**The untapped clinical potential - from combinatorial genomics to systems medicine**

The classic approach of learning biology involved making junk (point mutations, knockdown) and garbage (knockout) out of genes. We asked if the opposite was also possible i.e., could we make genes out of 'junk' DNA? To answer the question, we invented a simple and scalable method to artificially express non-coding DNA sequences and discovered interesting properties. This has led to the emergence of, what we call *combinatorial genomics* i.e., the ability to express sequences in different frames and possibilities based on user's specifications. To synthesize novel and functionally meaningful molecules out of existing genomic templates, we have developed a database that predicts potential properties of non-coding DNA products, if artificially expressed. The second part of our work is related to the emerging field of systems medicine. Our lab is involved in (a) construction of a virtual cell of Neisseria meningitidis with an aim to associate it with host-pathogen interactions (b) building diseasome i.e., linking all known human disorders with the corresponding genes (c) making a KEGG like resource of antibiotic synthesis pathways, and (d) developing karyotype-pathway-phenotype association map, to study how a deletion, for example, translates into network anomaly generating higher level phenotype. This work involves connecting clinical, experimental and computational domains.