Bioprocess Informatics to Accelerate Lentiviral Vector Process Development

Synthace

Oxford Biomedica

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1. Data are aggregated from multiple unit operations

Oxford Biomedica used a combination of spreadsheets and proprietary vendor software tools to interpret disparate portions of their dataset across their lentiviral vector development process.

The process of organizing, structuring, and presenting these data was shown to be cumbersome and resource-intensive when relying on the use of traditional tools.

Synthace's software platform, Antha® enabled Oxford Biomedica to automate upload, collation, organization, structuring, processing, visualization, and analysis of high-volume, high-density data streams from multiple unit operations.

Antha's bioprocess informatics capability **reduced the overall time from data generation to data interpretation from days to hours**, including a **~94% resource saving for a typical process analysis:**

- Raw to structured data: from 2.5 to 0.25 hours
- Structured to analyzed data: from 2.25 to 0.35 hours (two offline analyses) and from 1.5 to 0.25 hours (single offline analysis) per sample set

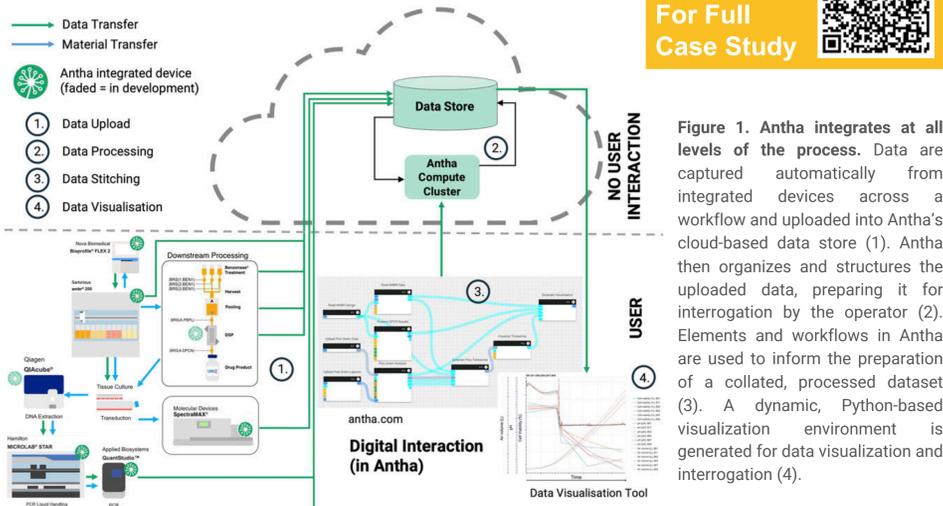**Click Here or Scan For Full Case Study**

Figure 1. Antha integrates at all levels of the process. Data are captured automatically from integrated devices across a workflow and uploaded into Antha's cloud-based data store (1). Antha then organizes and structures the uploaded data, preparing it for interrogation by the operator (2). Elements and workflows in Antha are used to inform the preparation of a collated, processed dataset (3). A dynamic, Python-based visualization environment is generated for data visualization and interrogation (4).

3. Reducing time spent structuring and visualizing data

Antha reduced time spent uploading data from disparate sources by 83% and reduced time spent structuring data by 92%.

Resulting in an **overall reduction in time spent from generating raw data to creating a structured dataset of 90%.**

Antha also enabled a **>80% saving in time spent creating basic plots** (incl. cellular, metabolite, and online bioreactor profiles) and functional titre plots and basic correlations.
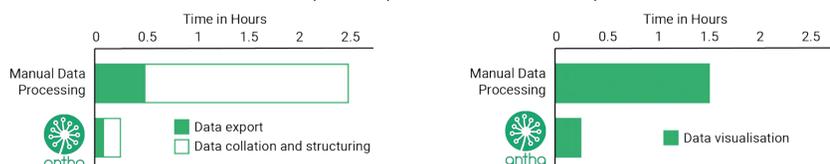

Figure 3. Antha greatly reduces time spent on structuring and visualizing bioprocess data. Left: The time needed to export, collate, and structure data are reduced by >80% each. The entire process, from generating raw data to creating a structured dataset, is shortened from 2.5 to 0.25 hours, resulting in a 90% time saving. Right: The time needed for basic plotting of bioprocess profiles, without online/offline overlay plotting, is reduced from 1.5 to 0.25 hours for a single offline analysis, resulting in a >80% time saving.

5. Time from data generation to insights reduced by 94%
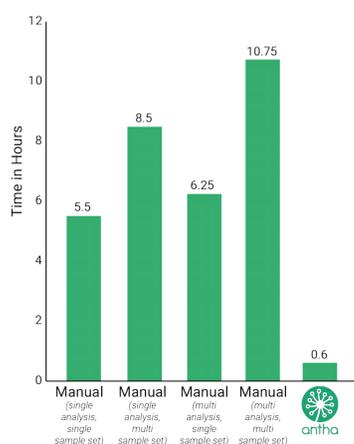
The more analyses undertaken by Antha, the greater the resource savings. For a typical vector bioprocess development run, time from raw data to insight is reduced from 10.75 to 0.6 hours, resulting in a ~94% reduction in resource demand.

"We're starting to deal with very big datasets, and some vendor software can be cumbersome and slow. Antha alleviates this problem by integrating offline data in a very user-friendly, comprehensive, and dynamic way."
- André Raposo, Group Lead - Computer-Aided Biology (CAB) Group, Oxford Biomedica

Figure 8. Manual vs Antha: approximate processing time from raw generated data to insight. Structuring of data is included in all options. Single analysis refers to qPCR, while multiple analyses also include dsDNA quantification. Multi-sample set is based on three sample plates generated by the process.

2. Drag and drop workflow design for ease-of-use and flexibility

Workflows for data processing are modular and designed to ease user interaction and interpretation.

Antha performs data structuring in two steps:

1. Data are uploaded, processed, and organized by device and time, ready for subsequent selection through the platform (Figure 1: upload stage)
2. Antha workflows are used to collate data from a single experimental run and contextualize those data as a single set ready for visualization and interrogation (Figure 2)

Information is passed between elements by connecting them together, enabling easy building and editing of complex data processing operations.

Strands feed into an element to provide a visualization environment for the structured dataset generated by the workflow. Oxford Biomedica's workflow is shown below (Figure 2).

The output is a structured, collated dataset that contains all of the selected data in the workflow and a visualization environment that contains those data for interrogation.
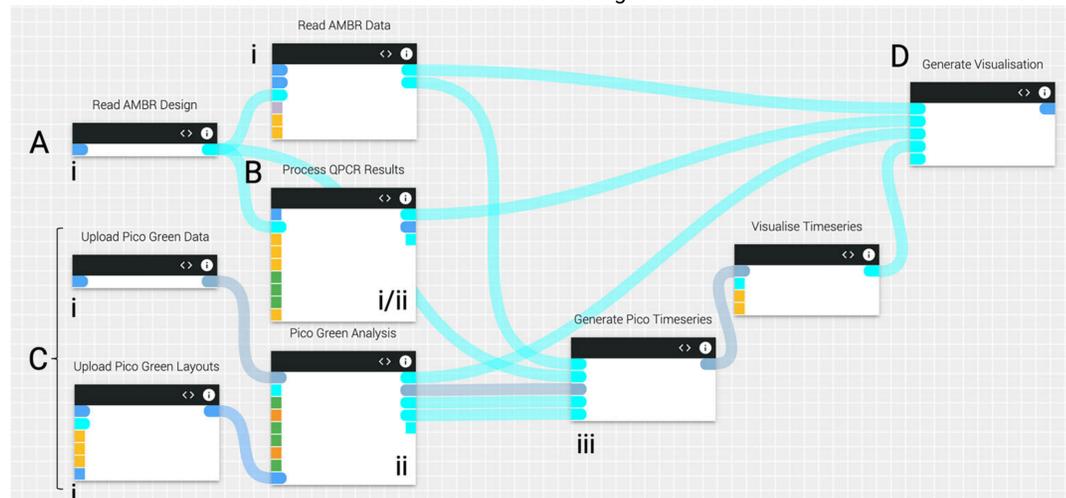

Figure 2. Antha's intuitive drag-and-drop interface allows users to easily design workflows for bioprocess data processing. Workflow steps are encoded by separate elements, connected in a specific order. Here, the workflow brings multiple disparate datasets together to form a single cohesive dataset, process analytics, and provide visualizations. Specific elements encode file selection and upload (i), data processing (ii), and data collation (iii) steps. Firstly, a complete online dataset from the 12-way ambr®250 HT system is selected as the basis for the timeseries by which the dataset will be aligned (A). Then, selected qPCR datasets (B) and PicoGreen® assay data (C) are processed and aligned to the online timeseries. Finally, the selected datasets are used to create a Python-based environment to enable dynamic exploration of structured data from the desired experimental run (D).

4. Automatic presentation of data for interrogation

Following execution of the Antha workflow, a user is presented with a dynamic visualization environment for exploring and interrogating a complete dataset.
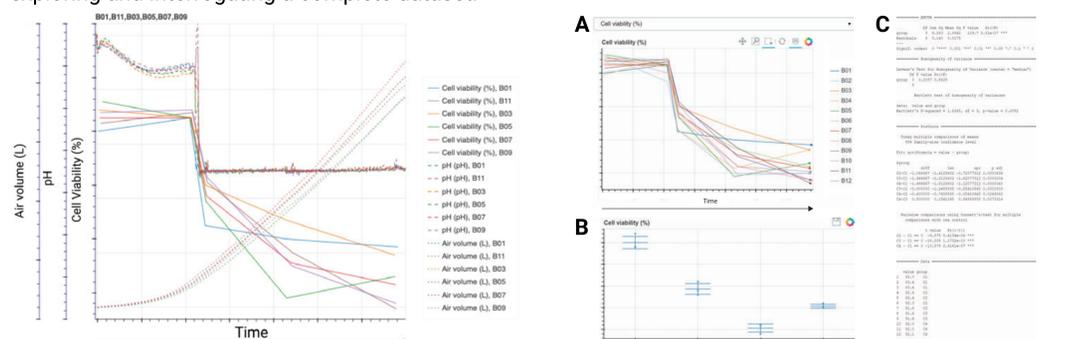

Figure 4. Multiplexed view of online/offline variables from multiple bioreactors.

Figure 5. Antha automates the basic statistical analysis of variance (ANOVA) and its visualization for selected data. Dynamic data selection (A), plotting of basic statistical analysis (B), and one-way ANOVA with post-hoc multi-comparison tests (Tukey and Dunnett's tests) (C).
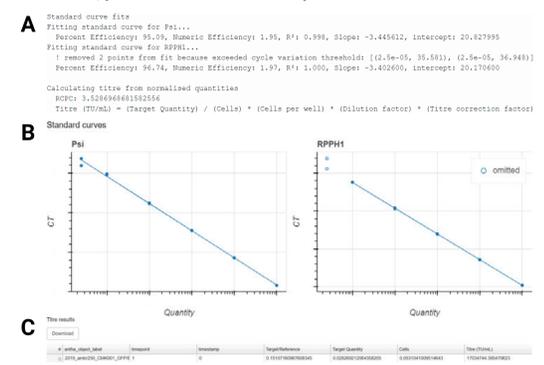

Figure 6. Antha automates processing and visualization of qPCR data. Standard curve information (A), plots (B), and final calculated titre data (C), presented in Antha's qPCR tab. Data have been anonymized: the values do not represent the actual data from Oxford Biomedica's development work.
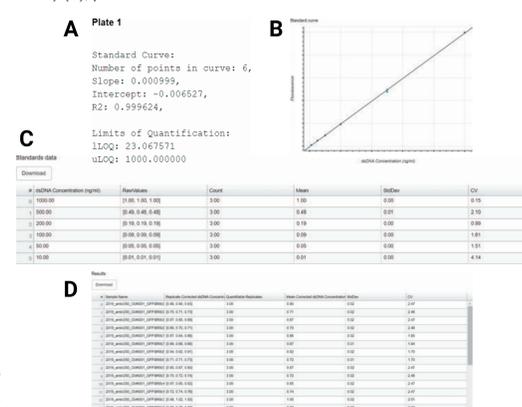
Figure 7. Antha automates processing of PicoGreen® assay data, including standard curves and comparison with assay acceptance criteria defined by the user. Standard curve summary information (A), plot (B), data (C), and final calculated values (D), presented in Antha's Pico tab. Data have been anonymized: the values do not represent the actual data from Oxford Biomedica's development work.

6. Advantages of Antha:

- Improved data integrity
- Equivalent performance to manual data processing for offline analytics
- Reduction in data export, collation, structuring, and visualization time (Figure 3)
- Provision of a single, cohesive dataset with minimal manual intervention
- Dynamic, sharable visualization environment for data exploration
- Generation of plots deemed too cumbersome by traditional means (e.g. online/offline overlays)
- Single software tool for handling data from across the bioprocess