tetrascience

Customer Story

Scaling mRNA stability analysis with automated chromatography data workflows

The Challenge

A leading biopharmaceutical company specializing in mRNA therapeutics uses reversed-phase ion-pair (RP-IP) chromatography to evaluate mRNA stability after exposure to stress conditions such as elevated temperature and shear. These high-throughput assays are critical for identifying promising candidates, but the underlying data workflows were slow, manual, and error-prone.

A key challenge is accurately identifying the target peak, as degradation products often share similar retention times with intact mRNA, resulting in overlapping peaks that are difficult to resolve without expert interpretation. Scientists attempted to compensate with a combination of manual processing and limited machine learning (ML) support, but several bottlenecks persisted:

- **Manual review** – Scientists spent significant time manually annotating target peaks in Thermo Scientific Chromeleon, especially for complex degradation patterns. The process was highly "point-and-click" and not scalable for high-throughput workflows.
- **Cumbersome data export** – Data for each sample had to be exported individually from Chromeleon, with transfers taking up to 15 minutes per file. While not requiring constant manual effort, the slow and fragmented process significantly delayed time to insight for each dataset.
- **Missing context** – The lack of critical metadata (e.g., column type, instrument ID, user name) reduced comparability, complicated traceability, and limited opportunities to analyze factors such as analyst-driven variability in stability trends.
- **Static ML model** – The peak prediction model could not learn from scientists' corrections in Chromeleon, requiring repeated manual verification with no improvement over time.
- **Risk of data loss** – Poorly resolved peaks could be misidentified or overlooked, undermining confidence in the data and affecting decisions tied to candidate selection.

These limitations not only delayed decision-making but also introduced variability and prevented the team from scaling its mRNA stability workflows effectively.

The Solution

The company turned to the Tetra Scientific Data and AI Cloud to automate and scale its chromatography data workflows. Key changes included:

- **Automated data ingestion** – Chromeleon data is now immediately and automatically captured by a Tetra Agent, eliminating manual exports and accelerating time to insight.
- **Contextualization and engineering** – Experimental metadata is added, and data is converted into a harmonized, vendor-agnostic format optimized for downstream analytics.
- **ML-driven peak prediction at scale** – The AI-ready data is automatically fed into the company's peak prediction model. Scientists can review and correct predictions, and those corrections are now captured as training data, enabling continuous model improvement.

Challenge:

A leading biopharma's mRNA stability workflow, based on RP-IP chromatography, was constrained by manual peak detection, slowing throughput and introducing variability into a critical analysis.

Solution:

The Tetra Scientific Data and AI Cloud automates data replatforming and engineering to eliminate manual bottlenecks, streamline peak detection, and scale machine learning.

Result:

- Saved up to 60 minutes of hands-on time per assay by automating data processing
- Reduced time to analysis by up to 24 hours through automated data transfer
- Enriched data with contextual metadata to unlock deeper insights
- Improved model performance through continuous feedback-driven learning

The Result

By streamlining and enhancing data workflows with TetraScience, the company achieved:

- **20–60 minutes of active scientist time saved per assay** through automated data processing
- **15 minutes saved per sample** (up to 24 hours per 96-well plate) by eliminating manual file exports and reducing the delay between data capture and analysis
- **Richer, more contextualized data** enabled deeper insight into variables such as analyst-driven variability and instrument performance
- **Improved ML accuracy** through a feedback loop that incorporates human-reviewed annotations to refine peak prediction over time

These improvements enabled scientists to spend more time performing assays and less time preparing and reviewing data. The structured data and feedback loops implemented through TetraScience provide a foundation for more accurate and efficient peak classification using ML. Ultimately, this approach supports faster decision-making, better candidate selection, and scalable screening of mRNA therapeutics.