Program

Monday

- 9:00 Thomas Prellberg

  Lattice Path Counting: where Enumerative Combinatorics and Statistical Mechanics meet

  A topic common to the two disciplines in the title of this talk is the wish to count truly large ensembles of structures. This talk will examine different ways of how the problem of lattice path counting is approached using methods from both of these areas. While enumerative combinatorics strives to ideally provide exact counting numbers, statistical mechanics rather deals with the thermodynamic limit of large system sizes, where concepts like entropy and energy are related to asymptotic growth. I will endeavour to close the gap between exact counting formulas from enumerative combinatorics and the approximate counting underlying the statistical mechanical approach, and to clearly define jargon particular to either discipline.

- 10:00 Coffee

- 10:20 EJ Janse Van Rensburg

  Modelling dense polymers by self-avoiding walks

  A dense polymer (for example in a polymer melt, or polymers in confined spaces in living cells) can be modelled by a lattice self-avoiding walk in a confined space. For example, in the square lattice a self-avoiding walk can be confined to a square. If the walk is very short compared to size of the square, then it is in an expanded phase, but when it is long, then it will start to fill the area of the square and is a compressed walk. In this talk I give a summary about modelling the free energy of a compressed walk by using Flory-Huggins theory (a mean field phenomenological theory of the free energy of dense polymer systems). We estimate numerically the Flory Interaction Parameter for square lattice self-avoiding walks, and also give an extrapolated estimate of the connective constant of Hamiltonian walks of a square. I will also produce tentative results on compressed and knotted lattice polygons in 3 dimensions.

- 11:00 Olya Mandelshtam

  Combinatorics of the ASEP on a ring and Macdonald polynomials

  The multispecies asymmetric simple exclusion process (ASEP) is a model of hopping particles of M different types hopping on a one-dimensional lattice of N sites. In this talk, we consider the ASEP on a ring with the following dynamics: particles at adjacent sites can swap places with either rate 1 or t depending on their relative types. Recently, James Martin gave a combinatorial formula for the stationary probabilities of the ASEP with generalized *multiline queues*. We will begin by describing the combinatorial methods we use to study the ASEP on a ring.

Furthermore, it turns out that by introducing additional statistics on the multiline queues, we get a new formula for both symmetric Macdonald polynomials P_λ and nonsymmetric Macdonald polynomials E_λ, where λ is a partition. For the second part of the talk, we will discuss the recent results and remarkable connection with Macdonald polynomials. This talk is based on joint work with Sylvie Corteel (Université Paris-Diderot) and Lauren Williams (Harvard).

- Lunch
- 16:00 Michael Deem

  Brain Modularity Mediates the Relation between Task Complexity and Performance

  Recent work in cognitive neuroscience has focused on analyzing the brain as a network, rather than as a collection of independent regions. Prior studies taking this approach have found that individual differences in the degree of modularity of the brain network relate to performance on cognitive tasks. However, inconsistent results concerning the direction of this relationship have been obtained, with some tasks showing better performance as modularity increases and other tasks showing worse performance. Our recent theoretical model suggests that these inconsistencies may be explained on the grounds that high-modularity networks favor performance on simple tasks whereas low-modularity networks favor performance on more complex tasks. I will review experiments being carried out by collaborators showing a negative correlation between individualsâĂŹ modularity and their performance on a composite measure combining scores from the complex tasks and a positive correlation with performance on a composite measure combining scores from the simple tasks. I will further present theory showing that a dynamic measure of brain connectivity termed flexibility is predicted to correlate in the opposite way with performance. I will review experiments confirming these predictions and also showing that flexibility plays a greater role in predicting performance on complex tasks requiring cognitive control and executive functioning. The theory and results presented here provide a framework for linking measures of whole-brain organization from network neuroscience to cognitive processing.
- 16:40 László Kozma

  Pattern avoidance: algorithmic connections
- 17:20 Open problem session

Tuesday

- 9:00 Sergi Elizalde

  A Markov-chain model of chromosomal instability

  Genomic instability allows cancer cells to rapidly vary the number of copies of each chromosome (karyotype) through chromosome missegregation events during mitosis, enabling genetic heterogeneity that leads to tumor metastasis and drug resistance. We construct a Markov chain that describes the evolution of the karyotypes of cancer cells. The Markov chain is based on a stochastic model of chromosome missegregation which incorporates the observed fact that individual chromosomes contain proliferative and anti-proliferative genes, leading to cells with varying fitness levels and allowing for Darwinian selection to occur. We analyze the Markov chain mathematically, and we use it to predict the long-term distribution of karyotypes of cancer cells. We then adapt it to study the behavior of tumors under targeted therapy and to model drug resistance. Vincent Vatter

  Less appreciated facets of permutation patterns

  The advances of Bevan, Bóna, Fox, Marcus, Tardos, et al. have made the asymptotic analysis of permutation patterns a prominent topic in combinatorics. I will attempt to survey other aspects of this study, hopefully exposing some gaps in the literature that ought to be filled (as opposed to "much-needed gaps in the literature", as the famous phrase goes). In particular, I will emphasize local containment bounds, universal permutations, reconstruction, mesh patterns, and more.

- 10:00 Coffee

- 10:20 David Bevan

  The curious behaviour of the total displacement

  The *total displacement* of a permutation $\sigma = \sigma_1 \ldots \sigma_n$ is $\mathsf{td}(\sigma) = \sum_i |\sigma_i - i|$. The ratio of the total displacement to the number of inversions, $R(\sigma) = \mathsf{td}(\sigma)/\mathsf{inv}(\sigma)$, is known to lie in the half-open interval $(1, 2]$ (unless σ is an increasing permutation, with no inversions).

  Let $\boldsymbol{\pi}_{n,m}$ denote a permutation chosen uniformly at random from the set of all n-permutations with exactly m inversions. In this talk, we consider the behaviour of the expected asymptotic displacement ratio $R[m] = \lim_{n\to\infty} \mathbb{E}\big[R(\boldsymbol{\pi}_{n,m})\big]$, as $m = m(n)$ increases from 1 to $\binom{n}{2}$.

  As long as $m = o(n)$, $R[m]$ takes the constant value of 2. Then, when $m \sim \alpha n$, $R[m]$ decreases as α increases, from 2 down to $2\log 2 \approx 1.3863$. However, once m becomes superlinear in n, $R[m]$ stalls again, at $2\log 2$, until $m = \Theta(n^2)$. Finally, when $m \sim \rho\binom{n}{2}$, $R[m]$ decreases from $2\log 2$, taking the value $\frac{4}{3}$ when $\rho = \frac{1}{2}$ and finally reaching 1 when $\rho = 1$.

We investigate how this curious behaviour can be explained in terms of the different effects that local and global constraints have on $\pi_{n,m}$.

- 11:00 Vincent Vatter

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- Lunch
- 16:00 Christine Heitsch

  The combinatorics of RNA branching

  Understanding the folding of RNA sequences into three-dimensional structures is one of the fundamental challenges in molecular biology. For example, the branching of an RNA secondary structure is an important molecular characteristic yet difficult to predict correctly. However, results from enumerative, probabilistic, and geometric combinatorics can characterize different types of branching landscapes, yielding insights into RNA structure formation.

- 16:40 Péter Erdős

  Sampling bipartite degree sequence realizations - the Markov chain approach

  How to analyze real life networks? There are myriads of them and usually experiments cannot be performed directly. Instead, scientists define models, fix parameters and imagine the dynamics of evolution.

  Then, they build synthetic networks on this basis (one, several, all) and they want to sample them. However, there are far too many such networks. Therefore, typically, some probabilistic method is used for sampling.

  We will survey one such approach, the Markov Chain Monte Carlo method, to sample realizations of given degree sequences. Some new results will be discussed.

Wednesday

- 9:00 István Miklós

  Computational complexity of sampling and counting genome rearrangements scenarios

  Most of the counting problems fall into one of the following 3 categories:

(a) In FP, that is, exactly solvable in polynomial time

(b) In the intersection of #P-complete and FPRAS, that is, exact polynomial solution does not exists (assuming that P $\neq$ NP) but efficient random approximation exists

(c) In #P-complete and outside of FPRAS, that is, cannot be well approximated even in a stochastic manner (assuming that RP $\neq$ NP).

The sampling counterparts usually follow the counting complexity and the there is a perfect uniform sampler, and approximate uniform sampler or any sampler is far from the uniform distribution.

There are several genome rearrangement models (sorting by reversals, SCJ, DCJ, etc.) and several tasks (counting the most parsimonious scenarios between two genomes, computing the number of median genomes, etc.), and for each combination of models and tasks, we are interested in the computational complexity of the so-emerging computational problem. The talk will focus on the recent results and open problems. Connections to enumerative combinatorics, statistical physics and network analysis will also be discussed.

- 9:40 Stéphane Vialette

  On Square Permutations

  Given permutations π and σ_1 and σ_2, the permutation π is said to be a *shuffle* of σ_1 and σ_2, in symbols $\pi \in \sigma_1 \sqcup\!\sqcup\, \sigma_2$, if π (viewed as a string) can be formed by interleaving the letters of two strings p_1 and p_2 that are order-isomorphic to σ_1 and σ_2, respectively. In case $\sigma_1 = \sigma_2$, the permutation π is said to be a *square* and $\sigma_1 = \sigma_2$ is a *square root* of π. For example, $\pi = 24317856$ is a square as it is a shuffle of the patterns 2175 and 4386 that are both order-isomorphic to $\sigma = 2143$ as shown in $\pi = {}^{2}{}_{43}{}^{17}{}_{8}{}^{5}{}_{6}$. However, σ is not the unique square root of π since π is also a shuffle of patterns 2156 and 4378 that are both order-isomorphic to 2134 as shown in $\pi = {}^{2}{}_{43}{}^{1}{}_{78}{}^{56}$.

  We shall begin by presenting recent results devoted to recognizing square permutations and related concepts with a strong emphasis on constrained oriented matchings in graphs. Then we shall discuss research directions to address square permutation challenges in both combinatorics and algorithmic fields.

- 10:20 Coffee

- 10:40 Jay Pantone

  Sorting Permutations with $\mathcal{C}$-machines

- 11:20 Seth Pettie

  Amortized Analysis of Data Structures via Forbidden 0-1 Matrices

  The amortized performance of a data structure is usually proved by designing and analyzing a "potential function", which is an accounting mechanism for letting faster-than-average operations pay for slower-than-average operations. In this talk I will survey an alternative method for analyzing amortized data structures that models executions by 0-1 matrices and bounds their weight using theorems on the density of such matrices avoiding 0-1 patterns.
- Lunch
- Free afternoon

Thursday

- 9:00 Cédric Chauve

  On the Median and Small Parsimony problems in some genome rearrangement Models

  The main goal of genome rearrangement problems is to compute evolutionary scenarios that can explain the order of genes observed in extant genomes. This naturally leads to questions about the order of genes in ancestral genomes, often of extinct species. If a species phylogeny is given, this problem is known as the Small Parsimony Problem, and in its simplest form, where a single ancestral genome is considered, the Median Problem. In this talk, I will first review several algorithmic results on the Median and Small Parsimony Problems, from initial intractability results to surprising tractability results, and then present some more recent results on the same problems in the context where duplicated genes are considered.
- 10:00 Coffee
- 10:20 Marilia Braga

  Family-Free Genomic Distance under DCJ
- 11:00 Robert Brignall

  Permutations and Permutation Graphs
- Lunch
- 16:00 Heather Smith

  Complexity of the Single Cut-or-Join Model and Partition Functions

  We survey computational complexity results for the Single Cut-or-Join model for genome rearrangement, a common mode of molecular evolution. Our main result, enumerating the most parsimonious median scenarios is $\#P$-complete, follows from a more general result for partition functions. In particular, calculating the partition function of optimal medians of binary strings with Hamming distance is #P-complete for several weight functions. This is joint work with István Miklós.

- 16:40 Alois Panholzer

  On some generalizations to trees of problems for permutations

  Various enumeration problems and statistics for permutations have been generalized to other combinatorial structures. In this talk we focus on some of such generalizations to labelled tree structures. In particular, some old and new results for random sequential adsorption, records, and local label-patterns in trees are discussed.

Friday

- 9:00 Fiona Skerman

  Permutations in labellings of trees

- 9:40 Jakub Sliacan

  Some $1xn$ generalized grid classes admit algebraic generating functions

- 10:20 Coffee