Statistical Genetics and Bioinformatics

RTI International offers advanced expertise in statistical genetics, genomics, and bioinformatics. Our researchers are experienced in an array of innovative genomics technologies and targeted analytical methods that can maximize genomic discovery. Whether the need is full project execution or support for a single aspect of an ongoing study, RTI can be an integral part of the collaboration.

Overview

RTI's statistical geneticists, statistical programmers, and bioinformaticians are experienced in the analysis of genome-wide association studies, next-generation sequencing, microarrays, proteomics, metabolomics, and integromic data. We are positioned to assist pharmaceutical and agribusiness companies with target identification and validation, basic and clinical sciences, pharmacogenomics, toxicogenomics, and other genomic studies.

Secure Services

RTI is committed to providing quality, secure deliverables, on time and within budget. We have a 120-node cluster that meets FIPS 140-2 moderate security and can assure that all data will be kept confidential and secure. If preferred, our staff can also conduct analysis in client-provided computing environments.

Our researchers routinely work with the complex and varied analytical needs of biomedical, clinical, basic science, and agricultural projects. RTI is GCP compliant, and our researchers are accustomed to working with personal health information, electronic medical records, and electronic data capture data. We select and implement state-of-the-art analytical methods based on project requirements and data type.

Statistical Genetics Expertise

RTI's researchers are experts in biostatistics, epidemiology, clinical studies, and the management of data. For complex studies, we serve as a coordinating center. We have leveraged these skills into genetics and functional genomics studies, with proven expertise in the following areas:

- Design of functional genomics studies
- Genome-wide association, imputation, CNC/aCGH
- Microarray analysis
- Metabolomics analysis
- Gel and mass spectrometric proteomic analyses
- Next-generation sequencing analysis
- Integromics/systems biology
- Discriminant analysis/model building
- Meta-analysis

Project Highlights

Stillbirth Coordination Research Network. RTI serves as the data coordinating center for the network, whose broad purpose is identifying the epidemiological, infectious, and genetic factors involved in stillbirth. RTI is currently conducting metagenomics and genome-wide copy number change analysis.

Population Genetics Analysis Program: Immunity to Vaccines/Infections. RTI and our partners are researching genetic variants and the consequent protein expression associated with responses to typhoid and cholera vaccines.

Consensus Measures for Phenotypes and Exposures (PhenX). This project is developing standard measures related to complex diseases, phenotypic traits, and environmental exposures. Use of these measures facilitates combining data from a variety of studies.

Genome-Wide Association Study (GWAS) of Heroin Abuse: A Multiethnic Study. This project's goal is to identify and characterize genetic determinants of heroin abuse in large samples of African Americans and European Americans by conducting a GWAS of heroin abuse, cross-population contrast mapping.

GWAS of HIV-1 Host Genetics among Injection Drug Users. The overarching goal is to identify and characterize genetic determinants of HIV 1 susceptibility and resistance in large samples of African American and European American injection drug users.

Recent Publications

Johnson, E. O., Hancock, D. B., Levy, J. L., Gaddis, N. C., Saccone, N. L., Bierut, L. J., Page, G. P. (2013). Imputation across genotyping arrays for genome-wide association studies: Assessment of bias and a correction strategy. *Hum Genet*, 132(5), 509–22.

Reddy, U. M., Page, G. P., Saade, G. R., Silver, R. M., Thorsten, V. R., Parker, C. B., et al. (2012). Karyotype versus microarray testing for genetic abnormalities after stillbirth. *New England Journal of Medicine*, 367(23), 2185–93.

Hsu, C. Y., Adams, J. P., No, K., Liang, H., Meilan, R., Pechanova, O., Barakat, A., Carlson, J. E., Page, G. P., Yuceer, C. (2012). Overexpression of CONSTANS homologs CO1 and CO2 fails to alter normal reproductive onset and fall bud set in woody perennial poplar. *PLoS One*, 7(9):e45448.

Hancock, D. B., Levy, J. L., Gaddis, N. C., Bierut, L. J., Saccone, N. L., Page, G. P., Johnson, E. O. (2012). Assessment of genotype imputation performance using 1,000 genomes in African American studies. *PLoS One*, 2012;7(11):e50610.

Jessen W. J., Miller, S. J., Jousma, E., Wu, J., Rizvi, T. A., Brundage, M. E., Eaves, D., Widemann, B., Kim, M. O., Dombi, E., Sabo, J., Dudley, A. H., Niwa-Kawakita, M., Page G. P., et al. (2012). MEK inhibition exhibits efficacy in human and mouse neurofibromatosis tumors. *Journal of Clinical Investigation*, doi:pii: 60578.

Hsu, C. Y., Adams, J. P., Kim, H., No, K., Ma, C., Strauss, S. H., Drnevich, J., Vandervelde, L., Ellis, J. D., Rice, B. M., Wickett, N., Gunter, L. E., Tuskan, G. A., Brunner, A. M., Page, G. P., et al. (2011). Flowering locus T duplication coordinates reproductive and vegetative growth in perennial poplar. *Proceedings of the National Academy of Sciences*, 108(26), 10756–61.

Garge, N., Pan, H., Rowland, M., Cargile, B. J., Cooley, P. C., Page, G. P., Bunger, M. K., & Zhang, X. (2010). Identification of quantitative trait loci underlying proteome variation in human lymphoblastoid cells. *Molecular and Cellular Proteomics, 9*(7), 1383–99.

Johnson, E. O., Chen, L. S., Breslau, N., Hatsukami, D. K., Robbins, T., Saccone, N. L., Grucza, R. A., & Bierut, L. (2010). Peer smoking and the nicotinic receptor genes: An examination of genetic and environmental risks for nicotine dependence. *Addiction, 105*(11), 2014–2022.

Hancock, D. B., Eijgelsheim, M., Wilk, J. B., Gharib, S. A., Loehr, L. R., Marciante, K. D., et al. (2009). Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. *Nature Genetics, 42*(1), 45–52.

Platts, A. E., Land, S., Chen, L., Page, G. P., Rasouli, P., Wang, L., Lu, Y., & Ruden, D. M. (2009). Massively parallel resequencing of the isogenic Drosophila melanogaster strain w(1118); iso-2; iso-3 identifies hotspots for mutations in sensory perception genes. *Fly (Austin), 3*(3), 192–203.

More Information

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