

# Background

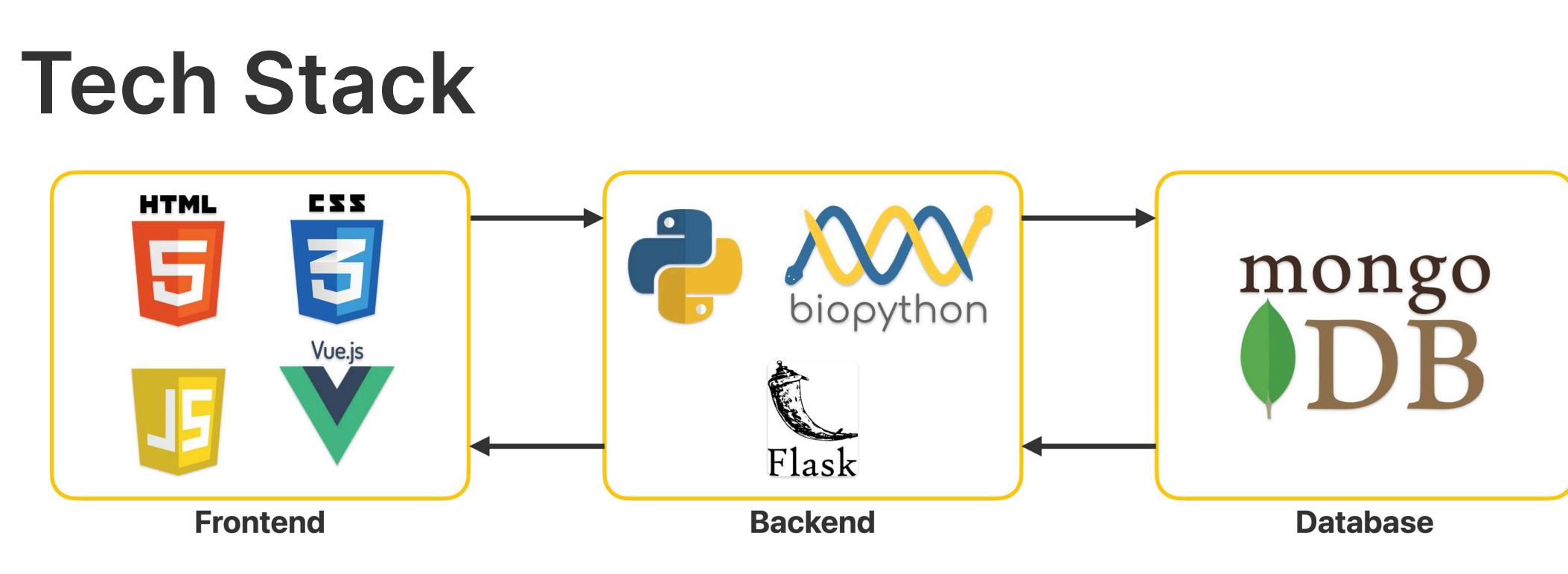
qPCR (quantitative Polymerase Chain Reaction) tests are widely used to detect infectious diseases by identifying specific genetic material. However, mutations in pathogen genomes can alter target regions, increasing the risk of false negatives and reducing the reliability of these assays. Maintaining the accuracy of qPCR reagents is essential for effective disease surveillance and diagnostics.

Currently, assay validation workflows are largely manual and depend heavily on third-party bioinformaticians to assess the impact of genetic mutations on assay performance. This process is time-consuming, inefficient, and does not scale well in the face of growing genomic data and emerging pathogen variants.



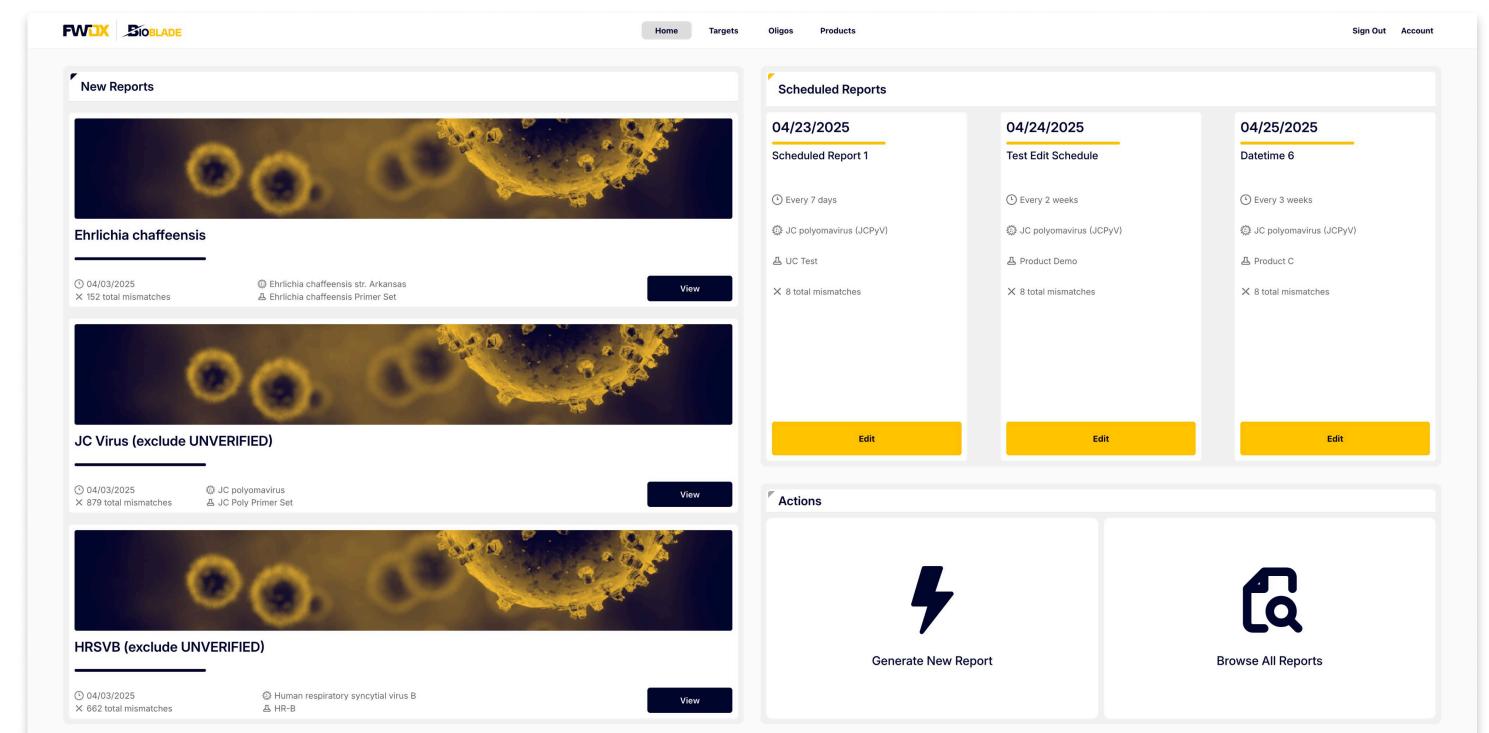
## Outcome

BioBlade eliminates the manual, resource-intensive steps traditionally required to validate qPCR assays and enhances the reliability of diagnostic testing. Through the development of a secure, web-based platform, we enable users across scientific disciplines to rapidly evaluate qPCR kit performance by comparing assay data to verified DNA reference sequences. This solution provides immediate, accurate insights into assay effectiveness, removes the dependency on external bioinformatics support, streamlines validation workflows, and strengthens confidence in disease detection and diagnostic outcomes.



# **Ensuring the reliability of qPCR reagents through** automatic detection of genetic mutations

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Wiki qPCR: A lab technique used to amplify and quantify DNA. Primers & Probes: Short DNA sequences or <i>oligos</i> used in qPCR to target specific genomic regions. Mutation: A change in the DNA sequence that may affect diagnostic assays. Sequence Alignment: A method to compare DNA sequences to identify variations. False Negative: A test result that incorrectly indicates the absence of a pathogen.	Ackno Fort Word • Dr. Je TCU Dep

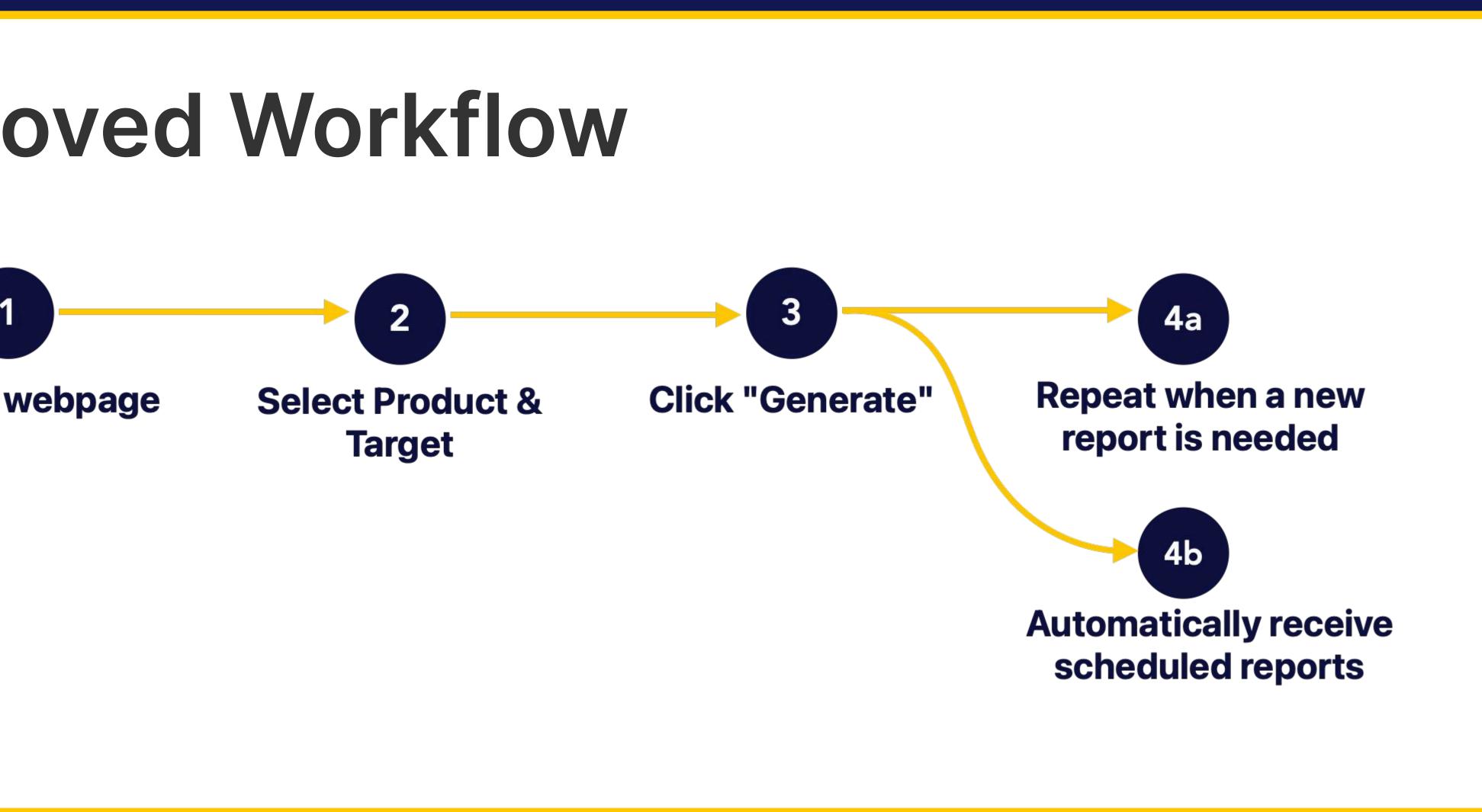
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# COLLEGE OF SCIENCE & ENGINEERING

### lenges

- uring the application integrates well with national and national genomic databases
- mizing architecture for high-volume data storage, enabling mless access and exceptional performance while minimizing astructure costs
- ementing a computationally fast but cost effective loyment strategy
- igating domain-specific biological terminology
- eraging cutting-edge CPU vector instruction optimization to ver ultra-fast global-local sequence alignments with aralleled performance and accuracy
- ementing advanced security protocols to safeguard Fort th Diagnostics proprietary information with industry-leading ection measures



# nary



- le leverages publicly available genomic sequence datasets vide enhanced curation, normalization, and enrichment of netadata, specifically benefiting qPCR manufacturers.
- latform enables clients to manage their proprietary cleotide sequences and product validation reports through itive web interface. This allows clients to validate their ts against real-world genomic sample data, ensuring cally significant product outcomes.

# owledgments

- orth Diagnostics
- Jerry Boonyaratanakornkit & Manuel Duval
- epartment of Computer Science
- 3ingyang Wei and the faculty for equipping us with the wledge and skills that enabled the creative and innovative tions presented in this project