

## APPLIED MATHEMATICS

Barak Sober (Hebrew University of Jerusalem)

*Exploring social patterns in ancient societies through variations in distribution of given names*

We present a novel application of ecological diversity statistics to analyze ancient societies through personal names preserved in archaeological records. Our approach adapts Hill Numbers and evenness measures to examine 1,058 personal names from the Hebrew kingdoms of Israel and Judah during the Iron Age II period (ca. 950-586 BCE), introducing specialized permutation test procedures to handle the small sample sizes characteristic of archaeological data.

The statistical analysis reveals significant differences in onomastic diversity patterns: Israel exhibits higher name diversity than contemporary Judah, Judah shows temporal decline over time, and the kingdoms display contrasting center-periphery geographic patterns. We validate our methodology using modern onomastic datasets from five countries, demonstrating that our statistical procedures remain robust for archaeological sample sizes. This work establishes a quantitative framework for extracting social insights from limited historical data and demonstrates the potential for applying diversity statistics beyond traditional contexts.

Inbar Seroussi (Tel Aviv University)

*Criticality in evolving scale-free graphs*

The evolution of epidemics and other contact processes depends on the interaction network between individuals. However, realistic networks are typically dynamic and change over time. In this talk, I will present a Susceptible-Infected-Recovered (SIR) model on an evolving graph, where the graph connections are resampled periodically. I will demonstrate that this model becomes critical for periodically resampled scale-free graphs with infinite variance, in the sense that the temporal average of the reproduction number converges to one, and the fraction of susceptible individuals converges to zero. This criticality is maintained for finite and infinite populations with high probability for all parameter values. Consequently, asymptotically, the entire population becomes infected, and there is no herd immunity.

Our model suggests a new route by which systems self-evolve into criticality without any fine-tuning. This is a joint work with Gil Ariel and Ofer Zeitouni.

Daniel Freedman (Tel Aviv University)

*Generative AI for molecules: semi-equivariant flows, sketchy diffusion, and quantum ground states*

Generative AI has made tremendous strides over the last few years in a wide variety of fields, including text, images, audio, and video. In this talk, we discuss the use of Generative AI techniques in the realm of molecules, emphasizing the incorporation of invariances to transformation groups, and covering three applications. In the first, we show an approach to the problem of generating molecules which will bind to a particular receptor molecule, a problem common in drug design. We design specialized normalizing flows which respect the physical invariances inherent in the problem, through the use of semi-equivariant networks. In the second application, we show how to adapt diffusion models to deal with this same problem. In particular, we address the size disparity between the receptor and the generated molecule, which can be problematic for learning as the receptor can overwhelm the training; we do so by creating a small sketch of the receptor, dubbed a

“virtual receptor.” In the final application, we address a problem common to chemistry, material science, and condensed matter physics: computing the quantum ground state of a molecule or material. We demonstrate an efficient method of solving the Electronic Schrödinger Equation by using a carefully designed antisymmetric normalizing flow to construct the wavefunction ansatz.

Yoram Louzoun (Bar-Ilan University)

*Efficient subgraph isomorphism in colored graphs*

Algorithms for the exact detection of a subgraph  $S$  within a larger graph  $G$  are currently limited to a small number of vertices in  $S$ . In colored graphs, the problem is simpler, given the constraint induced by the color match. We here propose VELCRO: (Very Efficient Large Colored gRaph-subgraph detectiOn) to detect very large colored subgraphs. VELCRO is based on efficient memory management to avoid multiplying the constraint memory cost for each vertex combination tested, smart traversal of vertices in  $S$ , and a constraint on the degree of the next vertex.

In short, VELCRO orders the vertices in  $S$  and opens a Depth First Search (DFS) in  $G$  to search pathways consistent with  $S$ . At each stage, VELCRO efficiently tests the constraints on unmatched vertices in  $S$ . The vertex order is optimized to prevent an exponential growth in the number of candidate trajectories. VELCRO stops a path when any vertex in  $S$  is constrained to have no possible match in  $G$ . We show the efficacy of VELCRO on simulated dense  $G(n, p)$ , real-world colored graphs, and real-world graphs with random coloring. VELCRO was tested on  $S$  of up to  $10^4$  vertices and on  $G$  up to millions of vertices and solves all cases within seconds to minutes. No current exact subgraph matching algorithm can search such large colored subgraphs.

In the specific case of rainbow cliques (a clique containing one vertex of each color), the task can be further optimized by reducing the search space to include the colored  $K$ -core. The search space limitation can be proposed as a general approach to improve the efficacy of the subgraph isomorphism problem.

Boaz Nadler (Weizmann Institute of Science)

*Completing large low-rank matrices from only few observed entries: a one-line algorithm with provable guarantees*

Suppose you observe very few entries from a large matrix. Can we predict the missing entries, say assuming the matrix is (approximately) low rank? We describe a very simple method to solve this matrix completion problem. We show our method is able to recover matrices from very few entries and/or with ill conditioned matrices, where many other popular methods fail. Furthermore, due to its simplicity, it is easy to extend our method to incorporate additional knowledge on the underlying matrix, for example to solve the inductive matrix completion problem, or completion with outliers. On the theoretical front, we prove that our method enjoys some of the strongest available theoretical recovery guarantees.

Jakob Waxman (Clalit Innovation)

*Using ML and AI to improve healthcare*

I will be presenting how at Clalit innovation we leverage machine learning, AI and big data to improve the delivery of healthcare, using a few different examples of projects. I will include a discussion around the challenges associated with implementation, the different considerations that impact our decision making, and the process we have developed for regulating AI in Clalit.