Model predicts number of species yet to be discovered regionally

April 3 2017, by Greg Borzo

UChicago researchers develop model for predicting number of species which breaks the number down by region—a new tool for biodiversity inventory and analysis. Credit: Jean Lachat

Many scientists have developed models to predict the total number of species on Earth—including those not yet discovered—of an animal or plant group, but University of Chicago researchers have developed the first such model that breaks the number down by region, providing a valuable new tool for biodiversity inventory and analysis.

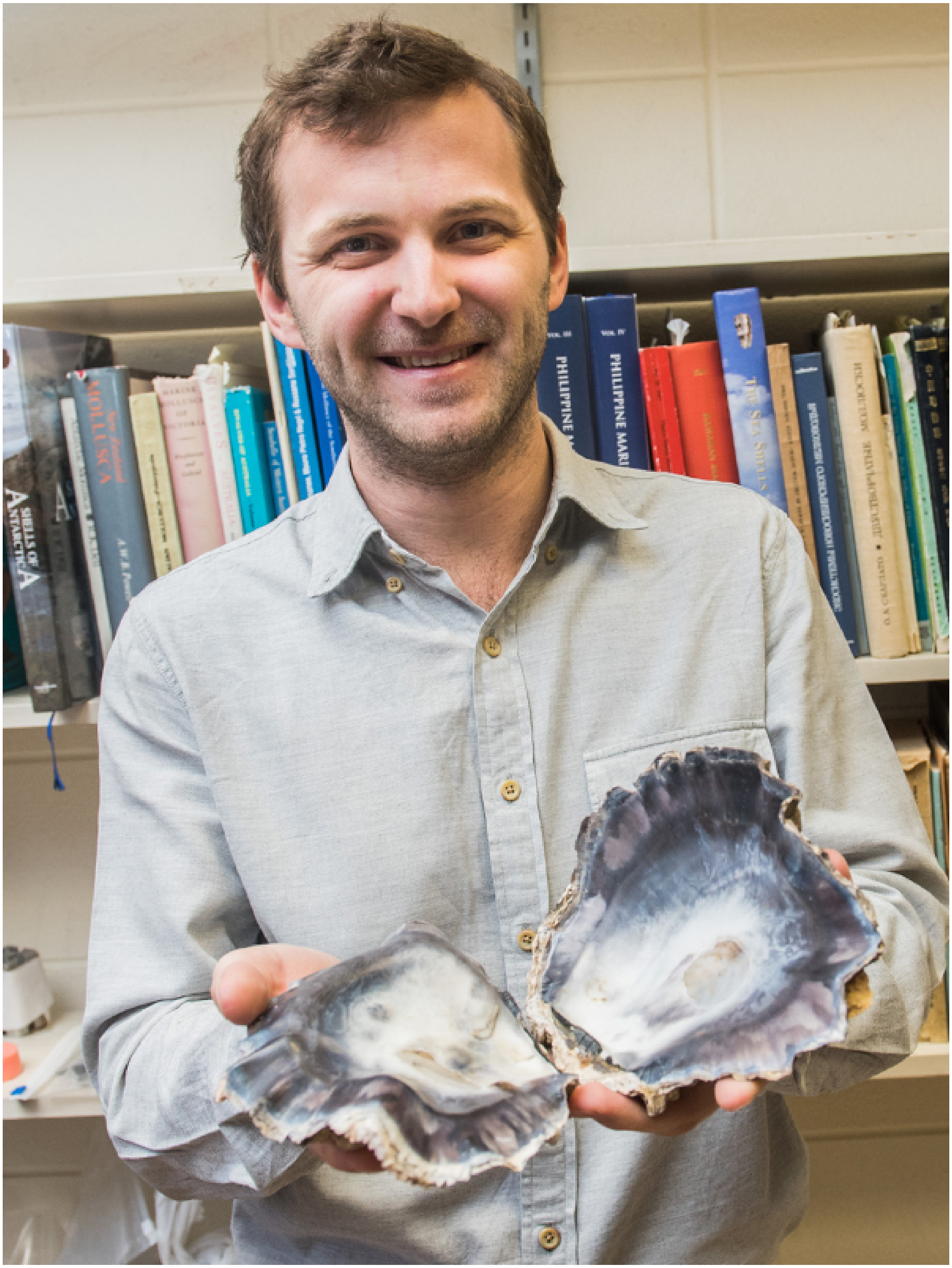
Using data about marine bivalves, the model estimates the number of undiscovered species living in a region based on the past rates of discovery and description of the species now known from that region. Regions with accelerating rates of discovery get higher projections for the number of species likely to live there, while regions with decreasing rates are likely to contain fewer undiscovered species. These models, broken down by region, take into account inconsistencies and disruptions in discovery efforts, cultural bias, warfare, uneven funding and other irregularities.

The research is described in a paper published in the early edition of the *Proceedings of the National Academy of Sciences*. The model aims to allow comparisons of species richness between regions that can be more useful than global numbers because the more specific and refined results help scientists establish more informed conservation priorities and understand ecological and evolutionary dynamics.

"This is the first time anyone has been able to predict in a robust, quantitative way the number of species that live in a specific region, and then rank those regions," said David Jablonski, a study co-author and the William R. Kenan Jr. Distinguished Service Professor of Geophysical Sciences. "There's a huge range of biological questions where it helps to have a strong picture of where the most biodiverse places are, and how they compare to the less biodiverse places. We wanted to put some numbers on how reliable the differences among regions are. And would they stack up in the same way 20 or 50 years from now, given past discovery patterns?"

While scientists have described about 1.6 million extinct and living species, some estimate that Earth could be home to 10 or even 100 times as many. The number of undescribed species is "staggering," Jablonski said, so this new model could help scientists figure out "how the natural world works."

Living bivalves constitute an ideal starting place for the model because they are widely dispersed and have been well studied over centuries. "Global distribution of bivalves, as well as extensive data on the living species, was critical," said Stewart Edie, a PhD student in geophysical sciences and lead author of the paper. "Bivalves have a long history of taxonomic study, which allowed us to demonstrate that the model's predictions are accurate through the many different eras of species discovery."


New Zealand MOLLUSCA
SHELLS OF ANTARCTICA
VOL. III
VOL. IV

PhD student Stewart Edie studies bivalves in the Henry Hinds Laboratory for Geophysical Sciences. Credit: Jean Lachat

For a baseline on marine bivalves, the authors started with the 220 species that Carl Linnaeus—the botanist whose statue overlooks the Midway Plaisance—described in 1758. Linnaeus wrote Systema Naturae, which laid out the classification system for life on Earth that is still used today.

For subsequent numbers, the authors turned to Jablonski's vast marine bivalve database of 5,744 species, with more than 62,000 records of where they are found. From this information, the researchers were able to establish patterns that they used to estimate the number of species of bivalves that live in 18 different geographic regions. They concluded that for the foreseeable future most of the newly described species would probably come from coastlines in the Indo-West Pacific region, a region that already has a massive level of biodiversity, but has far more to come, according to the model.

Knowing something about the underlying reasons why the history of bivalve discovery looks the way it does allowed the researchers to see how the model, which was built on the general statistical principles of discovery, performed across the pulses of discovery and quiet stretches of no discovery.

"As a result, we have a high level of confidence in the model and will continue to develop it so we can help to fill in gaps in our knowledge of biodiversity," Edie said. "In the meantime, we can pinpoint which diversity patterns that we are most, and least, confident in—given the data we have on hand right now."

The model is readily applicable to any biological group, he added. "Nearly all groups, from palm trees to tortoises, have a documented record of where and when their species were discovered. We can run those numbers through the model and predict how their biodiversity status will change, or not, with ongoing discoveries."

"This is a significant step forward because our model can be used to answer fundamental questions that conservationists and evolutionary biologists have regarding the spatial deployment of biodiversity, worldwide," Jablonski said.

Next steps will involve revising the model so it can account for more factors that influence discovery and description, such as body size, geographic range size, local abundance, water depth and other factors that make one animal more difficult to detect and collect than another. In addition, the model will be designed to take into account how such factors overlap and interact.

More information: Stewart M. Edie et al. Probabilistic models of species discovery and biodiversity comparisons, *Proceedings of the National Academy of Sciences* (2017). DOI: 10.1073/pnas.1616355114

Provided by University of Chicago