

Deeper than ancestry.com, 'EvoCor' identifies gene relationships

June 3 2014, by Ashley Wennersherron.

A frontier lies deep within our cells. Our bodies are as vast as oceans and space, composed of a dizzying number of different types of cells. Exploration reaches far, yet the genes that make each cell and tissue unique have remained largely obscure.

That's changing with the help of a team led by Gregorio Valdez, an assistant professor at the Virginia Tech Carilion Research Institute.

Valdez and his team designed a search engine – called [EvoCor](#) – that identifies [genes](#) that are functionally linked.

The name, a portmanteau of "evolution" and "correlation," points to the idea that genes with a similar evolutionary history and expression pattern have evolved together to control a specific biological process.

The project, described in May in the journal *Nucleic Acids Research*, may help medical scientists find ways to treat diseases that often have a genetic component, such as cancer or Alzheimer's disease.

A scientist types the name of a gene into a search box, and EvoCor quickly sifts through the evolutionary history of all mapped genes – human and otherwise.

EvoCor then compares the expression pattern of all genes to generate a list of candidate genes that function together with the query gene to drive a cellular process – from generating more energy for the cell to clearing

cellular debris. The scientist can use this list for the next stage of research.

"This platform allows researchers to generate lists of candidate genes quickly and at no cost," Valdez said. "EvoCor should speed the discovery of complex molecular mechanisms that control key cellular processes, including those that function to regenerate axons."

Most cellular functions—communication, division, death—result from a gene telling a cell how it's supposed to behave.

Scientists study how a gene is expressed and functions to determine, for example, eye color. The matter becomes more complicated when multiple genes with different functions are intricately related. Therein lies the problem. A researcher may start with one gene, but needs to know what other genes might play a part in influencing a particularly complex cellular function, such as the survival of neurons.

Once the other genes are known, the scientist can strategically study their function alone and as part of the larger network of genes.

To identify candidate genes, scientists have relied on expensive and time-consuming biochemical approaches. EvoCor takes advantage of the wealth of publicly available genome and [gene expression](#) datasets to generate a list of [candidate genes](#).

"It comes down to evolution," said James Dittmar, a fourth-year Virginia Tech Carilion School of Medicine student who is also a member of the Valdez laboratory and the first author of the journal article. "We took advantage of nearly 200 organisms with fully sequenced genomes to map out and compare the [evolutionary history](#) of all [human genes](#)."

Combing through the 21,000 human genes already mapped, 182

different genomes, and large gene expression datasets all maintained by the National Institutes of Health is a huge task. EvoCor makes it far more manageable.

"Scientists can now use EvoCor to take advantage of this massive amount of publicly available data to discover networks of genes without prior knowledge of their function," Valdez said.

When scientists fully understand every gene influencing a particular cellular output, they will have more options for developing therapeutics. In his own research, Valdez hopes to discover molecules that function to slow or halt cognitive and motor impairment caused by diseases and aging.

"We know of many genes that, when mutated, lead to disastrous outcomes," Valdez said. "But these genes don't function alone. EvoCor identifies functional partners and those partners could turn out to be better targets for therapeutics."

EvoCor was developed in collaboration with Lauren McIver, Pawel Michalak, and Harold "Skip" Garner, all scientists at the Virginia Bioinformatics Institute of Virginia Tech.

Valdez and his team plan to modify EvoCor further, so it can make even more powerful and specific predictions, easing the way for researchers trekking the new frontier.

More information: W. James Dittmar, Lauren McIver, Pawel Michalak, Harold R. Garner, and Gregorio Valdez. "EvoCor: a platform for predicting functionally related genes using phylogenetic and expression profiles." *Nucl. Acids Res.* first published online May 21, 2014 [DOI: 10.1093/nar/gku442](https://doi.org/10.1093/nar/gku442)

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