

Gene migration helps predict movement of disease

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Until recently, migration patterns, such as those adopted by birds all across the Amazonian rainforest, have not been thought to play an important role in the spreading of beneficial genes through a population.

Researchers have now, for the first time, been able to predict the chance of a gene spreading when given any migration pattern, potentially providing an insight into the migration patterns of <u>animals</u> throughout history.

Even more impressively, the concepts from these predictions can be applied to tracking the route of cancer through the body, and viruses or <u>bacteria</u> through a population.

The study, published today, 14 July 2011, in the Institute of Physics and German Physical Society's <u>New Journal of Physics</u>, has provided a computation to make these predictions, performed within seconds on a normal computer.

"Give me your migration pattern, I'll give you the chances of success of your mutant," said lead author Professor Bharum Houchmandzadeh, of CNRS and Laboratoire Interdisciplinaire de Physique.

A mutant is a gene that has been altered naturally so that its normal function, or expression of a trait, is affected. The large majority of mutations have damaging effects; however, some can be beneficial — the mutation may be able to help the organism withstand environmental



stress or help it reproduce more quickly.

As a result, beneficial mutations tend to become more common throughout a population.

Since the discovery that evolution is a chance game more than seventy years ago, evolutionary theorists have been calculating the chances of beneficial <u>mutations</u> making their way through a population, with little or no attention being paid to the effect that migrations might have on these chances.

One of the reasons for this disregard is the fact that migration patterns are very hard to evaluate due to their sometimes complex nature. Take, for instance, a species of plant situated along a river: the upstream plants can send their seeds down the river, but the reverse is impossible.

Previous research has found that there are two dominant types of migration pattern and the researchers have taken things one step further by applying a neat set of mathematical tools to represent those patterns.

The first migration pattern assumes that when you die, someone else's progeny will replace you. For example, a tree has to die to free up the space for another to grow in its place. For this type of behaviour, the researchers showed that migrations decrease the chance of a mutation spreading and that there is an upper limit to the chance of success.

The second migration pattern assumes that your progeny will kill someone and replace them; much like <u>viruses</u>, bacteria and cancer. For this type of behaviour, some migration patterns can greatly enhance the chance of a mutant's success and can even make it certain.

These calculations allow one to detect all the <u>migration patterns</u> when given the chance of success of a certain mutant.



Professor Houchmandzadeh continues, "Suppose we are speaking of the spread of epidemics. A virus can jump from one individual to another during a single encounter. The migration pattern in this case is then the network of people meeting each other.

"An epidemiologist could use our formulas to compute the best way to limit encounters between individuals and therefore slow the spread of epidemics."

More information: The fixation probability of a beneficial mutation in a geographically structured population Houchmandzadeh and Vallade 2011 New J. Phys. 13 073020 iopscience.iop.org/1367-2630/13/7/073020

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