Biomedimathics

Principal Investigators: Anita Kloss-Brandstätter

Background and previous findings

The aim of our bioinformatics team is to apply computer science to the field of molecular biology and medical genetics. Our group is concerned with the creation and advancement of databases, algorithms, computational and statistical techniques to solve practical problems arising from the management and analysis of genetic data.

High-throughput genotyping and phenotyping projects of large epidemiological study populations require sophisticated laboratory information management systems. We developed a database system for an efficient combination and management of phenotypes and genotypes (**eCOMPAGT**) deriving from genetic epidemiological studies. eCOMPAGT can store, administer and connect phenotype data with all kinds of genotype data.

Mitochondrial DNA (mtDNA) is widely being used for population genetics, forensic DNA fingerprinting and clinical disease association studies. The recent past has uncovered severe problems with mtDNA genotyping, not only due to the genotyping method itself, but mainly to the post-lab transcription, storage and report of mtDNA genotypes. The extended mtDNA version of **eCOMPAGT** was designed to enable error-free post-laboratory data handling of human mtDNA profiles.

As the determination of the mtDNA haplogroup affiliation is time-consuming and error-prone, we developed **HaploGrep**, a web-application designed to determine the most probable haplogroups of mtDNA haplotypes. With its sophisticated visualization tools, HaploGrep offers an all-in-one solution for quality assessment of mtDNA profiles in forensics, clinical and population genetics.

While several software packages support the determination of CNVs from SNP chip data, the downstream statistical inference of CNV-phenotype associations is still subject to complicated and inefficient in-house solutions, thus strongly limiting the performance of genome-wide association studies (GWAS) based on CNVs. We therefore developed **CONAN**, a freely available client-server software solution which provides an intuitive graphical user interface for categorizing, analyzing and associating CNVs with phenotypes (see Figure).

Ongoing work

- Cloud computing for CNV detection
- LIMS for SNP genotyping
- Graphics for mtDNA analysis

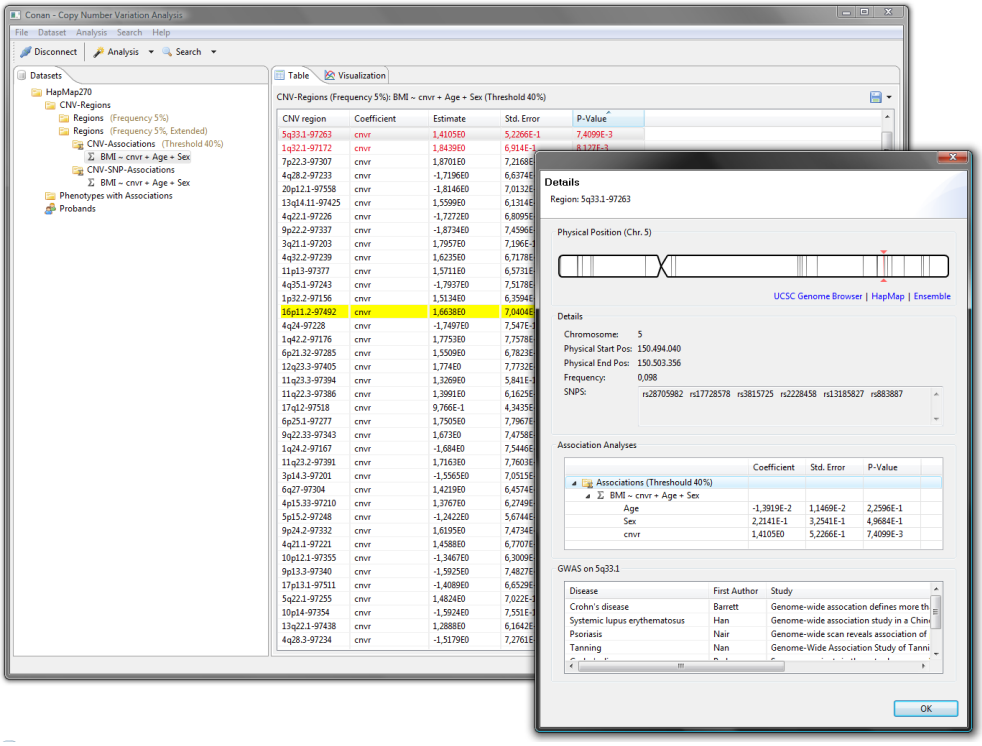

Figure: *Graphical User Interface of CONAN. All imported datasets, their calculated CNV regions and associated analyses are organized in a tree structure. All CNV regions of the current selected dataset or association analysis are shown as a table: Genome-wide significant CNVRs are highlighted in red and regions with already know associations from SNP-GWAS http://www.genome.gov/gwastudies/ are highlighted in yellow. Information about a specified CNVR is listed in a separate dialog.*

Team members:

Lukas Forer, Hansi Weissensteiner, Sebastian Schönherr, Dominic Pacher, Stefan Coassin, Florian Kronenberg

Main collaborators:

Günther Specht

Selected Publications:

1. Schoenherr S, Weissensteiner H, Coassin S, Specht G, Kronenberg F, Brandstätter A: eCOMPAGT - efficient Combination and Management of Phenotypes and Genotypes for Genetic Epidemiology. ***BMC Bioinformatics*** 10:139, 2009. [Pub-Med]
2. Weißensteiner H, Schönherr S, Specht G, Kronenberg F, Brandstätter A: eCOMPAGT integrates mtDNA: import, validation and export of mitochondrial DNA profiles for population genetics, tumour dynamics and genotype-phenotype association studies. ***BMC Bioinformatics*** 11:122, 2010. [Pub-Med]
3. Forer L, Schönherr S, Weissensteiner H, Haider F, Kluckner T, Gieger C, Wichmann HE, Specht G, Kronenberg F, Brandstätter A: CONAN: Copy Number Variation Analysis Software for Genome-Wide Association Studies. ***BMC Bioinformatics*** 11:318, 2010. [Pub-Med]
4. Kloss-Brandstätter A, Pacher D, Schönherr S, Weissensteiner H, Binna R, Specht G, Kronenberg F: HaploGrep: a fast and reliable algorithm for automatic classification of mitochondrial DNA haplogroups. ***Hum.Mutat.*** 32:25-32, 2011. [Pub-Med]