Cure cancer. Prevent future strokes. Treat night blindness. Ohio's bioscience researchers are using the Ohio Supercomputer Center to analyze vast amounts of genetic, molecular and environmental data to better understand human physiology and diagnose and treat diseases. The research on the following pages illustrates a sampling of these efforts.

BIOLOGICAL SCIENCES

Research Building III houses the Battelle Center for Mathematical Medicine, a new, $93 million facility that nearly doubled the dedicated research space at Nationwide Children's Hospital.

GENETIC ARCHITECTURE

Vieland develops PPL framework for data analysis

Genetic data analysis uses statistical methodology to map disease genes on the genome; statistical genetic research has long shifted from looking at a single gene disorder to complex diseases.

"When two genes interact to cause a clinically important phenotype, we can leverage genotypic information at one of the loci in order to improve our ability to detect the other," said Veronica Vieland, Ph.D., vice president for computational research and director, Battelle Center for Mathematical Medicine.

Vieland and researchers at the Center, which is part of the Research Institute at Nationwide Children's Hospital, have developed a class of linkage statistics, called the posterior probability of linkage (PPL), that allow for gene × gene interaction, parent of origin and many other genetic architectures. Implemented in KELVIN, a statistical genetic data analysis software package, the PPL framework treats trait model parameters as nuisance parameters and integrates them out of the likelihood rather than fixing them at arbitrary values.

Using KELVIN to model genetic architecture is computationally intensive and requires continuous software development. Ongoing software engineering focuses on extending the complexity of the calculations that KELVIN can perform in order to address emerging data analysis needs, including such things as multipoint likelihood calculations in large and complex pedigrees based on dense SNP maps and genetic analyses involving multiple interacting loci.

"We are expanding KELVIN and further developing the PPL framework, as well as implementing a web-based infrastructure to make the package more user-friendly to other investigators," Vieland said. "The considerable resources we have access to through the Ohio Supercomputer Center are an important component of what we need for this computationally intensive work."

PPL framework and its variants have been successfully applied to genetic data analysis for various genetic diseases, such as schizophrenia, autism and autoimmune thyroid disease. As Vieland works to refine KELVIN and the PPL framework, she also is more fully modeling the genetic architecture of schizophrenia, autism and bipolar disorder by evaluating the methods using simulations and applying them to public domain data sets that have been deposited by various research groups.

"By enhancing the power of our statistical and computational methods, we expect to shed new light on the genetic architecture of schizophrenia, autism and bipolar disorder," Vieland said.

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