Clinical and Genomic Risk Factors of Chronic Kidney Disease

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Chronic kidney disease (CKD) occurs when one suffers from gradual, but usually permanent loss of kidney function over time. At end stage of the renal disease (ESRD), kidney transplant or dialysis is necessary to stay alive. The incidence of CKD is reaching alarming levels in the U.S. and there is a rising prevalence of kidney failure, with poor outcomes and high cost. To date a few predictive factors for progression such as proteinuria have been detected and therapies such as ACE inhibitors, blood pressure control, and tight diabetes control can ameliorate the progression of renal disease. However, identification of those at risk to progress still remains a significant problem in the subjects receiving optimal therapy.

In this project we analyze a large-scale data consisting of 238 chronic kidney disease patients with hypertension and 77 clinical features and 113 single nucleotide polymorphisms (SNPs) obtained from the **African American Study of Kidney Disease and Hypertension Cohort Study**. We identify combinations of significant genomic and clinical features (combinatorial biomarkers) that accurately predict the progression of CKD and stratify patients into different risk groups. Our pattern-based approach produces an 80% accurate classification model that consists of 9 patterns for slow progressors and 10 patterns for fast progressors, where only **five clinical features** and **one SNP** are used in the description of patterns. The results of this study will be used as a basis for future studies where the ultimate goal is to identify new therapeutic targets for drug development.