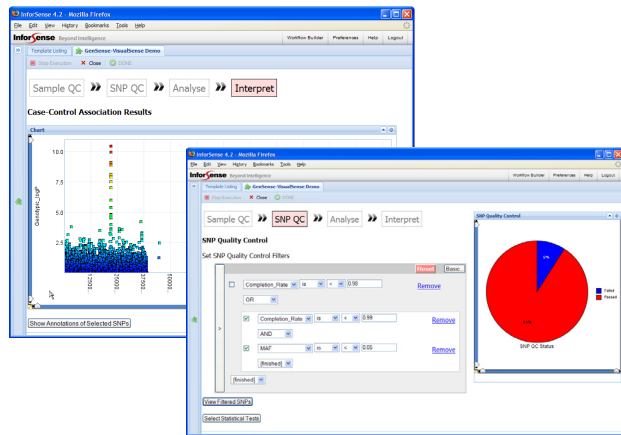


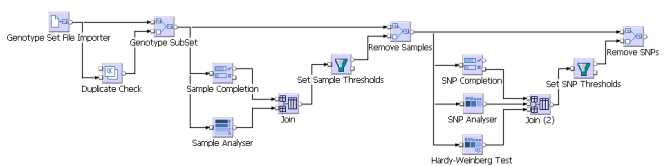
InforSense GenSense is a solution for analysing genotyping arrays. The system helps with the analysis of data from the latest generation of genotyping platforms. It has been specifically designed to aid the user with complex analyses to quickly find interesting SNPs and produce reports with easy to understand visualisations. GenSense supports data from Illumina BeadChips and Affymetrix GeneChip Mapping arrays as well as from HapMap, PrettyBase and LINKAGE formats.

GenSense allows you to easily analyse genome wide association data, including:

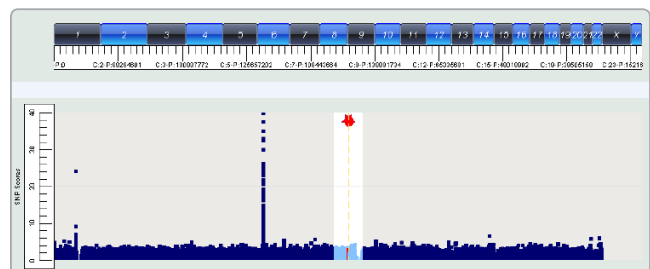
- Case Control and Candidate gene studies.
- Identify associations between genotypic and phenotypic data.
- Provide tools to support data management and analysis of genotypic and phenotypic data to more easily and automatically detect these associations.
- Out-of-the-box solutions, such workflows replicating the WTCCC analysis, as well as web portal services for GWA studies.
- Rank the most significant associations among case control studies.
- Look at frequencies of alleles in a sample population.
- Identify predictive and diagnostic biomarkers from significant associations.
- Provide intuitive and easily absorbed statistical and graphical summaries of large data sets.
- Link to current genomics data sources – Entrez Gene, HapMap, dbSNP, OMIM, Gene Ontology, UCSC Genome Browser.
- Compatibility with other InforSense solutions – Sequence Analysis and Toxicogenomics (BioSense), Pathway Analysis (GeneGO and Ingenuity), stratification of clinical trial data (ClinicalSense), workflow deployment as a web application for other scientists to use (VisualSense).
- Graphical traversal of genomic data sources, using NCBI, and other web services as search engine.



The system provides a customizable set of deployed workflows. The figures show a guided analysis of the WTCCC study using VisualSense.



Using workflows such as this: for quality control of genotyping data, large data sets can be filtered on call rate, allele frequency, genomic location and H-W equilibrium.



GenSense offers the user the possibility to visualize the sheer amounts of data at every step of the analytical process. Here, a view is shown of the SNP significance (-logP) across the human genome.

GenSense workflows give you a flexible way of customising the way in which you test, plan and run your analyses. The solution assists you all the way from data import, through quality control and filtering to data analysis and annotation.

Data Importing and Exporting

- Affymetrix GeneChip Mapping Array (BRLMM, BRLMM-P, Birdseed output and binary CHP)
- HapMap genotype format
- Illumina BeadStudio (Standard Final Report)
- LINKAGE format including PLINK
- PrettyBase format
- Generic Sample or SNP major format



Data Quality Control

- Genotype confidence score filtering
- Genotype call rate analysis by sample, SNP
- Duplicate sample detection
- Sample clustering by multidimensional scaling
- Filter using other summary statistics, such as heterozygosity rate and minor allele frequency
- Test for deviation from Hardy-Weinberg Equilibrium
- Mendelian inheritance check

Data Analysis

- Case-Control/Genotype/Phenotype Association Tests
 - Trend test
 - Chi-squared genotypic, allelic, dominant-recessive tests
 - Odds ratio, Relative risk
 - Fisher's exact test
 - Logistic regression and Likelihood ratio tests of association
- Haplotype Statistics
 - List alleles based on frequency; calculate marker variability
 - Cluster haplotypes
 - Determine recombination rates
- Calculate LD between all pairs of markers/SNPs
- Copy Number Analysis
- Genotype calling using Affymetrix Power Tools
 - BRLMM, BRLMM-P, Birdseed, Birdseed-v2

Annotation and Tool Integration

- SNP to Gene mapping using NetAffx, dbSNP and Entrez Gene
- Query and visualise in the UCSC Genome Browser
- Genome browser for visualisation of significant SNPs
- HaploView integration
- PLINK integration
- Optional R-genetics integration