

Method offers potential for understanding anti-bacterial resistance

April 9 2014

Biologists could gain a deeper understanding about how species have evolved – and even find ways to address antibiotic resistance – using tools that were developed recently at Stockholm's KTH Royal Institute of Technology.

A better method for identifying how [genes](#) evolve has been developed by an international team that includes Jens Lagergren, a professor in computer science and computational biology at KTH.

The new model and method offers a way to understand a gene's history, Lagergren says. But in the long term the research could potentially lead to better understanding of how species evolve and provide a basis for dealing with antibiotic resistance.

The evolution of a species can in many cases be depicted with a tree. The same can be said for describing the evolution of gene families, that is, closely-related genes that have similar functions with regard to the species they are found in.

Information carried by genes in one gene family can be altered by mutations of individual DNA positions, as well as through major events such as losses or duplications of entire genes.

The latter give rise to entirely new genes in a [gene family](#). In bacteria, genes often are transferred between individuals within the same species. They also jump from one species to another, which is how antibiotic

resistance spreads between different bacterial strains.

"Exploring how different gene families have emerged during evolution is important for understanding how different genes are related to one another," Lagergren says.

"Where there's a branch on gene tree, the gene has a new function," he says.

Lagregren worked with colleagues from KTH and Science for Life Laboratory (SciLifeLab) to develop probability models that provide a more detailed picture of how the [gene tree](#) has grown through evolution, and when genes eventually jumped from one species to another in the species tree.

By basing their methods on mathematical models and Bayesian analysis, the researchers succeeded in producing tools for biologists who are interested in jumping genes and the traits they carry with them.

"Bayesian analysis allows one to start from an observation that has been made in reality and see which model is most probable given this observation," Lagregren says. "This is too time-consuming to do by hand, but it is possible with the help of computers."

He applied the model to two sets of bacterial species, and found that the new method works much better than traditional, non-statistical methods.

"Right now it's pure, basic research to understand the genes' history," he says. "In the long run, however, the models can be used to provide a deeper understanding of how different species have evolved and are related to each other, not only through direct inheritance but also by gene transfer."

The method and model could be used in order to see the kinship between [species](#) more clearly than before.

And, Lagregren adds, the method could one day provide a basis for dealing with antibiotic resistance.

"The method describes an algorithm and associated software, which will be an important tool for researchers working with bacteria and the genes they transmit laterally, such as for [antibiotic resistance](#)," he says.

The work is of such importance that Jens Lagergren had a scientific article accepted in *Systematic Biology* (impact factor about 12).

More information: Joel Sjöstrand, Ali Tofigh, Vincent Daubin, Lars Arvestad, Bengt Sennblad, and Jens Lagergren. "A Bayesian Method for Analyzing Lateral Gene Transfer." *Syst Biol* first published online February 20, 2014 [DOI: 10.1093/sysbio/syu007](https://doi.org/10.1093/sysbio/syu007)

Provided by KTH Royal Institute of Technology

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