analysis identified upregulation of sustentacular cell specific cytokine expression and olfactory sensory neuron specific antiviral responses. Despite sparse infection pattern in the OE, widespread olfactory sensory neurons transcriptional and translational response are observed. We also observed shutoff of several olfactory sensory neuron markers in contrast to the upregulation of interferon stimulated genes. Viral infection induced widespread transcriptional reprogramming may be responsible for the comprise of olfactory sensory neuron function.

Cherenkov Radiation Generation using Drift-Biased Graphene Hyperbolic Structures

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Cherenkov radiation (CR) is an electromagnetic radiation that is produced when a charged particle moves faster than the phase velocity of light in a medium. From a quantum standpoint, the ultra-high energetic charged particles emit their energy to the photons while moving, then relax to a lower energy level. The accelerated electrons are conventionally produced by nuclear reactors or particle accelerators, which limits the on-chip applications. Recently, Cherenkov radiation has been experimentally explored by utilizing an external electronic beam nearby the hyperbolic plasmonic structures in visible frequency range. Using this feature, a threshold-less CR source has been proposed based on a hyperbolic metamaterial. In this paper, we generate Cherenkov radiation by applying drift-biased graphene hyperbolic structures, aiming to construct a miniaturized, broadband, and efficient source operating at terahertz and far infrared frequency range. We eliminate the need for external emitters, which makes the source more compatible with integrated devices. We calculate and optimize the emission rate by tuning the parameters such as the initial energy and chemical potential. In addition, we design the outcoupling mechanism to efficiently radiate the generated power to free space. Our theoretical and experimental efforts constitute a first step toward the development of high frequency solid-state sources based on CR.
The neuropathological landscape of Hispanic and Non-Hispanic White Decedents with Alzheimer’s disease

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The population of the United States is growing older and more diverse, resulting in diversity among those affected by Alzheimer Disease (AD). Scant neuropathologic studies have focused on brains of underrepresented ethnic groups, particularly Hispanics. We sought to characterize the neuropathologic landscape in non-Hispanic Whites (n = 185) and Hispanic (n = 92) individuals with AD evaluated across three Alzheimer’s Disease Research Centers (ADRCs-UC-San Diego, Columbia University, and UC-Davis). NHW were matched to Hispanics 2-1. Using semi-quantitative analyses (none [0], sparse [1], moderate [2], frequent [3]), we evaluated AD pathologic severity of plaques, tangles, and threads – within the posterior hippocampus, frontal, temporal, and parietal cortices. Evaluations were conducted by an expert blinded to demographics and group status. Ordinal logistic regression analyses revealed the frontal cortices to have significant higher neuritic plaque (p=0.02) and neuropil thread (P=0.01) densities in persons of Hispanic descent compared to age and gender matched NHWs (P=0.02), these pathologies had similar densities in hippocampal, parietal, and temporal cortices. The results indicate neuropathologic and neuroanatomic specific differences based on Hispanic ethnicity. Further research is needed to understand the contributions of demographic, genetic, and environmental factors to heterogeneous pathological presentations.
Poster abstracts

Characterizing Emissions from California Biomethane Facilities
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The Short-Lived Climate Pollutant Strategy is being implemented in California to reduce methane emissions by 40% from 2013 levels by 2030, along with reductions of black carbon and other pollutants. One way this can be achieved is through the production of renewable natural gas in the form of biomethane, which is created through anaerobic digestion applied on organic waste. To understand the extent to which anaerobic digestion may reduce greenhouse gases emissions, robust and reliable emissions rates must be established. The emissions rates at two facilities in California were measured to determine the potential emissions benefits of biomethane production from organic waste compared to composting technology. Yolo County’s Anaerobic Composter facility implements the anaerobic digestion and aerobic composting technology to produce renewable natural gas and compost as a by-product, and the Napa composting facility produces compost without the anaerobic digestion process (Fig. 1). Field measurements were conducted in four seasons to obtain a defensible estimate of annual emissions from both facilities. The data collected was used to formulate recommendations for facility management practices and quantify the role that biomethane would play within the Short- Lived Climate Pollutant Reduction Strategy.

Quantum Channel Monitoring via Quantum Wrappers
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When quantum computers become available and commercially viable, then they will be able to solve problems that are exponentially difficult for classical computers. The next question is how to interconnect and manage quantum computers for communication and distributed computing. Although there has been some progress in developing quantum computing, networking, and related device technologies, the quantum internet is far from reality. The reason is that the quantum bits are extremely fragile, and their fundamental principles forbid measurements or monitoring required for network control and management. However, the fragile qubits need to be transported and switched. To this end, we recently proposed a Quantum Wrapper Networking, and made some progress in transporting and monitoring of quantum bits. The key in quantum wrapper networks to wrap the quantum bits payload with classical header bits, and use them for switching, performance monitoring and inferring the quantum channel quality. In this symposium, we will present our preliminary experimental results for packetized transmission of the quantum bits with classical wrapper bits in a point-to-point link. We observe that it is possible to monitor the quantum channel quality without measuring quantum bits with the help of wrapper bits.
Impact of soil health management practices on soil hydraulic properties in irrigated agriculture: a meta-analysis

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Irrigated agriculture in semi-arid regions is becoming increasingly challenging with climate change, as rising temperatures and shifting precipitation patterns are making drought more likely and severe. Moreover, overreliance on groundwater to compensate for insufficient surface water resources has caused overdraft, prompting calls for alternative agricultural water management strategies. One such strategy includes adoption of soil health management practices, designed to promote soil ecological function, and provide co-benefits improving soil-water relations. Thus, the purpose of our meta-analysis is to quantify the effect of soil health management practices on soil hydraulic properties in irrigated agricultural systems. A systematic literature review was conducted to identify studies that measured the response of soil hydraulic properties following adoption of no/reduced tillage, cover crops, organic amendment, crop diversification, or crop-livestock integration (N=2722). We will next measure the effect of these soil health management practices on both direct and indirect indicators of water movement into, transmission throughout, and retention within soils: infiltration rate, saturated and unsaturated hydraulic conductivity, plant available water, soil water content, aggregate stability, and bulk density. The results will provide insight into which agricultural practices are most likely to enhance sustainable water management through changes in soil properties in semi-arid irrigated systems.


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BAQ13, a new autophagy inhibitor, has demonstrated remarkable efficacy in preclinical cancer models. Despite its self-assembly into nanoparticles, BAQ13 is not very stable and not well tolerated by high doses by intravenous administration in rodents. To address these limitations, the BAQ13 formulation was optimized by incorporating lipids to form more stable and tolerable lipid nanoparticles (LNP). Microfluidics was used to produce LNPs with tunable particle sizes (30-150 nm) and excellent distribution (PDI < 0.2) by adjusting lipid composition, ratios, and flow rate parameters. The optimal formulation was composed of BAQ13, DSPE-PEG2000, cholesterol, and soy PC (2:2:1:2) and was achieved at a flow rate ratio of 3:1 to 9:1 (H2O: ethanol). The resulting LNPs were 40 ± 5 nm in size and spherical in shape (confirmed by TEM). More importantly, they were more stable and showed good biocompatibility in vitro and higher tolerability in vivo, up to 40 mg/kg in mice. Large batches were produced continuously (several liters per minute) and stabilized with 9% sucrose for freeze-drying. The reconstituted formulation was deemed suitable for clinical use.
**Poster abstracts**

**Determination of gonad reproductive state using non-lethal ultrasonography in endangered black Haliotis cracherodii and white abalone Haliotis sorenseni**

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California abalone (Haliotis spp.) were once abundant; however, overharvesting, disease, loss of kelp forests, and habitat degradation have caused all seven species to decline. Today, black (H. cracherodii) and white abalone (H. sorenseni) are listed as federally endangered species. Efforts to conserve endangered abalone have been enacted; however, determination of the reproductive state of individual abalone can be difficult using traditional visual assessment. Ultrasonography is a well-recognized technology used to accurately and non-lethally assess gonad reproductive condition in fish, and more recently red abalone (H. rufescens). Here, we apply the use of ultrasound technology to monitor the gonad condition of endangered black and white abalone. Ultrasound assessments of the gonad were used to assess seasonal changes in reproductive development in black and white abalone. An ultrasound index score was used to categorize changes in gonad development, with a score of one being the lowest (gonad margin is wrapped slightly around the digestive gland or absent) and an index score of five being the greatest (gonad margin is thick and significantly compressing the digestive gland). Utilization of ultrasound technology can provide a more accurate estimate of abalone reproductive condition compared to visual gonad assessment and without using lethal histological methods.

**The Use of Passively Collected Data to Study the Evolution of Travel Demand**

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The pandemic brought the normal life to a halt around the world and induced significant changes in the travel behavior. However, there was heterogeneity in the adaption in the travel behavior within the society during pandemic. White-collar workers such as software professionals, accountants, etc. adopted remote work, the blue-collar workers such as construction workers, restaurant staff, etc., including frontline workers such as nurses, bus operators, etc., had to travel to their work locations and could not significantly shift to remote work. It is important to understand the variation in the adaptation in travel behavior to optimally allocate the resources (e.g., public transportation). The general approach to understand the heterogeneity in travel behavior within society involves hypothesis testing. The approach is well established; however, it is limited by the number of hypotheses that can be tested. We developed a data driven approach which can scan the northern Californian region to uncover the heterogeneity in the change in travel patterns in the neighborhoods without using sociodemographic information. The sociodemographic information can later be used to learn the causality for the heterogeneous behavior among neighborhoods. This novel data driven approach can get better insights of travel demand which can help transit agencies to introspect and prepare for any future health crisis.
Poster abstracts

Long-read genome sequencing accelerated the cloning of Pm69 by resolving the complexity of a rapidly evolving resistance gene cluster in wheat

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Gene cloning in repeat-rich polyploid genomes remains challenging. Here we describe a strategy for overcoming major bottlenecks in the cloning of the powdery mildew (Pm) resistance gene (R-gene) Pm69 derived from tetraploid wild emmer wheat (WEW). A conventional positional cloning approach encountered suppressed recombination due to structural variations, while chromosome sorting yielded an insufficient purity level. A Pm69 physical map, constructed by assembling ONT long-read genome sequences, revealed a rapidly evolving nucleotide-binding leucine-rich repeat (NLR) R-gene cluster. A single candidate NLR was identified within this cluster by anchoring RNASeq reads of susceptible mutants to ONT contigs and was validated by the virus-induced gene silencing (VIGS) approach. Pm69, comprising Rx_N with RanGAP interaction sites, NB-ARC, and LRR domains, is probably a newly evolved NLR discovered only in one location across the WEW distribution range in the Fertile Crescent. Pm69 was successfully introgressed into durum and bread wheat, and a diagnostic molecular marker could be used to accelerate its deployment and pyramiding with other resistance genes.

A Case Study Using California Olive Pomace For Potential Valorization Strategy Of Olive Oil Industry Byproducts By The Application In Avocado Oil-based Cosmetics

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This research project aims to assess the effectiveness of California olive pomace extract in avocado oil-based cosmetic cream. The resin-purified olive pomace extract (RPOPE) with 303 mg gallic acid equivalents (GAE)/g was used as a natural antioxidant. Four cream sample groups were formulated: negative antioxidant control without antioxidants, positive antioxidant control with 70 ppm of EDTA, and two experimental groups with 400 ppm and 800 ppm GAE of RPOPE. All samples were subjected to the treatment of 1ppm ferrous iron as prooxidants. The cream samples were incubated in the dark at 35°C for 2 weeks. Their L* a* b* color values were analyzed at week 0 and week 2. As for the L* value, the control groups exhibited no significant difference with average values, whereas the value displayed an inverse relationship with RPOPE concentration. On the other hand, A* and b* values increased with RPOPE concentration. The antioxidant capacity of the extract is evaluated with DPPH assay, suggesting that RPOPE has higher antioxidant activity than the control groups for both week 0 and week 2. Overall, the project demonstrates a potential valorization strategy of olive pomace as a value-added ingredient, improving the sustainability of the olive agricultural industry.
Transfer of Enterococcus faecium and Salmonella enterica during simulated postharvest handling of yellow onions

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The aim of the study was to investigate factors that influence bacterial transfer between yellow onions and dry food-contact surfaces. Rifampin-resistant Enterococcus faecium NRRL B-2354 or a five-strain cocktail of Salmonella were inoculated onto onions or polyurethane (PU) surfaces at 5 (moderate) or 7 (high) log CFU/cm². After the inoculum had dried, transfer from inoculated to uninoculated surfaces was conducted using a texture analyzer. After a preliminary assessment, a combination of five repeated 10 N, 30 s contacts was selected to understand other factors, including transfer direction (onion-to-PU vs PU-to-onion), recipient surface (PU and stainless steel [SS]), inoculum levels, bacterial species, and inoculum carriers. Percent transfer rate (TR) was calculated as a ratio of the population on the recipient surface to the source population. The TR of E. faecium was impacted by transfer direction but was not influenced by recipient surface or inoculum level (TR: 3 to 5%). The TR of Salmonella was higher than that of E. faecium at moderate inoculum levels (6 to 11%) but significantly lower at high levels (0.5 to 0.6%). The transfer was significantly impacted by inoculum carrier, with transfer rates of 61% (onion extract), 1.6% (peptone), and 0.30% (soil).