

Scientists unravel genetic 'hairballs'

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Fritz Roth uses model organisms to study gene mutations. Credit: Kevin Kelly

(Medical Xpress)—Some scientists call them "ridiculograms." Others use the term "hairballs."

They are scientific diagrams that contain important information, but that are so complex that no human being could decipher their secrets.

Hairballs often turn up in the field of genetics, especially among researchers who study genetic interactions. The [human genome](#) has between 20,000 and 25,000 genes. That's complicated enough, but many hereditary characteristics are caused not by a single gene, but by two, or 20 or 200 mutations conspiring together.

These relationships can change how individual genes affect an organism. What's more, any given gene can exhibit thousands of possible

characteristics and functions. Researchers create genetic network maps to document the nature and intensity of these interactions.

But the data is so complex, nuanced and interrelated that the sheer volume quickly becomes unmanageable. The maps become hairballs, which is a problem, given that genetic interactions can make the difference between health and sickness or even life and death. As mutations in genes change how they behave, they alter the likelihood of their owner falling prey to hereditary conditions like [heart disease](#), autism or many cancers.

Enter Fritz Roth and his research team.

"One of the obsessions in my lab has been with capturing shades of grey in what we know about genes," says Roth, who is appointed in U of T's Banting and Best Department of Medical Research and holds the Canada Excellence Research Chair in [Integrative Biology](#). He specializes in bioinformatics research, [solving problems](#) of previously intractable complexity by means of [powerful computers](#) that do sophisticated analysis.

Much of his research uses "model organisms"—simple forms of life like yeast, fruit flies, fish or worms. These organisms share many genes—and many [gene interactions](#)—with human beings. That allows researchers to study gene mutations that conspire to, for example, damage a yeast cell, and draw conclusions about where to look for parallels in a human being.

Roth's computers access huge—and growing—databases containing the combined results of many lifetimes of research into how genes behave in different species, what other genes they interact with and what kind of problems they cause when they get together. Bioinformatics turns hairballs into manageable information that can lead to the genes that, when mutated, perpetrate some of the most insidious attacks on human

health.

Roth likens it to a detective story where illness is the crime and the genetic suspects rarely work alone.

"We have facts about a gene, and we have facts about its relationships with other genes," Roth says. "Sometimes, there's guilt by association: genes expressed in heart muscle are more likely to be involved in heart disease. Genes that regulate cell division might be implicated in causing cancer."

Roth's work isn't quite like that of a police officer combing the databases for likely suspects. In his world, the computer itself is the detective, analyzing patterns, identifying suspicious- looking behaviour and shady acquaintances. The computer does the analysis and tells the researchers where they might best hunt for their culprits.

Bioinformatics arguably got its start with rudimentary databases created in the 1950s. Just in the past decade, though, a massive increase in computing power, a flood of new data and major advances in machine learning have transformed the field. As researchers like Roth turn hairball gene maps into solvable mysteries, it places scientists on the brink of a new level of sophistication in their understanding of how [genes](#) work together to make us who we are.

Provided by University of Toronto

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