

Decoding Data Challenges in Diagnostics Strand's Solutions

If you are a midsize to large diagnostic lab onboarding a new assay, or trying to scale an existing assay, here are some common challenges you may face and our potential solutions.



Increased TAT Due to High Sample Volumes:

YOUR CHALLENGE: 

Running only one flow cell at a time on DNAnexus leads to increased turnaround time (TAT) for samples and difficulty processing high sample volumes.

OUR SOLUTION: 

We update the pipeline to execute multiple samples simultaneously, utilizing the full computational power of DNAnexus.

Data Storage Issues:

YOUR CHALLENGE: 

Data storage on DNAnexus / AWS S3/ ICA has already reached several petabytes, making it difficult for labs to scale in terms of space and cost with the increased sample volumes.

OUR SOLUTION: 

We select a long-term storage solution and optimize the timing of data transfer. This involves determining which data types should be kept in an accessible storage and which should be moved to a deep archive storage. To ensure smooth workflows, we build detailed SOPs for data storage and archival. Additionally, we explore alternative cloud storage solutions on AWS or Azure, which are more cost-effective.

Data Transfer Across Platforms:

YOUR CHALLENGE: 

Moving data across various platforms (ICA to DNAnexus, DNAnexus to S3, etc.) is challenging due to the volume of data.

OUR SOLUTION: 

We write custom scripts to automate data transfer. We also consider incorporating available data management platforms to improve how data is copied, moved and managed.

Integration with LIMS:



The current integration with LIMS and other bioinformatics platforms needs optimization.



We tailor our solution to the specific needs of each laboratory. On a high level, we incorporate HL7 APIs for smooth integration between various systems.

Raw Data Access:



Raw data needs to be made available to partners through different channels.



We centralize all raw data in one portal, allowing users to download the required data to their preferred storage location.

Combining Multiple Data Types:



Multiple data types need to be combined for unified reporting.



We frequently combine various data types to facilitate comprehensive reporting. For instance, our tertiary analysis workflow in StrandOmics involves incorporating NGS results from StrandNGS along with the outcomes of other experiments, such as RNAseq and immunohistochemistry (IHC). This injection of multiple data types facilitates accurate summarization and customized reporting.

Launching and Tracking Pipelines:

YOUR CHALLENGE:



In addition to providing pipelines to be run, ICA offers an auto-launch feature that initiates, tracks, and reports the status of each pipeline. However, customized versions may be needed to obtain the required scale with this feature.

OUR SOLUTION:



We design an alternative customised system for launching pipelines and provide a tailored dashboard to track and monitor ICA run metrics. This system ensures a greater degree of surveillance and reliability in terms of pipeline failure reports and restarting runs.



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Our Genomics Solutions

We help you speed up the reporting of clinical NGS tests, both somatic and germline.

We enable pharmaceutical companies with clinical data and bioinformatics solutions for target discovery, translational research, and clinical research.

We help you build complex genomic software for managing and analyzing data and metadata from the entire gamut of omics modalities. We can help you accelerate releases and scale software operations.