

**PROGRAM OF THE
MINI-CONFERENCE ON APPLIED COMBINATORICS
WITH AN EMPHASIS ON SEARCH THEORY**

October 15: The day's program will be in Room 312 in the LeConte Building		
5:30- 6:30	Gyula O.H. Katona	Introduction to Search Theory and a result when the lie depends on the question
PIZZA PARTY		
October 16: The talks will be held in the CAS conference room, which is Room 231 in the Sumwalt Building		
8:30- 8:55	Ferdinando Cicalese	On Priced Function Evaluation
9:00- 9:25	Anthony J. Macula	Fibonacci Ensemble and High Fidelity DNA Codes
9:30- 9:55	Gábor Wiener	Rounds in Combinatorial Search
COFFEE BREAK		
10:30-10:50	Shahriar Shahriari	Chain partitions of normalized matching posets
10:55-11:15	Kelly Jordan	The Necklace Poset is a Symmetric Chain Order
11:20-11:40	Hua Wang	Trees with non-Sperner subtree poset
11:45-12:05	Jeremy Lyle	The Structure of Dense Graphs with Small Clique Number
LUNCH BREAK		
14:00-14:20	Darren Narayan	Minimal k -rankings and the rank number of P_n^2
14:25-14:45	Yubo Zou	Decycling of Fibonacci Cubes
COFFEE BREAK		
15:30-16:30	Charles J. Colbourn	Combinatorial Screening to Locate Interaction Faults
16:45-17:05	Dániel Gerbner	Algorithms finding interactions in some cases
17:10-17:30	Linyuan Lincoln Lu	An exact result and its application on hypergraph Turán numbers
17:35-17:55	Joshua Cooper	Discrete Stochastic Differentiation

ABSTRACTS

The abstracts are in the order of the talks.

Gyula O. H. Katona

Alfréd Rényi Institute of Mathematics, visiting at University of South Carolina
Search Theory and a result when the lie depends on the question

In the basic model of search an n -element set X is given which contains an unknown, but important element x . The goal is to find x . Questions of type "is $x \in A$?" can be asked for certain subsets $A \subset X$. The number of questions should be minimized necessary to find x . Another model is the traditional "search with lies" when the answers for the questions "is $x \in A$?" can be wrong with certain restrictions, but the chance of the false answer does not depend on x or A . The first part of the lecture will give a brief survey of this theory.

In the second half of the lecture the speaker will introduce a recent work with Krisztián Tichler in which the questions have a different nature. Namely one question is a partition Y, N, L of X . If $x \in Y$ the answer will be "yes" and we can be sure that x is in Y . The same if $x \in N$. However if $x \in L$ the the answer might be "yes" or "no", that is, no useful information is received. We found minimal algorithms finding an arbitrary x under such circumstances.

Ferdinando Cicalese

Università degli Studi di Salerno and Universitaet Bielefeld
On Priced Function Evaluation

A function f of n variables is to be evaluated. Let c_i be the cost of accessing the value of the i th variable. Knowing the values of some of the variables may determine the value of f . We provide algorithms for evaluating f by adaptively accessing values of the variables. The objective is to minimize the sum of the costs of the variables read. We evaluate the competitiveness of the algorithms in two settings: when the algorithm does or does not know the access costs c_1, \dots, c_n . We provide polytime algorithms with optimal and quasi-optimal competitiveness for several classes of functions.

Anthony J. Macula

State University of New York, College at Geneseo
Fibonacci Ensemble and High Fidelity DNA Codes

DNA nanotechnology often requires collections of oligonucleotides called DNA free energy gap codes that do not produce erroneous crosshybridizations in a competitive multiplexing environment. This talk addresses the question of how to design these codes to accomplish a desired amount of work within an acceptable error rate. Using a statistical thermodynamic and probabilistic model of DNA code fidelity, mathematical random coding theory methods and a connection to the Fibonacci numbers, theoretical lower bounds on the size of DNA codes are given. More importantly, DNA code design parameters, e.g., strand number, strand length and sequence composition, needed to achieve experimental goals are identified.

Gábor Wiener

Budapest University of Technology and economics
Rounds in Combinatorial Search

A set system $\mathcal{H} \subseteq 2^{[m]}$ is said to be separating if for every pair of distinct elements $x, y \in [m]$ there exists a set $H \in \mathcal{H}$ such that H contains exactly one of them. The search complexity of a separating system $\mathcal{H} \subseteq 2^{[m]}$ is the minimum number of questions of type " $x \in H$?" (where $H \in \mathcal{H}$) needed in the worst case to determine a hidden element $x \in [m]$. If we receive the answer before asking a new question then we speak of the *adaptive* complexity, denoted by $c(\mathcal{H})$, if the questions are all fixed beforehand, then we speak of the *non-adaptive* complexity, denoted by $c_{na}(\mathcal{H})$. If we are allowed to ask the questions in at most k batches then we speak of the *k-round* complexity of \mathcal{H} , denoted by $c_k(\mathcal{H})$. It is clear that $|\mathcal{H}| \geq c_{na}(\mathcal{H}) \geq c_1(\mathcal{H}) \geq c_2(\mathcal{H}) \geq \dots \geq c_m(\mathcal{H}) = c(\mathcal{H})$. A group of problems raised by G.O.H. Katona is to characterize those separating systems for which some of these inequalities are tight. In the lecture we are discussing set systems \mathcal{H} with the property $|\mathcal{H}| = c_k(\mathcal{H})$ for any $k \geq 3$. We give a necessary condition for this property by proving a theorem about traces of hypergraphs which also has its own interest.

Shahriar Shahriari

Pomona College *Chain partitions of normalized matching posets*

The talk is about recent results on a 30 year old conjecture of Griggs, which claims that normalized matching posets have a nested chain decomposition.

Kelly Jordan

University of South Carolina
The Necklace Poset is a Symmetric Chain Order

Let N_n denote the quotient poset of the Boolean lattice, B_n , under the relation equivalence under rotation. Griggs, Killian, and Savage proved that N_p is a symmetric chain order for prime p . In this paper, we settle the question of whether this poset is a symmetric chain order for all n by providing an algorithm that produces a symmetric chain decomposition (or SCD). We accomplish this by modifying bracketing from Greene and Kleitman. This allows us to take appropriate "middles" of certain chains from the Greene-Kleitman SCD for B_n . We also prove additional properties of the resulting SCD and show that this settles a related conjecture.

Hua Wang

University of Florida
Trees with non-Sperner subtree poset

Consider the poset of subtrees of a tree with respect to the inclusion ordering. It has been asked whether such posets are Sperner for all trees. While this question was answered in negative in 1995 with a counterexample, we show an infinite family of trees whose posets are non-Sperner.

Jeremy Lyle

Clemson University

The Structure of Dense Graphs with Small Clique Number

In this talk, we prove a general structural result about partitioning dense graphs which contain no clique of size r , which in particular allows us to extend results from triangle-free graphs and show that dense graphs of size n which contain no clique of size r and have minimum degree larger than $(2r - 5)/(2r - 3)n$ have chromatic number at most $r + 1$. Lastly, we will discuss other uses of this result, in particular as it applies to the binding number of a graph.

Darren Narayan

Rochester Institute of Technology, visiting University of South Carolina

Minimal k -rankings and the rank number of P_n^2

For a graph G , a k -ranking is a labeling of the vertices using integers between 1 and k inclusive such that whenever there are two vertices with the same label, every path connecting them contains a vertex of higher label. A ranking is minimal if the reduction of any label results in a violation of the above ranking property. The rank number of a graph is the minimum k that can occur in a minimal ranking. The arank number is the maximum k that can appear in a minimum ranking. We investigate rank and arank numbers for paths, cycles and related graph families.

Yubo Zou

University of South Carolina

Decycling of Fibonacci Cubes

The decycling number $\nabla(G)$ of a graph G is the smallest number of vertices that can be deleted from G so that the resultant graph contains no cycle. A Fibonacci string of order n is a binary string of length n with no two consecutive ones. The Fibonacci cube of order n is the graph whose vertices are the Fibonacci strings of length n such that two vertices are adjacent if they differ in just one position. The family of Fibonacci cubes has applications in interconnection topologies. In this talk, we will study the decycling number of the Fibonacci cubes. Lower and upper bounds of the decycling number for the Fibonacci cubes will be presented, as well as the exact value of the decycling number for $n < 8$.

Charles J. Colbourn

Arizona State University

Combinatorial Screening to Locate Interaction Faults

Let $\{F_1, \dots, F_k\}$ be a set of k factors. Each factor F_i has a set V_i of v_i allowed values. A covering array of strength t and type $(v_1 \cdots v_k)$ having N tests is an $N \times k$ array with the property that choosing any t columns (factors) i_1, \dots, i_t , each of the $\prod_{j=1}^t v_{i_j}$ possible t -tuples of values for F_{i_1}, \dots, F_{i_t} appears at least once in a test as the values of the corresponding factors. (In other words, for every t factors, every possible combination of values is tested at least once.) We call such a choice of t factors and values for each a t -way interaction.

Covering arrays have been widely used to detect the presence of unexpected interactions among factors; examples of applications include component-based software testing, integrated circuit I/O testing, developmental genetic networks, materials development, and combinatorial drug design. One way to use a covering array in a screening experiment is to run each of the N tests to produce a binary response vector; the presence of a '1' in the ℓ th position indicates that an unexpected interaction arose in the execution of the ℓ th test. A standard use would be for defect detection. Covering arrays can in this way detect the presence of certain unexpected interactions, but may be unable to locate them. Indeed many different combinations of interactions can lead to the same response vector, and hence the unexpected interactions involved cannot be deduced.

We explore a generalization of covering arrays. A (d, t) -locating array is a covering array of strength t so that if there are at most d unexpected t -way interactions, we can uniquely determine from the response vector which interactions arose. This location condition imposes a cover-free property on the array; indeed considering the subsets of tests in which t -way interactions arise produces a d -cover-free family. We pose many questions on the existence of (d, t) -locating arrays, and answer a few.

Dániel Gerbner

University of South Carolina

Algorithms finding interactions in some cases

Let $\{F_1, \dots, F_n\}$ be a set of n factors. Each factor F_i has a set V_i of v_i allowed values. A choice of some factors and their values is called an interaction. A choice of the values of all the factors (a realization) is either "wrong" or "good".

In our cases the values of all the factors are 0 and 1. In other words, every possible choice of values corresponds a subset of $\{1, \dots, n\}$. Let \mathcal{F} be the family of "wrong" sets. We suppose \mathcal{F} is monotone, i.e. if $A \subset B \subset \{1, \dots, n\}$ and $A \in \mathcal{F}$ then $B \in \mathcal{F}$. In this case the smallest "wrong" interactions are the minimal members of \mathcal{F} . One test can ask subsets of $\{1, \dots, n\}$ if they are in \mathcal{F} or not. Our goal is to find all the minimal members of \mathcal{F} .

In this generality it has been solved by Hansel. We examine some cases when some restrictions are known on the family of minimal members of \mathcal{F} .

Linyuan Lincoln Lu

University of South Carolina

On families of subsets with a forbidden subposet

Let $\mathcal{F} \subset 2^{[n]}$ be a family of subsets of $[n] = \{1, 2, \dots, n\}$. For any poset H , we say \mathcal{F} is H -free if \mathcal{F} does not contain any subposet isomorphic to H . For a fixed poset H , let $\text{La}(n, H)$ be the maximum size of H -free families $\mathcal{F} \subset 2^{[n]}$. We give bounds on $\text{La}(n, H)$ in terms of H .

Joshua Cooper

University of South Carolina

Discrete Stochastic Differentiation

Suppose that a random walker on a vertex-weighted graph chooses neighboring vertices at each step with probabilities in proportion to those vertices' weights. If the walker is started at a "source" vertex, and stops when she reaches a "sink" vertex, one may ask, what is the expected number of visits (i.e., occupation times) to each vertex? The answer is simple to derive from standard Markov Chain theory, but the inverse question, which we term "discrete stochastic differentiation" (DSD) is apparently wide open: given a graph with designated source and sink, for which vectors of occupation times is it possible to find a corresponding weighting of the vertices of G ? How does one find it if it exists? We state a natural conjecture and several results about DSD. We also discuss a few promising applications to machine learning and educational psychology.