



### **Supplementary Figure 1. Data flow through T2D-Db application**

The entire data flows through eight categories. Query from the user passes from the front-end to the back-end through the CGI scripts and vice-versa. SNP Map, Heat Map and Interaction Map are the three maps used for visual display of SNP data, Microarray data and Protein-Protein Interaction data respectively. Java Web Start is used to launch the Heat Map and Cytoscape application. In SNP Map, the genes are displayed along with markers within a specified genomic region range. The Gene information is obtained from the NCBI Gene Entrez Database. A Flat-file database is also maintained in order to store the FASTA sequence files for each gene.