Combating Liver Cancer with DeepMine, a Novel Deep Learning Algorithm

Retchin, Michael

Retchin, Matthew

Hepatocellular carcinoma (HCC) has the shortest survival time of any cancer, and affects more than 850,000 people worldwide as the second leading cause of cancer-related mortality. Understanding the molecular basis of HCC can aid in discovering effective targets for therapy. MicroRNA-1202 (miR-1202) is downregulated in HCC-recurring and chronic HCV-infected sera, suggesting a potential tumor suppressing role in HCC. To predict potential biological effects of miR-1202 in HCC, a novel deep learning (artificial intelligence) algorithm called DeepMine was developed with a deep belief network. By incorporating several open-source softwares to determine binding site properties, DeepMine predicted putative targets of miR-1202. Of predicted targets, staphylococcal nuclease domain containing protein 1 (SND1) was identified as highly overexpressed in HCC. SND1 levels were evaluated in miR-1202 transfected HCC cell lines, and proliferation and apoptosis were analyzed. MiR-1202 transfected cells showed significant SND1 knockdown, and stable clones showed reduced cell viability and increased apoptotic pathway activity. Additionally, DeepMine outperformed currently available human miRNA target prediction algorithms in standard metrics. Thus, an antagonistic pathway relating miR-1202 with oncogene SND1 was identified and characterized, and miR-1202 was demonstrated to be a potent inhibitor of HCC. These findings may aid in saving the lives of patients with HCC. In addition, the development of DeepMine provides researchers with a powerful tool for developing targeted therapies for a range of diseases.

Awards Won:

First Award of $5,000

Intel ISEF Best of Category Award of $5,000