requires that the organism can adapt to external/non-genetic perturbations (homeostasis) and that the transmitted genotype is robust to internal/genetic changes (genetic robustness) so as to preserve the success of the progenitor phenotype. Biologically and mathematically, a priori, these two concepts are unrelated: Homeostasis is a dynamic property and is a direct product of natural selection. Genetic robustness is a static property that is unnecessary for homeostasis. It is, however, essential for evolution to occur and seems to coexist with homeostasis in many biological processes. Despite its central role in the evolutionary process, the rationale for selection for genetic robustness is still controversial. It has been suggested that genetic robustness is a by-product of homeostasis but the origins of this putative relationship have never been investigated in a general theoretical context.

Here, we find a strong statistical correlation between adaptive homeostasis and genetic robustness in N-node enzymatic networks, providing a foundation for the unitary character of evolutionary fitness. We investigate the scaling properties of these networks and extract topological motifs that are necessary and/or sufficient to achieve adaptive homeostasis and/or genetic robustness. Furthermore, we map out the robustness/homeostasis space of these topologies. This correlation and the identification of design principles renders the deciphering and reconstruction of complex biological networks more feasible as we narrow down the search space for possible design principles in biology.

**2528-Pos Board B547**

**Indirect Competitive Reaction between Enzymes with Different Diffusivity**

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Diffusion process of molecules within heterogeneous medium shows a peculiar behavior termed anomalous diffusion. Here the motions of molecules are hindered by the obstacles, which constitute the heterogeneity of the environment. Accordingly, compared to homogeneous medium, the area that a molecule moves for a given time is smaller for heterogeneous medium. This affects the reaction process deeply (especially for diffusion limited reactions) and the classical formulation based on mass action law fails to describe the process and a formulation based on the Fractal reaction theory is necessary [Kopelman, Science 1988].

In this study we analyzed the indirect competitive reaction between enzymes with different sizes. We assume that for larger enzymes obstruction due to molecular crowding makes the environment heterogeneous to it. On the other hand for smaller enzymes the environment is assumed to be homogeneous due to smaller obstruction effects from the molecular crowding. Accordingly there is a difference in the diffusivity, one with normal diffusivity and the other with anomalous diffusivity. We would like to discuss the physiological implications of this effect using Lattice Monte Carlo simulation and theoretical analysis based on the Fractal reaction theory.

**2529-Pos Board B548**

**Rationalizing the Catalytic Activity of an Unusual Oxidoreductase (FucO)**

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Enzyme-catalyzed processes often exhibit exquisite stereo- and regiospecificities. Following from this, there is great interest in using enzymes to catalyze stereospecific reactions outside the cell, for example, for the design of novel therapeutics as well as the selective synthesis of fine chemicals, where product purity is essential. A biocatalytically important class of enantioselective enzymes are oxidoreductases, which catalyze the interconversion of alcohols, aldehydes and ketones, thus providing important building blocks for organic synthesis. Among them, the NAD⁺ dependent diol oxidoreductase (FucO), from *Esherichia coli* have shown strict regiospecificity for the oxidation of primary alcohols, high stereospecificity for the 5-enantioomer of 1,2-propanediol, and also a strong preference for short-chained substrates of about 2 to 4 carbons in length. In addition to this, the enzyme has an unusual pH profile, displaying its highest activity at high pH values of around 10. At present, the molecular details of the mechanism for the reaction catalyzed by FucO remain unclear.

We present here a detailed study of the catalytic activity of FucO, including identification of catalytically important residues. The radical pH dependence of catalysis found for this enzyme is also analyzed, using 1-propanol as model substrate, for which extensive experimental data is available. This study provides the basis for further rationalization and redesign of the regio- and enantiospecificity of this enzyme, as well as its pH dependence.

**2530-Pos Board B549**

**Diffusion of Public Goods Prevents Coexistence of Cooperators and Cheaters in a Stochastic Competition Model**

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Many organisms secrete diffusible extracellular factors to engineer their local environment. Diffusion of these factors leads to long-range intercellular interactions with local competition, creating the possibility of cooperation but also the risk of exploitation by non-producing neighbors. Despite the risk of exploitation, diffusible resources are widespread in nature, occurring even in dense multi-species communities. In local interaction models, coexistence is commonly observed between cooperators (corresponding to resource producers) and cheaters (corresponding to nonproducers). However, we find that including the diffusion of resources completely prevents coexistence in an analogous spatial model. Instead, we find population dynamics similar to simple competition, either neutral or biased, with no balancing selection that would favor coexistence. We conclude that in crowded environments diffusible resources generally favor nonproducers, and suggest that regular eras of population expansion are required for producers to thrive.

**2531-Pos Board B550**

**Heterogeneity in Protein Copy Numbers induces Metabolic Variability in Modeled E. coli Populations**

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Heterogeneity in isogenic population of bacteria arises due to inherent stochasticity in the process of gene expression as well as local environmental fluctuations. Advances in quantitative fluorescence imaging of *Esherichia coli* has enumerated such heterogeneity in terms of protein copy numbers at genome scale. In this study we use genome scale model of metabolism for *Ecoli* to investigate the effect of this variability on their growth rates and metabolic pathway usage. Results suggest wide variation in growth rate of single cells around the bulk measurement obtained via optical density measurements. This prediction is in agreement with the variation in growth rates measured experimentally at single cell level. We also predict variability in metabolic pathway usage among these cells owing to tradeoffs between energy efficiency and enzyme usage efficiency. All the variability in metabolism can be attributed to variability in expression of few genes. This integration of a metabolic model, which is a bottom up reconstruction from the genome, with single cell proteomics data gives us new insight into the effect of noise on the physiology of cell populations.

**2532-Pos Board B551**

**Faithful Models of Viral Fitness can be Inferred from Mutation Patterns in Viral DNA Sequences Sampled from a Population**

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A detailed understanding of fitness landscapes of viruses can be exploited to computationally screen candidate vaccines and therapeutic drugs. Inverse Ising models inferred using techniques rooted in entropy maximization have recently been proposed as accurate fitness landscapes for certain proteins of HIV. Such landscapes are parameterized based on statistical quantities measured from population sequence ensembles, like the average probabilities of mutation at single amino acid sites, pairs of sites etc. Since individual sequences in the ensemble have evolved under diverse immune responses, patterns of mutation in such data can reflect systematic biases arising from immune escape rather than intrinsic fitness requirements. Therefore, delineating the role of immune pressure in shaping mutational patterns in the population and understanding how intrinsic fitness can be faithfully inferred from sequence data is important. We performed simulations of a discrete molecular quasispecies model that reveals the essential role of immune pressure in driving viral evolution on its intrinsic fitness landscape. Our simulations show that in the absence of immune pressure the virus remains frozen in its ground state and mutations that reflect the correlation structure of its fitness landscape are not selected at the population level. In the presence of immune pressure, there is an intermediate mutation rate per site per generation that favors viral adaptation and selects mutations. We studied an analytical mapping our quasispecies model to an equilibrium 2-D Ising system. Analyzing the resulting Hamiltonian using variational mean field theory enabled us to derive analytical expressions for the