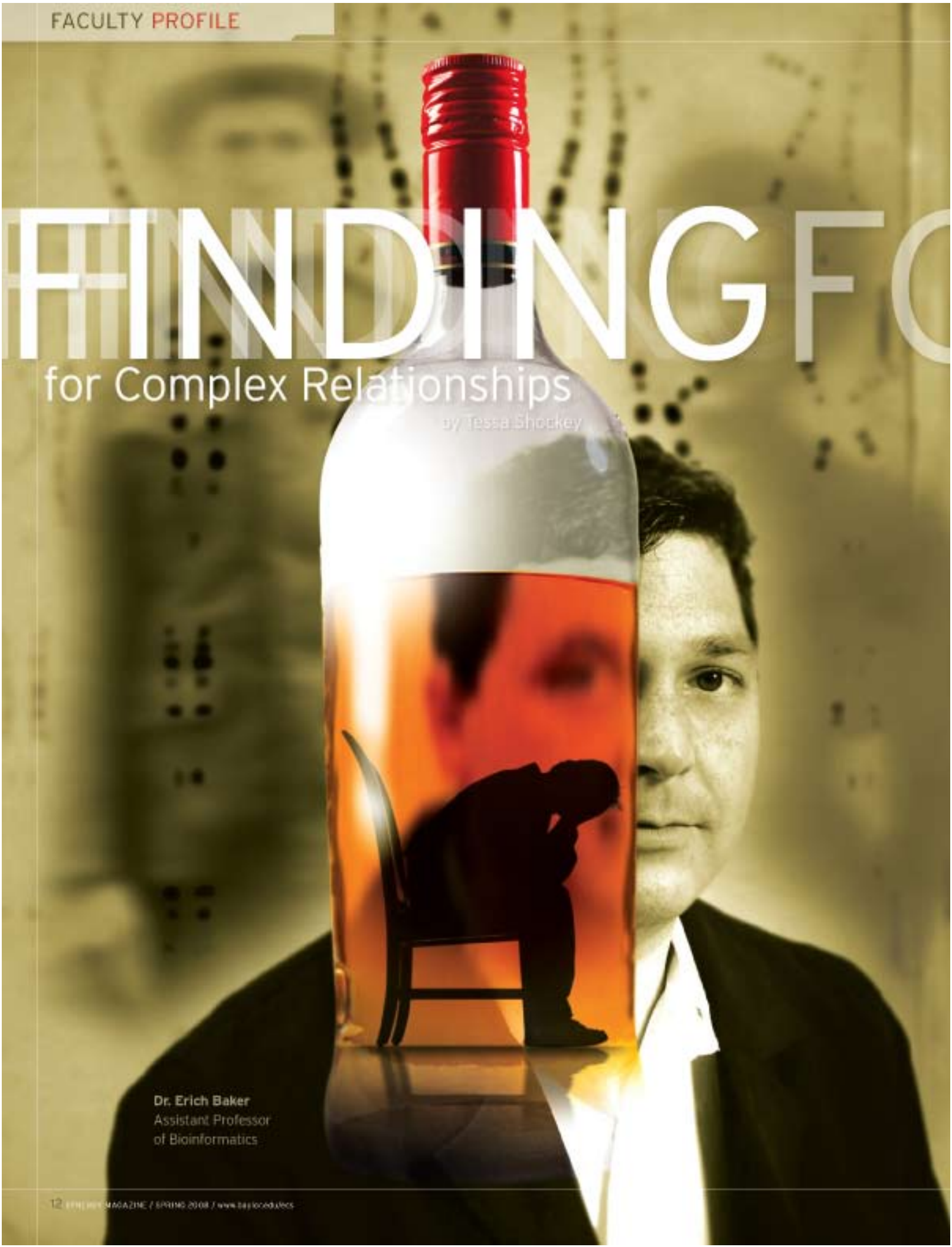
FINDING FO

for Complex Relationships

by Tessa Shockey



Dr. Erich Baker
Assistant Professor
of Bioinformatics

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DR. ERICH BAKER, ASSISTANT PROFESSOR IN BIOINFORMATICS, seeks to discover and implement means of sifting databases to uncover connections that might unlock answers to complex disorders, particularly alcoholism and post traumatic stress.

He is in charge of the database portion of the Integrative Neuroscience Initiative on Alcoholism (INIA)-Stress project, funded by the National Institute on Alcohol Abuse and Alcoholism.

The purpose of the project is to compile data on neural responses to stress and alcohol in hopes of better understanding how genes relate and affect alcoholism. Baker is part of a team of researchers, computer scientists and programmers that are compiling research and creating models to do so.

"[We're] taking information from all different technologies into a central computational system that will allow you to discover new trends by connecting the data together," Baker says. "For this particular project, the INIA-Stress project, I am actually in charge of the database behind it."

The database will sort through information and make relational connections.

"Traditionally, databases are really good at some things and really poor at other things. One of the things they are really poor at discovering are fuzzy relationships between things," he says.

Baker's model employs computer science graph theory to make binary connections in order to build larger graph models to help describe complex traits of alcoholism.

"Relational databases have come a long way, yet a fundamental question like that [alcoholism] is hard to answer," Baker says.

Alcoholism's genes are difficult to define because there are multiple genes with complex traits that may be interconnected.

"Complex traits are much more difficult because they have that fuzzy relationship that's hard to find a one-to-one connection with," he says. "So by discovering these new genes that are involved ... in this process we can understand complex traits and alcoholism."

The INIA-Stress project has made tremendous strides in the first year, and they hope to build on the computational tools in the upcoming two years.

Researchers also are running tests on mice, but hope to translate the experiment data to humans. Baker says that the program eventually will run tests on honeybees, canines and monkeys.

This research is conducted through Oak Ridge National Laboratories, where Baker did his post-doctoral work in human genome project. His research involved the *Shewanella* organism that is used in breaking down toxic materials through bioremediation.

Baker also is contributing to research in a study on Post Traumatic Stress Disorder, which, like alcoholism, doesn't have a single cause.

"If it had a single cause, it would be much easier to understand," he says.

Baker and the researchers are building a system where individual researchers can "store their data, curate their data, and hopefully make it easier for them to discover more connections in their data and other researchers in PTSD project," he says. The database will allow for data on genetic sequences of individuals that have PTSD.

"RELATIONAL DATABASES HAVE COME A LONG WAY..."

Baker is a co-investigator for the *Shewanella* and the PTSD projects, and a co-primary investigator on the INIA-Stress project.

Within the classroom, he works to develop the next generation of researchers for this interdisciplinary field. Baylor's bioinformatics major equips students to find computational tools and learn how to apply them.

Rachel Adams, a senior bioinformatics major, notes "When I discovered the intersection of computer science, chemistry, the life sciences, statistics and informatics through the bioinformatics major at Baylor, it seemed to be a fit for my academic interests."

Students, Baker says, are prepared "both to know how to use computational tools and also, on the life sciences side, to get a good overview of what is computable, what's not computable and what needs to be computed." ▸