

## FULLY-AUTOMATED BIOREACTOR PROCESS CONTROL ELIMINATES HANDS-ON TIME THROUGH CLOSED-LOOP CLOUD SOFTWARE INTEGRATION

Adam R. Carcella, Asimov  
Nick De La Torre, Asimov  
Lucas Corley, Asimov  
Will Johnson, Asimov  
Kevin D. Smith, Asimov  
Alec A.K. Nielsen, Asimov

Key Words: Ambr15, multi-omics, automation, microbioreactor, process control

Synthetic biology and multi-omics analysis have the potential to substantially increase the performance of engineered cell lines, but to develop an understanding of the link between genotype and phenotype, highly scalable processes for bioreactor control and data analysis are needed. Over the past decade, the Ambr15 automated microbioreactor system has become an industry standard for high-throughput cell line screening and media development; the BioProfile Flex2 is also commonly integrated to automate sampling for each bioreactor vessel. However, even with most bioreactor operations fully automated, data collection, calculation, and analysis is typically performed off-line and process changes are often manually adjusted within the Ambr15 software. Collectively, these manual steps increase operator hands-on time and introduce the potential for human error.

By leveraging the full capability of the Ambr15 software, we have eliminated all manual steps in data collection, calculation, and process control. We developed an Ambr15 process with dynamic feed control determined by glucose uptake rate (GUR) and integral viable cell count (IVCC), which are calculated in the Ambr15 software. Moreover, we connected our Ambr15 system to an open platform communications (OPC) server, enabling continuous data collection over the course of an experiment. Data is parsed and stored in a BigQuery data lake with direct connectivity to a master data analytics package, allowing us to analyze and compare data across experiments and modalities, and calibrate predictive computational models of the bioprocess. Overall, this integrated system reduces operator hands-on time by approximately 60% per experiment and minimizes the chance for human error. In summary, we streamlined our Ambr15 process to develop a truly “hands-off” workflow from experiment initiation through data analysis, enabling a truly scalable process for cell line characterization from multi-omics data.