Network Study of Human Disease Genes

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Recent advances in genomic and phenotypic data collection provide us with an opportunity to assess the properties of disease-associated human genes on a large scale. However, studies on genetic mutations were concentrated to disease genes with Mendelian inheritance. Here we extend the previous studies to include another set of disease genes from collection of association studies which have not yet been characterized from network-biology perspective. We classify the human disease genes into three classes based on their disease-phenotypic and genetic contexts and compare their properties in the context of human interactome and transcriptome.
Statistical topography of fitness landscapes

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The adaptive evolution of a population under the influence of mutations and selection is governed by the structure of the underlying fitness landscape. Previous theoretical studies of topographical quantities on fitness landscapes have mostly focused on local properties such as local maxima.

Here we investigate the global property of accessible paths traversing the complete genome configuration space towards the global optimum. Numerical and analytical studies and comparison to empirical data suggest a surprising universality across almost all established theoretical models, indicating high accessibility of the globally optimal configuration in the biologically relevant limit of very long genome sequences.
Scale-free correlations in bird flocks

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From bird flocks to fish schools, animal groups often react to environmental perturbations as if of one mind. Most studies in collective animal behaviour have aimed to understand how a globally ordered state emerges from simple behavioural rules. Less effort has been devoted to understanding the origin of collective response, namely the way the group as a whole reacts to its environment. We argue that collective response in animal groups is achieved through scale-free behavioural correlations.

By reconstructing the three-dimensional position and velocity of individual birds in large flocks of starlings, we measured to what extent the velocity fluctuations of different birds are correlated to each other. We found that the range of such spatial correlation does not have a constant value, but scales with the size of the flock. This result indicates that behavioural correlations are scale-free: the change in the state of one animal affects and is affected by that of all other animals in the group, no matter how large the group is.

Scale-free correlations extend maximally the effective perception range of individuals, thus compensating for the short-range nature of the inter-individual interaction and enhancing global response to perturbations. Our results suggest that flocks behave as critical systems, poised to respond maximally to environmental perturbations.
The integration of community membership for the coral network of the Great Barrier Reef

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Abstract

The exchange of genetic information between coral reefs through the transport of larvae can be described in terms of networks that capture the linkages between distant populations. A key question arising from these networks is the determination of the highly connected modules (communities). Communities can be defined using genetic similarity or distance statistics between multiple samples but due to limited specimen sampling capacity the boundaries of the communities remain unresolved across the seascape. In this study we use the microsatellite composition of individual corals, then we statistically compare sample populations using a genetic dissimilarity measure (F\textsubscript{ST}) to create a complex network. This network involved sampling 1,025 colonies from 22 collection sites and examining 10 microsatellites loci. The links between each sampling site were given a strength that was created from the pairwise F\textsubscript{ST} values. The result is a directional weighted network describing the genetic dissimilarity between each sampled population. From this network we then determined the community structure using leading eigenvectors within graph theory. However given the limited sampling conducted the representation of the regional genetic structure was incomplete. To assist with defining the boundaries of the genetically-based communities we also integrated the communities derived from a hydrodynamic network. The hydrodynamic network though comprehensive was of smaller spatial extent than our genetic sampling. A Bayesian Belief network was developed to integrate the overlapping communities. The results indicate the population structure of the Great Barrier Reef and where future genetic sampling should take place to complete biodiversity mapping.
The susceptible-infectious-recovered (SIR) model describes the evolution of three species of individuals which are subject to an infection and recovery mechanism. A susceptible $S$ can become infectious $I$ with a certain infection rate by an infectious type provided that both are in contact. That type may recover $R$ with a rate and from then on stay immune. Due to the coupling between the different individuals, the model is nonlinear and out of equilibrium. We adopt a stochastic individual-based description where individuals are represented by nodes of a graph and contact is defined by the links of the graph. Mapping the underlying Master equation into a quantum formulation in terms of spin operators, the hierarchy of evolution equations can be solved exactly for arbitrary initial conditions on a linear chain. In case of uncorrelated random initial conditions the exact time evolution for all three individuals of the SIR model is given analytically. Due to fluctuations, isolated regions of susceptible individuals evolve and unlike in the standard mean-field SIR model one observes a finite stationary distribution of the susceptible. The exact results for the ensemble averaged population size are compared with simulations for single realizations of the process. The model is extended to the SIRS model in which the $R$ type becomes again of $S$ type with time delay.