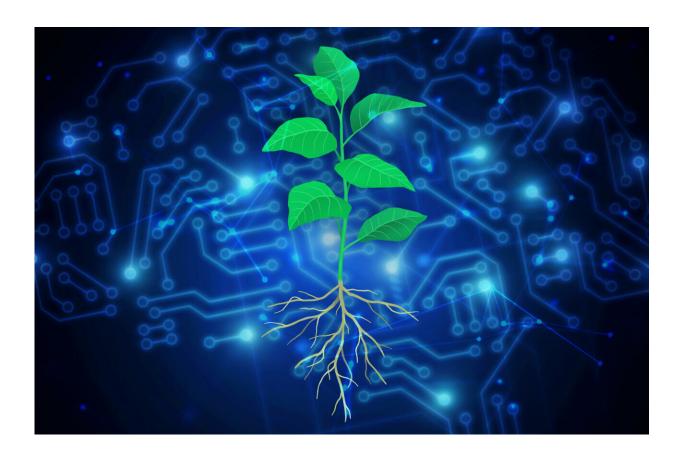# Artificial intelligence helps scientists engineer plants to fight climate change

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A green leafy plant with its roots exposed on a background of abstract computer imagery representing SLEAP. Credit: Salk Institute

The Intergovernmental Panel on Climate Change (IPCC) has declared that removing carbon from the atmosphere is now essential to fighting

climate change and limiting global temperature rise. To support these efforts, Salk Institute scientists are harnessing plants' natural ability to draw carbon dioxide out of the air by optimizing their root systems to store more carbon for a longer period of time.

To design these climate-saving plants, scientists in Salk's Harnessing Plants Initiative are using a sophisticated new research tool called SLEAP—an easy-to-use artificial intelligence (AI) software that tracks multiple features of root growth. Created by Salk Fellow Talmo Pereira, SLEAP was initially designed to track animal movement in the lab. Now, Pereira has teamed up with plant scientist and Salk colleague Professor Wolfgang Busch to apply SLEAP to plants.

In a study published in *Plant Phenomics*, Busch and Pereira debut a new protocol for using SLEAP to analyze plant root phenotypes—how deep and wide they grow, how massive their root systems become, and other physical qualities that—prior to SLEAP—were tedious to measure. The application of SLEAP to plants has already enabled researchers to establish the most extensive catalog of plant root system phenotypes to date.

Moreover, tracking these physical root system characteristics helps scientists find genes affiliated with those characteristics, as well as whether multiple root characteristics are determined by the same genes or independently. This allows the Salk team to determine which genes are most beneficial to their plant designs.

"This collaboration is truly a testament to what makes Salk science so special and impactful," says Pereira. "We're not just 'borrowing' from different disciplines—we're really putting them on equal footing in order to create something greater than the sum of its parts."

Prior to using SLEAP, tracking the physical characteristics of both

plants and animals required a lot of labor that slowed the scientific process. If researchers wanted to analyze an image of a plant, they would need to manually flag the parts of the image that were and weren't plant—frame by frame, part by part, pixel by pixel. Only then could older AI models be applied to process the image and gather data about the plant's structure.

What sets SLEAP apart is its unique use of both computer vision (the ability for computers to understand images) and deep learning (an AI approach for training a computer to learn and work like the human brain). This combination allows researchers to process images without moving pixel by pixel, instead skipping this intermediate labor-intensive step to jump straight from image input to defined plant features.

"We created a robust protocol validated in multiple plant types that cuts down on analysis time and human error, while emphasizing accessibility and ease-of-use—and it required no changes to the actual SLEAP software," says first author Elizabeth Berrigan, a bioinformatics analyst in Busch's lab.

Without modifying the baseline technology of SLEAP, the researchers developed a downloadable toolkit for SLEAP called sleap-roots (available as open-source software here). With sleap-roots, SLEAP can process biological traits of root systems like depth, mass, and angle of growth.

The team tested the sleap-roots package in a variety of plants, including crop plants like soybeans, rice, and canola, as well as the model plant species Arabidopsis thaliana—a flowering weed in the mustard family. Across the variety of plants trialed, they found that the novel SLEAP-based method outperformed existing practices by annotating 1.5 times faster, training the AI model 10 times faster, and predicting plant structure on new data 10 times faster, all with the same or better

accuracy than before.

Together with massive genome sequencing efforts for elucidating the genotype data in large numbers of crop varieties, these phenotypic data, such as a plant's root system growing especially deep in soil, can be extrapolated to understand the genes responsible for creating that especially deep root system.

This step—connecting phenotype and genotype—is crucial in Salk's mission to create plants that hold on to more carbon and for longer, as those plants will need root systems designed to be deeper and more robust. Implementing this accurate and efficient software will allow the Harnessing Plants Initiative to connect desirable phenotypes to targetable genes with groundbreaking ease and speed.

"We have already been able to create the most extensive catalogue of plant root system phenotypes to date, which is really accelerating our research to create carbon-capturing plants that fight climate change," says Busch, the Hess Chair in Plant Science at Salk. "SLEAP has been so easy to apply and use, thanks to Talmo's professional software design, and it's going to be an indispensable tool in my lab moving forward."

Accessibility and reproducibility were at the forefront of Pereira's mind when creating both SLEAP and sleap-roots. Because the software and sleap-roots toolkit are free to use, the researchers are excited to see how sleap-roots will be used around the world. Already, they have begun discussions with NASA scientists hoping to utilize the tool not only to help guide carbon-sequestering plants on Earth, but also to study plants in space.

At Salk, the collaborative team is not yet ready to disband—they are already embarking on a new challenge of analyzing 3D data with SLEAP. Efforts to refine, expand, and share SLEAP and sleap-roots will

continue for years to come, but its use in Salk's Harnessing Plants Initiative is already accelerating plant designs and helping the Institute make an impact on climate change.

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