About the Bioinformatics Core
The Bioinformatics Core is a component of the Comprehensive Transplant Center (CTC), formed in 2009, at Northwestern University (NU). The Core works as a platform such that CTC and other NU researchers could do collaborative research projects involving:

- Genomics Data Analysis
- Proteomics Data Analysis
- Metabolomics Data Analysis
- Pathway and Function Analysis based on Databases
- Sequence and regulatory element Analyses based on Databases

With the introduction of new technology in biological world, for recording experimental data, amount of big-data has increased rapidly in the medical domain. This served as the driving force for CTC towards developing a core facility that could analyze such high throughput and/or high-dimensional biological data arising from diverse technology platforms, including but not limited to,

- Arrays - Gene expression, transcript/isoform, SNP, Exon, methylation, proteins
- Next Generation Sequencing - DNA-seq, RNA-seq, WES, ChIP-seq, etc.

To perform computationally expensive analyses, Core utilizes NU’s High Performance Computing Cluster, QUEST.

Mission
The Bioinformatics Core at Comprehensive Transplant Center is committed to provide exceptional care, pioneering research and the training of the next generation of transplant clinicians and researchers.

The mission of the Core is to provide state-of-the-art bioinformatics training and analytic support services to investigators interested in basic, pre-clinical, clinical and epidemiological transplant studies within Northwestern.

Facts
Bioinformatics core serves interested investigators in the Northwestern University community and has performed bioinformatics analyses for more than 100 projects. The Core has helped Principal Investigators to secure funding support from various funding agencies including National Institutes of Health. Ongoing and planned research efforts at the CTC and its collaborators take full advantage of the emerging and evolving technologies:

- Microarray (RNA expression, exon array, DNA methylation array, etc.)
- Next generation sequencing (DNaseq, RNAseq, etc.)
- Top-down proteomics from NU Evanston Campus
- RBM (Rules-Based Medicine Multi-Analyte Profiles assays)
- SUSHI (Simultaneous Ultrasensitive Subpopulation Staining/Hybridization In Situ)

Examples:
- Analysis of the plasma and urine from kidney and liver transplant recipients using RBM for proteomic signature
- Gene expression profiling of the whole blood from kidney and liver transplant recipients with Affymetrix DNA microarray
- Gene expression profile of the tolerance mouse model of islet transplant using Illumina Array from NU genomics core

Services
The Core contains state-of-the-art computing and analytical software packages for analyzing wide range of data. It provides various analysis services, including but not limited to,

- Class comparisons
- Pathway Analyses
- Gene Function enrichment analysis
- Class discovery and pattern recognition
- Class prediction
- Genome Wide Association Studies (GWAS)

We are always interested in collaborations, and will attempt to accommodate any proposed project, large or small.

Getting Started
To discuss starting a project using the Bioinformatics Core please contact:

Dr. Manoj Kandpal
Research Assistant Professor
Department of Surgery
Director, Bioinformatics Core, CTC
kandpal@northwestern.edu
1-312-503-2310