The Center for Combating Pandemics
Tel Aviv University

TCCP

4th annual conference

Abstracts

The Steinhardt Museum of Natural History
Tel Aviv University

Wednesday, May 28, 2025

08:30-09:00 **Registration and coffee** | Reception hall

09:00-09:10 **Opening statements** | Auditorium

Prof. Dan Peer, TAU VP for R&D
Prof. Itai Benhar, Director of the TCCP

PLENARY LECTURE | Auditorium

09:10-10:00 **Prof. Dorit Nitzan,** Ben-Gurion University

Advanced Degrees in Emergency Management: The View from Ben-Gurion University

In an era defined by pandemics, armed conflict, climate crises, and technological threats, the need for advanced education in emergency management has never been more urgent. Ben-Gurion University of the Negev offers a forward-looking Master's Program in Emergency Medicine—Preparedness and Response to Disasters—designed to equip professionals with the skills and insight needed to lead through complexity.

The curriculum integrates core competencies in public health and epidemiology with leadership, coordination, and decision-making across the full emergency cycle: prevention, preparedness, response, and recovery. It emphasizes etics, legal aspects, Resilience, as well as logistics, data management, risk communication, community engagement, health diplomacy, and a rights-based approach to vulnerability and resilience. Teaching is interactive, scenario-driven, and deeply connected to real-world practice in Israel and globally.

The program is tailored for professionals with field experience—defence, security, lufe-saving and the health workforce (e.g. nurses, doctors, paramedics, veterinarians, public health officers), social workers, educators, emergency responders, local authority personnel, logisticians, legal experts, and humanitarian actors—and all professionals seeking to deepen their impact and formalize their expertise. Delivered in a one or two -days-per-week format, the program enables working professionals to study while continuing their field engagement.

This presentation will showcase how a dynamic, interdisciplinary graduate program can serve as a model for preparing ethical, effective, and agile leaders in emergency management—leaders capable of bridging systems, sectors, and communities in times of crisis.

10:00-10:20 **Coffee break** | Reception hall

SESSION 1 THE IMPACT OF EXTERNAL FACTORS ON DISEASE DYNAMICS AND PUBLIC HEALTH RESPONSES DURING PANDEMICS | Auditorium

Chair: Prof. Itai Benhar, Director of the TCCP, Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences

10:20-10:50 **Prof. Sigal Alon,** Department of Sociology and Anthropology, Faculty of Social Sciences, Tel Aviv University

Work Orientation through the Lens of the COVID-19 Disruption: Temporal and Positional Variations of Work Centrality and Job Satisfaction

Disasters reveal the key values that define society (Drabek, 2007), and COVID-19 is no exception. This significant disruption since WWII allows us to harness our sociological imagination and revisit the roots of work orientation. By examining several snapshots from 2016 to 2023, this investigation assesses the sensitivity of attachment to the world of work (work centrality) and job satisfaction to contextual arrangements. Workers' attitudes are anchored at two structural levels: first, the broader macro context (before, during, and after the COVID-19 period) to capture temporal variation, and second, subjective job quality to capture positional variation. The goal is to evaluate the intersection of temporal and positional variations, specifically how sensitive the relationship between workers' subjective job quality and work orientation is to the macro context. The empirical investigation employs a twin-pronged strategy. The first part fits a polynomial specification, generating three-dimensional surface plots that provide precise and sensitive visualizations of the relationship between work orientation and subjective job quality. The second part implements a novel discrete category analysis based on a categorical specification, facilitating summarization, quantification, and statistical testing of temporal and positional variations. This method is particularly suitable for assessing complex relationships in large-scale, multi-period, and multi-faceted designs. The findings reveal the significant impact of the pandemic disaster on work orientation and the connection between workers' subjective job quality and work orientation. The emerging stratification patterns in work orientation in 2020 persisted until 2023, the final observation window. These findings emphasize the necessity for a dynamic perspective to understand work orientation and its relevance in interpreting labor market dynamics.

10:50-11:20 **Dr. Moran Bodas,** School of Public Health, Faculty of Medical and Health Sciences, Tel Aviv University

The effect of risk messaging framing (altruism versus Individualism) on compliance with health guidelines during a future pandemic

Public adherence to health guidelines during pandemics is critical for disease mitigation, particularly in the absence of medical countermeasures. This study examined the impact of risk communication framing (self-protection vs. altruism-based messaging) on public compliance with health regulations. A longitudinal, intervention-based study was conducted with 523 Israeli adults, randomized into three groups: altruism-based messaging, self-protective messaging, and a control group. Participants completed questionnaires before, immediately after, and two weeks following the intervention.

Findings revealed a significant increase in behavioral intention immediately following the intervention, particularly in the altruism-based messaging group (mean increase: 5.35 to 5.57, $p < 0.01$). However, a comparable decline in behavioral intention was observed across all groups at the two-week follow-up. Repeated measures ANOVA indicated a significant time effect ($F = 9.76$, $p = 0.02$) and an interaction effect for messaging style ($F = 3.25$, $p = 0.039$). Correlational analyses demonstrated a strong positive association between behavioral intention and attitudes toward health guidelines, in particular concerning viewing mask-wearing as an altruistic act and intention to adhere with health guidelines ($r=0.270$, $p<0.01$).

The study highlights the short-term effectiveness of altruism-based risk communication in enhancing compliance with public health measures. However, maintaining these behavioral changes over time remains a challenge, underscoring the need for sustained messaging strategies. Future research should explore methods to reinforce prosocial behavior to improve long-term adherence during public health crises.

האפקט של מסגור מסרים (אלטרואיזם מול אינדבידואליזם) על כוונה להיענות להנחיות בריאות בזמן פנדמיה

רקע: היענות הציבור להנחיות בריאותיות במהלך מגפות היא קריטית לצמצום התפשטות מחלות, במיוחד בהיעדר אמצעים רפואיים מונעים. עם זאת, רתימת הציבור להיענות להנחיות בריאות בזמן מגפה נותרת אתגר משמעותי, כפי שהדגימה מגפת הקורונה. מרבית מאמצי ההסברה ותקשורת הסיכונים מתמקדים בסיכון האישי ולא בתועלת החברתית שבעמידה בהנחיות.

מטרה: מחקר זה בחן את ההשפעה של מסגור תקשורתי של סיכונים (הגנה עצמית לעומת מסרים מבוססי אלטרואיזם) על היענות הציבור להנחיות בריאותיות במקרה של מגפה עתידית אפשרית.

שיטה: בוצע מחקר אורך מבוסס קבוצות השוואה (ביקורת והתערבות) בקרב 523 מבוגרים ישראלים, אשר הוקצו אקראית לשלוש קבוצות: מסרים מבוססי אלטרואיזם, מסרים להגנה עצמית וקבוצת ביקורת (ללא הסברה). המשתתפים השלימו שאלונים לפני ההתערבות, מיד לאחריה ושבועיים לאחריה.

תוצאות: הממצאים הצביעו על עלייה משמעותית בכוונה ההתנהגותית להיענות להנחיות מיד לאחר ההתערבות, במיוחד בקבוצת המסרים מבוססי האלטרואיזם (עלייה ממוצעת: 5.35 ל-5.57,, $p<0.01$). עם זאת, נצפתה ירידה דומה בכוונה ההתנהגותית בכל הקבוצות לאחר שבועיים. ניתוח ANOVA למדידות חוזרות הראה אפקט זמן מובהק ($F = 9.76$, $p = 0.02$) ואפקט אינטראקציה לסגנון המסרים ($F = 3.25$, $p = 0.039$). ניתוחים מתאמיים הראו קשר חיובי חזק בין הכוונה ההתנהגותית לעמדות כלפי הנחיות בריאותיות, במיוחד בנוגע לתפיסת עטית מסכה כמעשה אלטרואיסטי וכוונה להיענות להנחיות הבריאותיות ($r = 0.270$, $p < 0.01$).

מסקנות: המחקר מדגיש את האפקטיביות קצרות הטווח של תקשורת סיכונים מבוססת אלטרואיזם בהגברת הציות להנחיות בריאות הציבור. עם זאת, שמירה על השינויים ההתנהגותיים לאורך זמן נותרת אתגר, המצביע על הצורך באסטרטגיות תקשורת סיכונים מתמשכות. מחקרי המשך צריכים לבחון דרכים לחיזוק התנהגות פרו-חברתית לשיפור ההיענות ארוכת הטווח במהלך משברים בריאותיים.

11:20-11:50 **Prof. Judith Berman,** Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences, Tel Aviv University

Antifungal drug resistance and tolerance in pathogenic yeasts

Fungal infections cause more than 2.4 million deaths a year and the rise in prevalence of fungal infections, pathogens intrinsically resistant to clinically available drugs, and the ability of fungi to survive while testing as susceptible to these drugs. Considerable mortality is associated with serious fungal infections caused by fungal isolates that test as susceptible to the few clinically available antifungal drugs. While patient immune status, drug dynamics and kinetics play their part in treatment failures, the ability of infecting fungi to survive despite their exposure to antifungal therapies is a major reason for the high mortality. We study antifungal drug resistance (which is rare) and antifungal drug tolerance—the ability of some cells, in an isolate that tests as drug-susceptible, to grow slowly and continue to survive and evolve in the presence of the drug. We use Candida albicans (a common commensal of the microbiome and a frequent cause of systemic fungal infections with 30->50% mortality). Tolerance to

azole antifungals (the most widely prescribed class of antifungals) is quite common, likely explains a proportion of clinical treatment failures, and appears to involve many different stress response pathways. Our research aims to understand how tolerance is acquired and is maintained, and how best to prevent both processes, at multiple scales of biology: the species-wide scale, where we compare sequences, proteomes and phenotypes across >1700 isolates to identify the many different routes that C. albicans can use to tolerate stress; the isolate scale, where pathways in a representative set of individual strains are dissected; and at the single cell scale, where we study how individual cells in the population differ from one another in their metabolic and physiological states. Ultimately, a species wide understanding of relevant pathways and cellular shifts in metabolic state will inform approaches to inhibit or stop fungal proliferation during infections.

11:50-12:20 **Prof. Oren Kobiler,** Department of Clinical Microbiology and Immunology, Faculty of Medical and Health Sciences, Tel Aviv University

Enhanced Recombination in Herpes Simplex Viruses is Induced by Antiviral Drugs

Herpes simplex viruses cause significant health complications within human populations. Currently, the only available treatments for these viruses are antiviral drugs that inhibit viral replication. Viral recombination plays an important role in these viruses' replication and evolution. We developed a fluorescent-based assay to assess HSV-1 recombination, which, when combined with a deep machine learning model, becomes a powerful tool for evaluating viral recombination rates. Our results indicate that common antiviral drugs, when used at clinically relevant concentrations, not only inhibit viral replication but also increase viral recombination and the accumulation of defective genomes. Additionally, we observed an increase in interspecies recombination between HSV-1 and HSV-2 in the presence of these drugs. Based on our findings, we conclude that limited inhibition of viral replication may enhance viral diversification.

12:20-13:20 **Lunch**

SESSION 2 BIOLOGICAL AND SYSTEMIC STRATEGIES FOR UNDERSTANDING AND COMBATING DISEASE

Chair: Prof. Adi Stern, Faculty of Life Sciences

13:20-13:50 Dr. Ofer Cornfeld, Be Free Israel

Integrating Macroeconomic and Public Health Impacts in Social Planning Policies for Pandemic Response

Infectious disease outbreaks with pandemic potential present challenges for mitigation and control. Policymakers make policy decisions in order to reduce disease-associated morbidity and mortality while also minimizing socioeconomic costs. There remains a paucity of decision tool frameworks that integrate epidemic and macroeconomic dynamics.

Here, we propose and analyze an econo-epidemic model to identify robust planning policies to limit epidemic impacts while maintaining economic activity. The model couples epidemic dynamics, behavioral change, economic activity, and feasible policy plans informed by respiratory disease threats of pandemic concern. We compare alternative fixed, dynamic open-loop optimal control, and feedback control policies via a welfare loss framework.

We find that open loop policies that adjust employment dynamically while maintaining a flat epidemic curve outperform fixed employment reduction policies. However, open loop policies are sensitive to misestimation of disease strength and feedback between economic activity and transmission, leading to potentially significant increases in welfare loss. In contrast, feedback control policies guided by open loop dynamical targets of the time-varying reproduction number perform near-optimally when parameters are well-estimated, while significantly outperforming open loop policies whenever disease features and behavioral response are misestimated -- as they inevitably are.

These findings present a template for integrating principled economic models and control theory with epidemic scenarios to identify vulnerabilities in policy responses and expand policy options in preparation for future pandemics.

13:50-14:20 **Prof. Marcelo Ehrlich,** Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences, Tel Aviv University

Control of protein translation: a critical battleground in viral infection and antiviral responses, and a promising therapeutic target

Protein synthesis is crucial for both viral replication and antiviral defenses. As such, in all cells, and infected cells in particular, translation is under tight and complex regulation to ensure the expression of the correct amounts of specific protein repertoires. Mechanistically, this is achieved through a combination of structural elements of mRNA molecules and alterations to the expression and activity of protein kinases that phosphorylate translation regulators. The eukaryotic initiation factor 2α kinases (EIF2AK1-4) and the mechanistic target of rapamycin (mTOR) are the primary mediators of this mechanism and are thus differentially regulated in infected cells. Specifically, in the context of interferon-mediated antiviral responses, cells attempt to shut down protein synthesis to arrest viral replication. Consequently, viruses are equipped with various mechanisms that enable them to counteract this inhibition. Moreover, restoration or exacerbation of these cellular capabilities may serve as an efficient antiviral tactic. We examine these contrasting scenarios by studying: (i) the differential ability of oncogenes encoded by viruses that infect primates (SV40-Large T antigen or HPV16-E6E7 proteins) to inhibit human but not murine PKR, using a novel human-PKR knock-in mouse, and (ii) by developing and characterizing a novel antiviral compound that targets translation-regulatory kinases.

14:20-14:50 **Prof. Dudu Burstein,** Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences, Tel Aviv University

Plasmids Fight Back: Anti-Defense Systems Boost Conjugation Efficiency

Bacterial defense mechanisms, including CRISPR-Cas, restriction-modification systems, and SOS-response genes, have evolved to prevent the invasion of mobile genetic elements. Despite these barriers, plasmids efficiently transfer within bacterial populations through conjugation, driving gene mobilization and the global spread of antimicrobial resistance, which threatens modern medicine. Using comparative genomics and functional analyses, we show that the leading region of plasmids, the first to enter recipient cells, is a hotspot for an extensive repertoire of anti-defense systems, encoding anti-CRISPR, anti-restriction, anti-SOS, and other counter-defense proteins. We further identified in the leading region a prevalence of promoters known to allow expression from single-stranded DNA, facilitating rapid protection

against bacterial immunity during the early stages of plasmid establishment. We performed conjugation experiments with anti-defense genes in different locations of the plasmid and demonstrated the importance of their position in the leading region for efficient conjugation. These results indicate that focusing on the leading region of plasmids could lead to the discovery of diverse anti-defense genes. Combined, our findings reveal an intricate evolutionary strategy for plasmid dissemination, provide foundations for developing efficient conjugative delivery systems for natural microbial communities, and offer potential tools to combat the "silent pandemic" of antimicrobial resistance.

14:50-15:20 **Prof. Uri Ashery,** Sagol School of Neuroscience, School of Neurobiology Biochemistry & Biophysics, Faculty of Life Sciences, Tel Aviv University

Developing a Biological Definition for Synucleinopathies based on Alpha-Synuclein Aggregates Using Super Resolution Microscopy

Objectives: Alpha-synuclein (aSyn) is a synaptic protein that plays a role in synaptic vesicle trafficking and neurotransmitter release through interactions with SNARE proteins. Irregular aggregation of aSyn is known to occur in many synucleinopathies like Parkinson's disease (PD), Multiple system atrophy (MSA), and Dementia with Lewy Bodies (DLB). However, it is unknown whether the organizations of the aSyn aggregates are similar or different in these diseases. Our main aim is to characterize the different aSyn aggregate species in the various diseases and to study if aSyn aggregate inhibitors have a similar effect on these aSyn aggregates simultaneously and to understand the biological implications of altered aggregate characteristics.

Methods: To characterize the aSyn aggregates in detail, we use a novel super-resolution imaging technique, direct Stochastic Optical Reconstruction Microscopy (dSTORM). Together with an in-house analysis platform "dSTORM Analyzer", which provides quantitative measures such as aggregate size, number of molecules, density of aggregates alongside additional parameters.

Results: We applied dSTORM on different cell types including mouse cortical neurons, MSA cell lines, PD patients' skin, and human-induced pluripotent-stem-cell derived models to study the aSyn aggregates in different synucleinopathies. aSyn aggregates in mouse cortical neurons range in size, between 30-220 nm, similar to the aSyn aggregate size range in striatal mouse neurons. Similarly, aSyn aggregates in skin biopsies from PD patients have an average radius of 75nm. Currently, we are examining aSyn aggregation in MSA cell lines and the effects of an aSyn aggregate modifier on the aggregates' parameters.

Conclusions: As the precise molecular organization of aSyn aggregates in different synucleinopathies is currently unclear, this approach can provide new information about aggregates' size, density, and composition. This can elucidate changes between aSyn aggregates in different species and diseases to contribute to our understanding regarding whether similar drugs can help in all synucleinopathies or how they can be modified for specific diseases.

15:20-15:45 **Coffee break** | Reception hall

SESSION 3 STUDENTS LECTURES – INCLUDING RECIPIENTS OF TCCP SCHOLARSHIPS

Chair: Prof. Udi Sommer, Faculty of Social Sciences

15:45-16:00 **Arielle Kaim** (Prof. Bruria Adini's Lab) School of Public Health, Faculty of Medical and Health Sciences, Tel Aviv University

Evaluating the Effectiveness of Emergency Medical Team Field Hospital Deployments in Pandemic Response: A Novel Assessment Tool

The COVID-19 pandemic highlighted the immense strain placed on healthcare systems globally, emphasizing the urgent need for surge capacity. To manage the overwhelming patient load, field hospitals were introduced to support existing healthcare infrastructures. Defined by the World Health Organization, field hospitals are mobile healthcare facilities intended for rapid deployment in emergency situations. These units provided essential care in non-traditional settings; however, multiple challenges emerged during their operation in the pandemic. Existing literature on COVID-19 field hospitals documented persistent issues, including shortages in human resources, disruptions in supply chains, and structural limitations.

This study aimed to develop and validate a tool for evaluating the effectiveness of field hospitals during pandemics. Its objectives were to identify key performance indicators (KPIs) relevant to field hospital operations, create an evaluation tool based on these indicators, and validate the tool through a pilot study. A cross-sectional exploratory study was conducted with one field hospital team under classification, involving volunteers from both logistical and clinical roles.

The study was carried out in several phases. Initially, the evaluation tool was developed based on an extensive literature review and semi-structured interviews with COVID-19 field hospital directors. The tool was then validated by 20 content experts, and a

modified Delphi technique was used to reach consensus on the relative weight of each performance indicator. Finally, a full-scale pandemic response simulation was conducted, covering all aspects of field hospital operations. During this simulation, the tool was applied and refined using both objective and subjective metrics, and its dissemination occurred throughout and following the exercise.

The research provided a robust framework for assessing field hospital performance, ensuring the delivery of efficient, effective, and evidence-based care during health emergencies.

The findings offer valuable insights for enhancing preparedness strategies and improving the adaptability of healthcare systems in times of crisis.

16:00-16:15 **Roza Izgilov** (Prof. Dafna Benayahu's Lab) Department of Cell and Developmental Biology, Faculty of Medical & Health Sciences, Tel Aviv University

Advanced glycation end products (AGEs) alter tissue stiffness and lead to metabolic dysfunction

Type 2 diabetes (T2D) and obesity have emerged as global pandemics, significantly impacting public health and healthcare systems worldwide. A critical yet underexplored area in the pathogenesis of these metabolic disorders involves the role of Advanced Glycation End-products (AGEs). AGEs, formed through non-enzymatic glycation processes under hyperglycemic conditions, induce structural changes and dysfunction in proteins, influencing metabolic pathways and tissue characteristics.

This research investigates the specific impacts of AGEs, particularly methylglyoxal (MGO)-derived AGEs, on adipose tissue metabolism and cellular microenvironment. Our recent studies demonstrated that exposure to MGO alters protein structure. The current project employs multidisciplinary approaches to elucidate how these molecular changes contribute to adipocyte niche stiffness and impaired cellular signaling pathways, findings that are mirrored in diabetic animal models.

The insights gained from this study aim to deepen our understanding of how nutritional and metabolic factors influence the progression of T2D and obesity pandemics.

16:15-16:30 **Asaf Pras** (Prof. Hadas Mamane's Lab) School of Mechanical Engineering, Faculty of Engineering, Tel Aviv University

Nowcasting Fecal Coliforms Risk Categories in real-time and in-situ

Access to safe drinking water is essential for public health; however, the timely detection of microbial contamination, specifically fecal coliforms (FC), remains challenging due to delays in conventional water testing methods. This study evaluated machine learning (ML) and deep learning (DL) models to predict real-time FC contamination risk categories using readily measurable water parameters. Utilizing approximately 85,000 water samples from India, classified into five WHO-defined risk levels, models including Random Forest (RF), XGBoost, logistic regression, recurrent neural networks (RNN), and long short-term memory (LSTM) were developed. Incorporating parameters such as temperature, pH, turbidity, electrical conductivity, dissolved oxygen, total dissolved solids, source type, and location, the RF model achieved the highest accuracy (76.1%), outperforming the LSTM model (74.1%). Both models effectively identified extreme contamination events but struggled with intermediate levels. Findings highlight the potential of machine learning (ML) for real-time microbial contamination prediction, emphasizing the significance of extensive historical data in enhancing model accuracy and supporting effective water quality management.

16:30-16:45 **Yoav Dan (Prof Lihi Adler Abramovich's Lab) Department of Oral Biology,** The Goldschleger School of Dental Medicine, Faculty of Medical & Health Sciences, Tel Aviv University

Encapsulated Enzyme as an Antibacterial Treatment

The increasing prevalence of antibiotic-resistant infections presents a serious challenge to public health worldwide. As traditional antibiotics lose effectiveness, there is a growing need for alternative strategies that can mitigate bacterial pathogenicity without contributing to resistance. One such approach targets bacterial communication systems that regulate collective behaviors such as virulence, toxin production, and biofilm formation. By disrupting these signaling pathways, it is possible to attenuate bacterial activity without directly killing the cells, thus reducing selective pressure for resistance. Enzymes capable of degrading these signaling molecules offer a promising method of intervention. However, their practical application is hindered by limited stability under physiological and environmental conditions. Encapsulation within self-assembling peptide-based nanostructures provides a solution, offering protective carriers that improve enzyme stability, extend shelf

life, and preserve functionality. These biocompatible assemblies can shield the enzymes from degradation while maintaining their ability to interfere with bacterial communication. This encapsulation-based strategy holds significant potential as a new class of antibacterial treatment. It combines targeted action with enhanced stability, making it suitable for various applications. By supporting the development of non-antibiotic therapies, this work contributes to the broader effort to address the global antibiotic resistance crisis through innovative and sustainable solutions.

16:45-17:00 **Dafna Tussia-Cohen** (Dr. Tsachi Hagay's Lab) Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences, Tel Aviv University

Using comparative genomics to discover resistance mechanisms against infectious diseases

Most emerging infectious diseases in humans are caused by pathogens originating from animals. Many of these animals are adapted to these pathogens and display mild or asymptomatic infection. For example, the Egyptian fruit bat can be infected by Ebolavirus - a lethal virus for humans - without any significant symptoms. Reptiles are also thought to be more resistant to various infections in comparison with mammals. In my research, I compare the innate immune response between human and animals thought to have unique adaptations to resist pathogens. By using comparative genomics analysis, I detect differences between these species in specific immune pathways. These evolutionary differences can then be leveraged to find new treatments for infectious diseases in humans.

In my first project I discovered that the complement system genes are highly and uniquely expressed in bat epithelial cells, unlike in corresponding human and mouse cells. This high expression in bat cells before infection can provide a rapid inhibition mechanism against a range of invading pathogens in gut and lung of bats.

Using a similar comparative approach, I now focus on peripheral blood mononuclear cells (PBMCs) from a range of representative reptiles and study their innate immune response to pathogens in comparison to mammalian PBMCs.

17:00-17:15 **Elya Wygoda** (Prof. Tal Pupko's Lab), Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences, Tel Aviv University

How do sequences diverge? Accurate modelling of indel and substitution events

Understanding how biological sequences change over time is important for studying bacterial pathogens. This talk explores whether the patterns of insertions and deletions (indels) in protein sequences can help distinguish between effector and non-effector proteins in bacteria. While much of the research in molecular evolution has focused on substitution patterns, indels provide additional information about evolutionary history that has been severely lacking.

We developed an Approximate Bayesian Computation (ABC) method to determine indel patterns from multiple sequence alignments (MSAs) of effector proteins. This method estimates insertion rates, deletion rates, and length distributions of indel events by comparing real sequences to simulated ones.

A challenge with ABC methods is that they need many simulations to be accurate. The second part of my talk will focus on making our sequence simulations faster without losing accuracy. I will describe how we improved our algorithms to speed up simulations, making it practical to analyze protein MSAs from bacterial effectors and non-effectors.

By applying these methods to effector and non-effector proteins, we aim to improve our prediction tools for identifying secreted effectors in pathogenic bacteria, which could help us better understand how bacteria interact with their hosts at the molecular level.

17:15 **Closing remarks** | Auditorium