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NAPPN Annual Conference Abstract: The *OPEN Series* Design Philosophy, Putting High Throughput Phenotyping Into the Hands of Users

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Predictive biology is the ability to predict a biological outcome from known inputs (and vice versa). Complex and urgent problems, such as climate change and a growing global population, requires a better grasp of predictive biology approaches. However, predictive biology requires a deep understanding of the *genome-to-phenome* relationship within an organism. The field of genomics has accelerated rapidly in the last few decades with technological advances that have helped reduced the costs of genomics research and easy-to-use computational tools. Phenomics technologies has not advanced at the same rate. Many phenotyping systems are expensive to own, require special training to use, focus on narrow areas of research, and produce large amounts of data with no standards of storage and documentation.

We propose a design philosophy for high-throughput phenotyping systems called the *OPEN Series*. This philosophy focuses on systems that use off-the-shelf commercial products and open-source software to make high quality phenotyping systems efficiently and for use by general users. In addition, the *OPEN Series* focuses on integrating cloud-based image processing through the NSF-funded cyberinfrastructure *CyVerse,* thus allowing users to share and process data remotely. We've worked to integrate this philosophy into our own phenotyping systems, *OPEN leaf* and *OPEN root*, to great success. We hope to export our work in creating accessible and affordable phenotyping system to labs across the globe to accelerate our understanding of the genome-to-phenome relationship for predictive biology.