Rachel Karchin, the William R. Brody Faculty Scholar for the Whiting School of Engineering from 2013 to 2019, is a leading translational computational biologist. She develops novel algorithms and software to analyze genomic data and interpret its impact on cancer, the immune system and tumor evolution.

As a core member of the Johns Hopkins University Institute for Computational Medicine, Karchin has created leading-edge tools to interpret genomic variants, identify cancer drivers, model multivariate biomarkers of cancer prognosis and of tumor evolution. An international team of cancer geneticists, gastroenterologists and surgeons recently published a new clinical protocol, which offers substantial improvements over the current standard of care for pancreatic cyst patients, based on her lab’s innovative Multivariate Organization of Combinatorial Alterations (MOCA) algorithm, which integrates clinical, imaging, and genetic biomarkers into interpretable classifiers for clinical decision making. Her contributions to the field are extensive. Fifteen years ago, Karchin was among the first to apply computational statistical learning algorithms to the problem of predicting variant pathogenicity, which has become a standard practice in bioinformatics. Additionally, she helped to pioneer statistical learning methods to infer the importance of variants of uncertain significance in the BRCA1 and BRCA2 genes in support of genetic counseling of individuals being evaluated for hereditary breast and ovarian cancer.

A co-holder of multiple current or pending patents and software licenses, Karchin led the mutation modeling and analysis team for some of the first whole-exome sequencing studies of tumors at the Sidney Kimmel Cancer Center, Johns Hopkins University School of Medicine. Her team developed CHASM, the first widely used statistical learning method to predict somatic driver missense mutations in tumors and, subsequently, used in numerous cancer sequencing studies. Her team’s CRAVAT variant interpretation decision support framework is widely used by genomics researchers, with an open source version OpenCRAVAT introduced in 2019.

Karchin holds joint appointments in Hopkins’ Computer Science Department and the Department of Oncology and is a member of the Cancer Biology Program and of the Multidisciplinary Pancreatic Cyst Team, both with the Kimmel Cancer Center. Since 2007, she is an Affiliate Member for the McKusick-Nathans Institute of Genetic Medicine at Hopkins’ School of Medicine. Karchin co-led The Cancer Genome Atlas (TCGA) PanCan Atlas Essential Genes and Drivers Analysis Working Group (2017-2018).

Inducted in 2017 into the College of Fellows of the American Institute for Medical and Biological Engineering, Karchin was recipient of a National Science Foundation CAREER Award in 2008. She is a member of: International Society for Computational Biology; American Association for the Advancement of Science; American Society of Human Genetics; American Association for Cancer Research; Society for Immunotherapy of Cancer; and American Institute for Medical and Biological Engineering. She currently serves on the editorial boards of *Human Mutation*, *Human Genetics*, and *PLoS Computational Biology* and on numerous review groups. Among the advisory boards on which she currently serves are the ClinGen Sequence Variant Interpretation Group, the Critical Assessment of Genome Interpretation organization and the Human Genome Variation Society, of which she is on the board of Directors.

A frequent conference speaker, session chair, and workshop leader, Karchin co-chaired the May 2019 RECOMB satellite meeting on Cancer Computational Biology and chaired the Gordon Research Conference on Human Genetic Variation & Disease (2016-2018). Additional conference leadership includes her role as vice chair of the Gordon Research Conference on Human Single Nucleotide Polymorphisms and Disease (2014-2016) and symposium co-chair of the Cancer Computational Biology, American Association of Cancer Research 2017 meeting.

She received a B.S. in Computer Engineering (1998) and M.S. (2000) and Ph.D. (2003) in Computer Science from the University of California, Santa Cruz and completed her postdoctoral work at the University of California, San Francisco in the Department of Biopharmaceutical Sciences.