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PREFERENTIAL ATTACHMENT WITHOUT VERTEX GROWTH: EMERGENCE OF THE GIANT COMPONENT

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We study the following preferential attachment variant of the classical Erdős–Rényi random graph process. Starting with an empty graph on n vertices, new edges are added one-by-one, and each time an edge is chosen with probability roughly proportional to the product of the current degrees of its endpoints (note that the vertex set is fixed). We determine the asymptotic size of the giant component in the supercritical phase, confirming a conjecture of Pittel from 2010. Our proof uses a simple method: we condition on the vertex degrees (of a multigraph variant), and use known results for the configuration model.

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ASYMPTOTIC DISTRIBUTION OF BERNOULLI QUADRATIC FORMS

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Consider the random quadratic form $T_n = \sum_{1 \le u < v \le n} a_{uv} X_u X_v$, where $((a_{uv}))_{1 \le u,v \le n}$ is a $\{0, 1\}$-valued symmetric matrix with zeros on the diagonal, and $X_1, X_2, \ldots, X_n$ are i.i.d. $\mathrm{Ber}(p_n)$, with $p_n \in (0, 1)$. In this paper, we prove various characterization theorems about the limiting distribution of T_n, in the sparse regime, where $p_n \to 0$ such that $\mathbb{E}(T_n) = O(1)$. The main result is a decomposition theorem showing that distributional limits of T_n is the sum of three components: a mixture which consists of a quadratic function of independent Poisson variables; a linear Poisson mixture, where the mean of the mixture is itself a (possibly infinite) linear combination of independent Poisson random variables; and another independent Poisson component. This is accompanied with a universality result which allows us to replace the Bernoulli distribution with a large class of other discrete distributions. Another consequence of the general theorem is a necessary and sufficient condition for Poisson convergence, where an interesting second moment phenomenon emerges.

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CONVEX HULLS OF PERTURBED RANDOM POINT SETS

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We consider the convex hull of the perturbed point process comprised of n i.i.d. points, each distributed as the sum of a uniform point on the unit sphere $\mathbb{S}^{d-1}$ and a uniform point in the d-dimensional ball centered at the origin and of radius n^α, $\alpha \in (-\infty, \infty)$. This model, inspired by the smoothed complexity analysis introduced in computational geometry (*J. Comput. Geom.* **7** (2016) 101–144; *J. ACM* **51** (2004) 385–463), is a perturbation of the classical random polytope. We show that the perturbed point process, after rescaling, converges in the scaling limit to one of five Poisson point processes according to whether α belongs to one of five regimes. The intensity measure of the limit Poisson point process undergoes a transition at the values $\alpha = \frac{-2}{d-1}$ and $\alpha = \frac{2}{d+1}$ and it gives rise to four rescalings for the k-face functional on perturbed data. These rescalings are used to establish explicit expectation asymptotics for the number of k-dimensional faces of the convex hull of either perturbed binomial or Poisson data. In the case of Poisson input, we establish explicit variance asymptotics and a central limit theorem for the number of k-dimensional faces. Finally, it is shown that the rescaled boundary of the convex hull of the perturbed point process converges to the boundary of a parabolic hull process.

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ON THE LIMITATIONS OF SINGLE-STEP DRIFT AND MINORIZATION IN MARKOV CHAIN CONVERGENCE ANALYSIS

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Over the last three decades, there has been a considerable effort within the applied probability community to develop techniques for bounding the convergence rates of general state space Markov chains. Most of these results assume the existence of drift and minorization (d&m) conditions. It has often been observed that convergence rate bounds based on single-step d&m tend to be overly conservative, especially in high-dimensional situations. This article builds a framework for studying this phenomenon. It is shown that any convergence rate bound based on a set of d&m conditions cannot do better than a certain unknown optimal bound. Strategies are designed to put bounds on the optimal bound itself, and this allows one to quantify the extent to which a d&m-based convergence rate bound can be sharp. The new theory is applied to several examples, including a Gaussian autoregressive process (whose true convergence rate is known), and a Metropolis adjusted Langevin algorithm. The results strongly suggest that convergence rate bounds based on single-step d&m conditions are quite inadequate in high-dimensional settings.

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HIGH-DIMENSIONAL CENTRAL LIMIT THEOREMS BY STEIN'S METHOD

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We obtain explicit error bounds for the d-dimensional normal approximation on hyperrectangles for a random vector that has a Stein kernel, or admits an exchangeable pair coupling, or is a nonlinear statistic of independent random variables or a sum of n locally dependent random vectors. We assume the approximating normal distribution has a nonsingular covariance matrix. The error bounds vanish even when the dimension d is much larger than the sample size n. We prove our main results using the approach of Götze (1991) in Stein's method, together with modifications of an estimate of Anderson, Hall and Titterington (1998) and a smoothing inequality of Bhattacharya and Rao (1976). For sums of n independent and identically distributed isotropic random vectors having a log-concave density, we obtain an error bound that is optimal up to a $\log n$ factor. We also discuss an application to multiple Wiener–Itô integrals.

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CENTRAL LIMIT THEOREMS FOR COMBINATORIAL OPTIMIZATION PROBLEMS ON SPARSE ERDŐS–RÉNYI GRAPHS

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For random combinatorial optimization problems, there has been much progress in establishing laws of large numbers and computing limiting constants for the optimal values of various problems. However, there has not been as much success in proving central limit theorems. This paper introduces a method for establishing central limit theorems in the sparse graph setting. It works for problems that display a key property which has been variously called "endogeny," "long-range independence" and "replica symmetry" in the literature. Examples of such problems are maximum weight matching, λ-diluted minimum matching, and optimal edge cover.

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GRAPHON-VALUED STOCHASTIC PROCESSES FROM POPULATION GENETICS

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The goal of this paper is to construct a natural class of graphon-valued processes arising from population genetics. We consider finite populations where individuals carry one of finitely many genetic types and change type according to Fisher–Wright resampling. At any time, each pair of individuals is linked by an edge with a probability that is given by a type-connection matrix, whose entries depend on the current types of the two individuals and on the current empirical type distribution of the entire population via a fitness function. We show that, in the large-population-size limit and with an appropriate scaling of time, the evolution of the associated adjacency matrix converges to a random process in the space of graphons, driven by the type-connection matrix and the underlying Fisher–Wright diffusion on the multi-type simplex. In the limit as the number of types tends to infinity, the limiting process is driven by the type-connection kernel and the underlying Fleming–Viot diffusion.

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CUTOFF FOR A ONE-SIDED TRANSPOSITION SHUFFLE

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We introduce a new type of card shuffle called *one-sided transpositions*. At each step a card is chosen uniformly from the pack and then transposed with another card chosen uniformly from *below* it. This defines a random walk on the symmetric group generated by a distribution which is nonconstant on the conjugacy class of transpositions. Nevertheless, we provide an explicit formula for all eigenvalues of the shuffle by demonstrating a useful correspondence between eigenvalues and standard Young tableaux. This allows us to prove the existence of a total-variation cutoff for the one-sided transposition shuffle at time $n \log n$. We also study a weighted generalisation of the shuffle which, in particular, allows us to recover the well-known mixing time of the classical random transposition shuffle.

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LOCALIZATION ON 5 SITES FOR VERTEX REINFORCED RANDOM WALKS: TOWARDS A CHARACTERIZATION

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We continue the investigation of the localization phenomenon for a vertex reinforced random walk on the integer lattice. We provide some partial results towards a full characterization of the weights for which localization on 5 sites occurs with positive probability, and make some conjecture concerning the almost sure behavior.

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ERGODIC ROBUST MAXIMIZATION OF ASYMPTOTIC GROWTH

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We consider the problem of robustly maximizing the growth rate of investor wealth in the presence of model uncertainty. Possible models are all those under which the assets' region E and instantaneous covariation c are known, and where the assets are stable with an exogenously given limiting density p, in that their occupancy time measures converge to a law governed by p. This latter assumption is motivated by the observed stability of ranked relative market capitalizations for equity markets. We seek to identify the robust optimal growth rate, as well as a trading strategy which achieves this rate in all models. Under minimal assumptions upon (E, c, p), which in particular allow for an arbitrary number of assets, we identify the robust growth rate with the Donsker–Varadhan rate function from occupancy time large deviations theory. We also explicitly obtain the optimal trading strategy. We apply our results to the case of drift uncertainty for ranked relative market capitalizations. Here, assuming regularity under symmetrization for the covariance and limiting density of the ranked capitalizations, we explicitly identify the robust optimal trading strategy.

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STOCHASTIC ANALYSIS OF EMERGENCE OF EVOLUTIONARY CYCLIC BEHAVIOR IN POPULATION DYNAMICS WITH TRANSFER

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Horizontal gene transfer consists in exchanging genetic materials between microorganisms during their lives. This is a major mechanism of bacterial evolution and is believed to be of main importance in antibiotics resistance. We consider a stochastic model for the evolution of a discrete population structured by a trait taking finitely many values, with density-dependent competition. Traits are vertically inherited unless a mutation occurs, and can also be horizontally transferred by unilateral conjugation with frequency dependent rate. Our goal is to analyze the trade-off between natural evolution to higher birth rates on one side, and transfer which drives the population towards lower birth rates on the other side. Simulations show that evolutionary outcomes include evolutionary suicide or cyclic re-emergence of small populations with well-adapted traits. We focus on a parameter scaling where individual mutations are rare but the global mutation rate tends to infinity. This implies that negligible subpopulations may have a strong contribution to evolution. Our main result quantifies the asymptotic dynamics of subpopulation sizes on a logarithmic scale. We characterize the possible evolutionary outcomes with explicit criteria on the model parameters. An important ingredient for the proofs lies in comparisons of the stochastic population process with linear or logistic birth–death processes with immigration. For the latter processes, we derive several results of independent interest.

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PHASE TRANSITION IN RANDOM TENSORS WITH MULTIPLE INDEPENDENT SPIKES

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Consider a spiked random tensor obtained as a mixture of two components: noise in the form of a symmetric Gaussian p-tensor for $p \geq 3$ and signal in the form of a symmetric low-rank random tensor. The latter is defined as a linear combination of k independent symmetric rank-one random tensors, referred to as spikes, with weights referred to as signal-to-noise ratios (SNRs). The entries of the vectors that determine the spikes are i.i.d. sampled from general probability distributions supported on bounded subsets of $\mathbb{R}$. This work focuses on the problem of detecting the presence of these spikes, and establishes the phase transition of this detection problem for any fixed $k \geq 1$. In particular, it shows that for a set of relatively low SNRs it is impossible to distinguish between the spiked and nonspiked Gaussian tensors. Furthermore, in the interior of the complement of this set, where at least one of the k SNRs is relatively high, these two tensors are distinguishable by the likelihood ratio test. In addition, when the total number of low-rank components, k, of the p-tensor of size N grows in the order $o(N^{(p-2)/4})$ as N tends to infinity, the problem exhibits an analogous phase transition. This theory for spike detection is also shown to imply that recovery of the spikes by the minimum mean square error exhibits the same phase transition. The main methods used in this work arise from the study of mean field spin glass models, where the phase transition thresholds are identified as the critical inverse temperatures distinguishing the high and low-temperature regimes of the free energies. In particular, our result formulates the first full characterization of the high temperature regime for vector-valued spin glass models with independent coordinates.

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GLIVENKO–CANTELLI THEOREMS FOR INTEGRATED FUNCTIONALS OF STOCHASTIC PROCESSES

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We prove a Glivenko–Cantelli theorem for integrated functionals of latent continuous-time stochastic processes. Based on a bracketing condition via random brackets, the theorem establishes the uniform convergence of a sequence of empirical occupation measures towards the occupation measure induced by underlying processes over large classes of test functions, including indicator functions, bounded monotone functions, Lipschitz-in-parameter functions, and Hölder classes as special cases. The general Glivenko–Cantelli theorem is then applied in more concrete high-frequency statistical settings to establish uniform convergence results for general integrated functionals of the volatility of efficient price and local moments of microstructure noise.

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DISCREPANCY BOUNDS FOR A CLASS OF NEGATIVELY DEPENDENT RANDOM POINTS INCLUDING LATIN HYPERCUBE SAMPLES

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We introduce a class of γ-negatively dependent random samples. We prove that this class includes, apart from Monte Carlo samples, in particular Latin hypercube samples and Latin hypercube samples padded by Monte Carlo.

For a γ-negatively dependent N-point sample in dimension d we provide probabilistic upper bounds for its star discrepancy with explicitly stated dependence on N, d, and γ. These bounds generalize the probabilistic bounds for Monte Carlo samples from Heinrich et al. (*Acta Arith.* **96** (2001) 279–302) and C. Aistleitner (*J. Complexity* **27** (2011) 531–540), and they are optimal for Monte Carlo and Latin hypercube samples. In the special case of Monte Carlo samples the constants that appear in our bounds improve substantially on the constants presented in the latter paper and in C. Aistleitner and M. T. Hofer (*Math. Comp.* **83** (2014) 1373–1381).

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DERIVATION OF COUPLED KPZ-BURGERS EQUATION FROM MULTI-SPECIES ZERO-RANGE PROCESSES

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We consider the fluctuation fields of multi-species weakly-asymmetric zero-range interacting particle systems in one dimension, where the mass density of each species is conserved. Although such fields have been studied in systems with a single species, the multi-species setting is much less understood. Among other results, we show that when the system starts from stationary states with a particular property, the scaling limits of the multi-species fluctuation fields, seen in a characteristic traveling frame, solve a coupled Burgers SPDE, which is a formal spatial gradient of a coupled KPZ equation.

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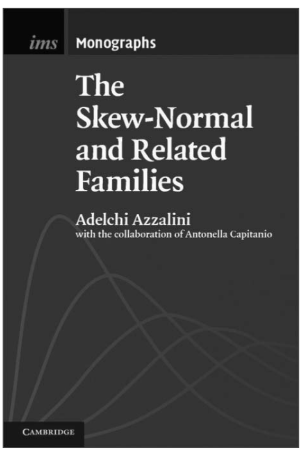

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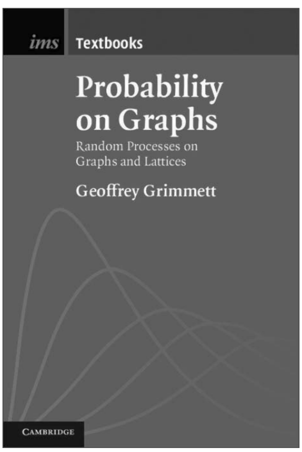

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