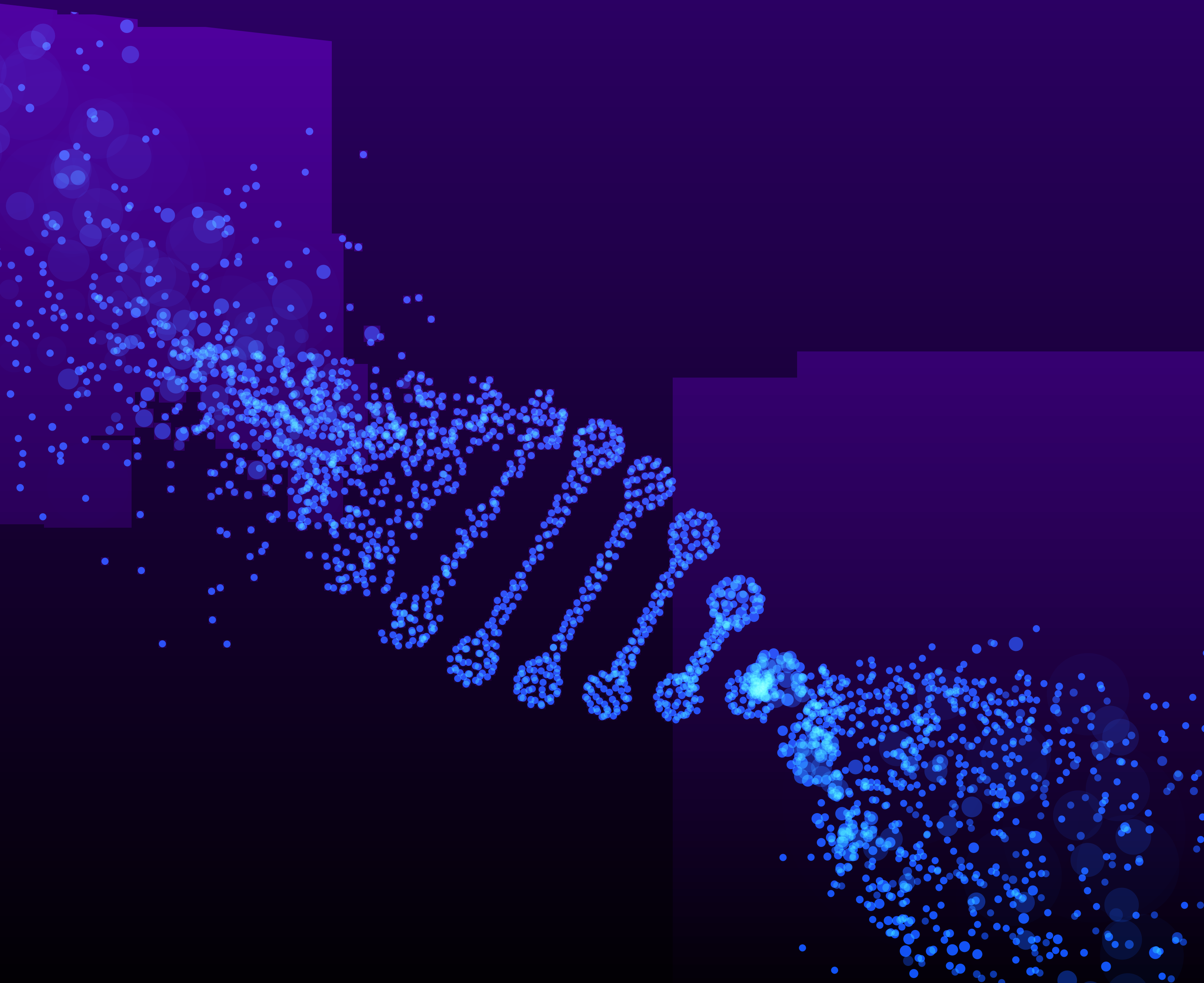
excelra

Where data means more

CASE STUDY

Bioinformatics pipeline development



Objective

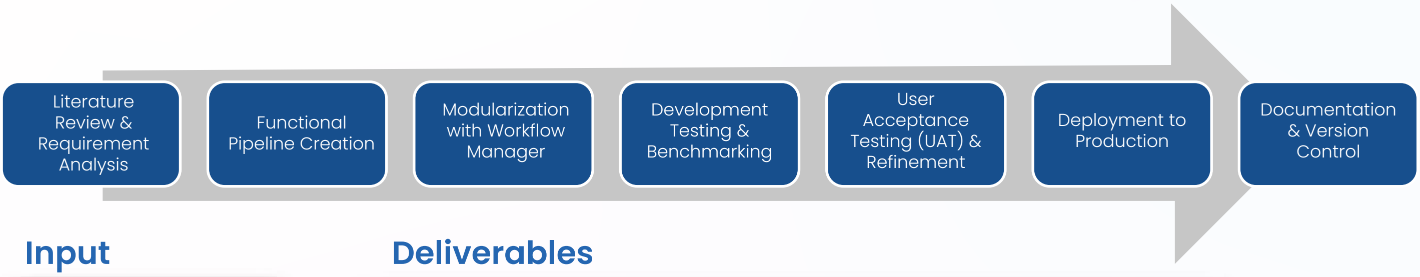
- Develop and implement robust pipelines tailored to each data-type for comprehensive analysis
- Additionally, provide essential bioinformatics support to enhance the capabilities of the Computational Oncology department in conducting cutting-edge research.

Challenges

- Data complexity: Managing diverse biological data formats and structures.
- Algorithm selection: Choosing suitable tools and algorithms for analysis tasks.
- Performance optimization: Ensuring efficiency in speed, resource usage, and scalability.
- Integration challenges: Integrating multiple tools and modules while maintaining compatibility.

Workflow (overall)

- Data complexity: Managing diverse biological data formats and structures.



Literature Review & Requirement Analysis

Functional Pipeline Creation

Modularization with Workflow Manager

Development Testing & Benchmarking

User Acceptance Testing (UAT) & Refinement

Deployment to Production

Documentation & Version Control

Input

Data types

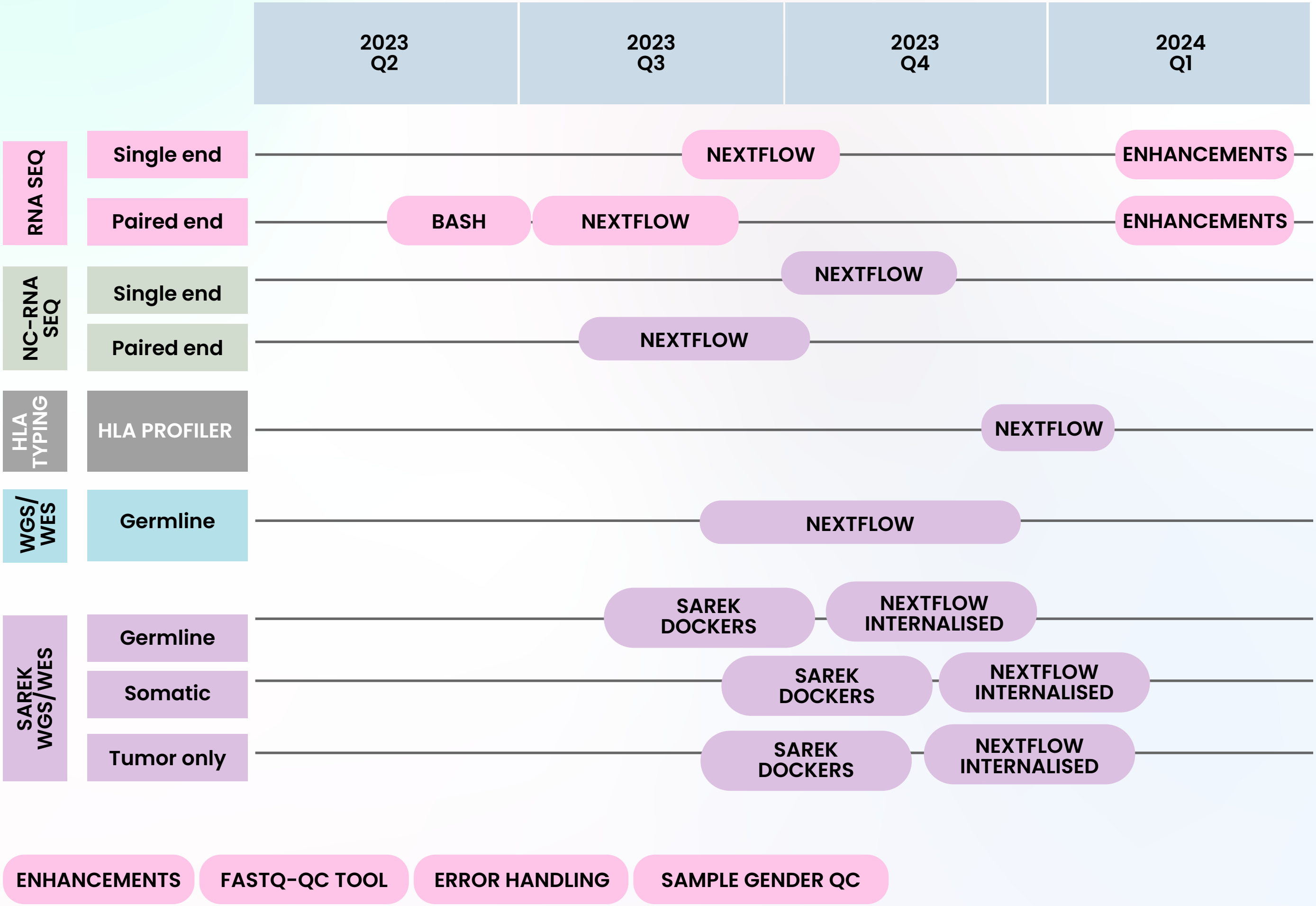
1. RNA-Seq
2. scRNA-Seq
3. WGS
4. WES

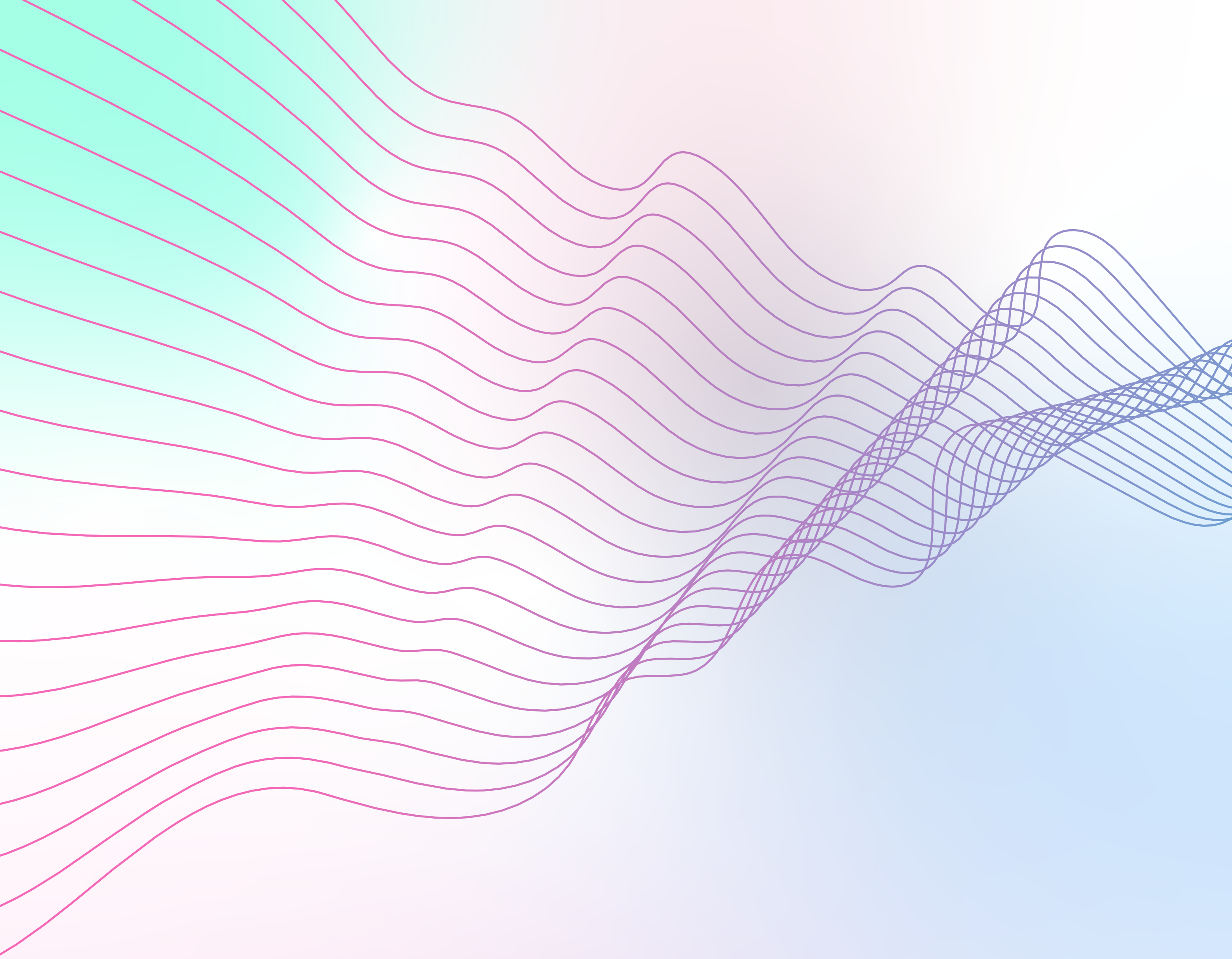
Deliverables

Production ready pipelines:

1. RNA-Seq pipeline (Single and paired-end)
2. scRNA-Seq pipeline (single end and paired end)
3. HLA typing pipeline
4. Germline WGS/WES pipeline
5. SAREK pipeline (Germline, somatic and Tumor)

Results


2023 Q2
2023 Q3
2023 Q4
2024 Q1
RNA SEQ
Single end
NEXTFLOW
ENHANCEMENTS
Paired end
BASH
NEXTFLOW
ENHANCEMENTS
NC-RNA SEQ
Single end
NEXTFLOW
Paired end
NEXTFLOW
HLA TYPING
HLA PROFILER
NEXTFLOW
WGS/ WES
Germline
NEXTFLOW
SAREK WGS/WES
Germline
SAREK DOCKERS
NEXTFLOW INTERNALISED
Somatic
SAREK DOCKERS
NEXTFLOW INTERNALISED
Tumor only
SAREK DOCKERS
NEXTFLOW INTERNALISED
ENHANCEMENTS
FASTQ-QC TOOL
ERROR HANDLING
SAMPLE GENDER QC



Where data means more

excelra

SAN FRANCISCO • BOSTON • LONDON • GHENT/GENT
UTRECHT • HYDERABAD

Connect with our experts: marketing@excelra.com

www.excelra.com