6-WEEK MENTOR-LED PROGRAM

Bioinformatics × Artificial Intelligence

From raw sequencing reads to deployed AI models — genomics, single-cell and spatial omics, protein structure prediction, generative drug design and reproducible cloud pipelines.



6	6	40+	1
Weeks, mentor-led	Live industry projects	Tools & frameworks	Deployed MVP capstone

WHAT THE PROGRAM COVERS

Genomics & Variants

NGS QC, alignment, GATK / DeepVariant calling, structural variants and long-read phasing.

Single-Cell & Spatial

Scanpy / Seurat workflows, scVI integration, trajectories, Visium and Xenium deconvolution.

Structure & Drug Design

AlphaFold3, ESM-2 protein language models, docking, MD intuition and generative binders.

ML, Graphs & MLOps

GNNs on biological networks, genomic transformers, GWAS/PRS, Nextflow and deployment.

THE END-TO-END PIPELINE YOU WILL BUILD

Raw reads to deployed model

01
Raw reads
FASTQ / BAM ingestion

02
QC & align
FastQC, STAR, GATK

03
Quantify
Counts, matrices, VCF

04
Model
ML, GNNs, AlphaFold3

05
Interpret
Pathways, SHAP, ACMG

06
Deploy
Nextflow, Docker, app

ADVANCED SPECIALISATION TRACKS

AI / STRUCTURE

Protein Language Models

ESM-2 embeddings and AlphaFold3 confidence metrics to predict function, stability and mutation effects.

SINGLE-CELL

Spatial Multi-Omics

Map transcripts back to tissue architecture with Visium and Xenium, then deconvolve cell neighbourhoods.

GENERATIVE

De Novo Molecule Design

Diffusion and flow models that generate binders, then score them with docking and MD sanity checks.

CLINICAL

Variant Interpretation

ACMG classification, pharmacogenomics and polygenic risk scores with reporting-grade rigour.

NETWORKS

Graph Learning on Biology

GNNs over PPI, pathway and drug–target graphs for repurposing and synthetic-lethality discovery.

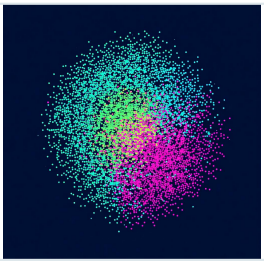
ENGINEERING

Reproducible Bio-Pipelines

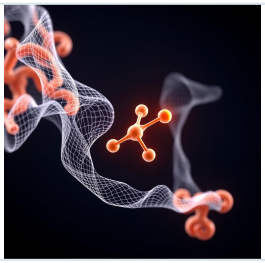
Nextflow, containers and cloud storage: workflows a reviewer can rerun on the first try.



PREDICTED FOLDS



SINGLE-CELL UMAP



LIGAND DOCKING

WEEK-BY-WEEK CURRICULUM

Weeks 1 – 3

WEEK 01

FOUNDATION

Bioinformatics Foundations & AI Integration

TOPICS COVERED

- Central dogma for data people: DNA → RNA → protein
- Biological data formats: FASTA, GenBank, VCF, GFF, BAM/CRAM
- NCBI, Ensembl, UniProt, PDB — programmatic access via REST APIs
- Data cleaning, missing values, batch effects and outliers
- Pairwise & multiple sequence alignment (global vs local)
- Hidden Markov models and profile search (HMMER)

TOOLS & FRAMEWORKS

BLAST | Clustal Omega | MAFFT | Biopython | HMMER

Live Project 1 — Sequence retrieval, alignment & annotation pipeline

WEEK 02

CORE

Genomics, Variants & Transcriptomics

TOPICS COVERED

- Short vs long read sequencing: Illumina, PacBio HiFi, Nanopore
- QC → alignment → variant calling (GATK best practices, DeepVariant)
- RNA-Seq workflow: quantification, normalisation, DE testing
- Pathway & gene-set enrichment: GO, KEGG, Reactome, GSEA
- Structural variants, CNVs and long-read phasing
- Cloud-scale genomics with cost-aware compute

TOOLS & FRAMEWORKS

FastQC | STAR | Salmon | DESeq2 | GATK | DeepVariant

Live Project 2 — RNA-Seq differential expression & pathway report

WEEK 03

ADVANCED

Single-Cell & Spatial Omics

TOPICS COVERED

- scRNA-seq chemistry, droplet demultiplexing, ambient RNA removal
- Dimensionality reduction: PCA → UMAP; clustering & marker discovery
- Cell-type annotation, label transfer and reference mapping
- Trajectory inference, RNA velocity and pseudotime
- Spatial transcriptomics: Visium, Xenium, deconvolution
- Batch integration with Harmony, scVI and scANVI

TOOLS & FRAMEWORKS

Scanpy | Seurat | scVI | Squidpy | CellRanger

Live Project 3 — Single-cell atlas: clustering, annotation & trajectory

WEEK-BY-WEEK CURRICULUM

Weeks 4 – 6

WEEK 04

ADVANCED

Structural Bioinformatics & AI Drug Discovery

TOPICS COVERED

- Protein structure hierarchy, folds and domain architecture
- AI structure prediction: AlphaFold3, ESMFold, RoseTTAFold
- Protein language models & embeddings for function prediction
- Molecular docking, scoring functions and virtual screening
- Molecular dynamics essentials and free-energy intuition
- Generative chemistry: diffusion models, de novo binder design

TOOLS & FRAMEWORKS

AlphaFold3 | ESM-2 | AutoDock Vina | RDKit | DeepChem | PyMOL

Live Project 4 — Fold prediction + docking & lead prioritisation

WEEK 05

FRONTIER

Machine Learning & Systems Biology

TOPICS COVERED

- Feature engineering on omics matrices; leakage & cross-validation traps
- Graph neural networks on PPI and pathway networks
- Transformers for genomic sequence (Enformer, DNABERT-style models)
- Multi-omics integration: MOFA, autoencoders, late fusion
- GWAS, polygenic risk scores, fine-mapping and Mendelian randomisation
- Explainability for clinical trust: SHAP, attention attribution

TOOLS & FRAMEWORKS

PyTorch | scikit-learn | PyG | PLINK 2 | Cytoscape | MOFA+

Live Project 5 — Disease-risk model with GWAS features + explainability

WEEK 06

FRONTIER

Pipelines, MLOps & Translational Deployment

TOPICS COVERED

- Reproducible workflows with Nextflow / Snakemake + nf-core
- Containers, Conda envs and version-pinned reproducibility
- Cloud genomics on AWS/GCP; object storage & spot compute
- Experiment tracking, model registries and drift monitoring
- Metagenomics, pathogen surveillance and genomic epidemiology
- Ethics, consent, HIPAA/GDPR and clinical reporting standards

TOOLS & FRAMEWORKS

Nextflow | Docker | MLflow | Streamlit | Kraken2 | Nextstrain

Live Project 6 — Deployed MVP: end-to-end pipeline + interactive app

OUTCOMES

What you walk away with

01

Read biology like data

Move fluently between raw reads, matrices, structures and networks without losing the biology.

02

Ship reproducible analysis

Every result you produce is containerised, versioned and rerunnable by someone else.

03

Apply AI where it earns its place

Know when a transformer beats a t-test — and how to validate either honestly.

04

Publish a portfolio MVP

A deployed, interactive bio-app with documented methods that recruiters can actually open.

WHO THIS IS FOR

- Life-science students & researchers
- Data analysts moving into biotech
- Software engineers entering genomics
- Pharma & clinical research associates
- MSc / PhD candidates needing compute skills
- Founders building health-tech products

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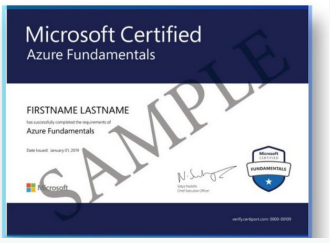
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