Resource Summary Report

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ALCHEMY

RRID:SCR_005761
Type: Tool

Proper Citation

ALCHEMY (RRID:SCR_005761)

Resource Information

URL: http://alchemy.sourceforge.net/

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Description: ALCHEMY is a genotype calling algorithm for Affymetrix and Illumina products which is not based on clustering methods. Features include explicit handling of reduced heterozygosity due to inbreeding and accurate results with small sample sizes. ALCHEMY is a method for automated calling of diploid genotypes from raw intensity data produced by various high-throughput multiplexed SNP genotyping methods. It has been developed for and tested on Affymetrix GeneChip Arrays, Illumina GoldenGate, and Illumina Infinium based assays. Primary motivations for ALCHEMY''s development was the lack of available genotype calling methods which can perform well in the absence of heterozygous samples (due to panels of inbred lines being genotyped) or provide accurate calls with small sample batches. ALCHEMY differs from other genotype calling methods in that genotype inference is based on a parametric Bayesian model of the raw intensity data rather than a generalized clustering approach and the model incorporates population genetic principles such as Hardy-Weinberg equilibrium adjusted for inbreeding levels. ALCHEMY can simultaneously estimate individual sample inbreeding coefficients from the data and use them to improve statistical inference of diploid genotypes at individual SNPs. The main documentation for ALCHEMY is maintained on the sourceforge-hosted MediaWiki system. Features * Population genetic model based SNP genotype calling * Simultaneous estimation of per-sample inbreeding coefficients, allele frequencies, and genotypes * Bayesian model provides posterior probabilities of genotype correctness as quality measures * Growing number of scripts and supporting programs for validation of genotypes against control data and output reformating needs * Multithreaded program for parallel execution on multi-CPU/core systems * Non-clustering based methods can handle small sample sets for empirical optimization of sample preparation techniques and accurate calling of SNPs missing genotype classes ALCHEMY is written in C and developed on the GNU/Linux platform. It should compile on any current GNU/Linux distribution with the development packages for the GNU Scientific Library (gsl) and other development packages for standard system libraries. It may also compile and run on Mac OS X if gsl is installed.

Abbreviations: ALCHEMY

Synonyms: ALCHEMY - An automated population genetic model driven SNP genotype calling method

Resource Type: source code, software resource

Defining Citation: PMID:20926420

Keywords: diploid, genotype, snp, bio.tools

Funding: NSF 0606461

Availability: GNU General Public License

Resource Name: ALCHEMY

Resource ID: SCR_005761

Alternate IDs: biotools:alchemy, nlx_149227

Alternate URLs: https://bio.tools/alchemy

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250401T060409+0000

Ratings and Alerts

No rating or validation information has been found for ALCHEMY.

No alerts have been found for ALCHEMY.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Baltazar MD, et al. (2019) QTL mapping for tolerance to anaerobic germination in rice from IR64 and the aus landrace Kharsu 80A. Breeding science, 69(2), 227.

Rahman MA, et al. (2017) Mapping QTLs using a novel source of salinity tolerance from Hasawi and their interaction with environments in rice. Rice (New York, N.Y.), 10(1), 47.

Ye C, et al. (2015) Identifying and confirming quantitative trait loci associated with heat tolerance at flowering stage in different rice populations. BMC genetics, 16, 41.

Fang Z, et al. (2014) Two genomic regions contribute disproportionately to geographic differentiation in wild barley. G3 (Bethesda, Md.), 4(7), 1193.

Trijatmiko KR, et al. (2014) Meta-analysis of quantitative trait loci for grain yield and component traits under reproductive-stage drought stress in an upland rice population. Molecular breeding : new strategies in plant improvement, 34(2), 283.