



Job Title: Senior Computational Biologist, Multi-Omics (Crop Genomics)

Location: Ghent, Belgium (on-site)

Department: Artificial Intelligence

Type: Full-time

About Rainbow Crops

Rainbow Crops leverages multiplex genome editing, precision breeding, and AI to engineer crops with the genetic superpower to adapt to climate challenges, reduce chemical inputs, and enhance nutritional value. By targeting complex traits and improving multiple characteristics simultaneously, our technology tackles plant traits that have historically been difficult to enhance. We partner with seed companies and nonprofits to develop and make these advanced plant genetics accessible, benefiting farmers, consumers, and the environment, while driving sustainability and global food security. www.rainbowcrops.com

Position Overview

We are seeking a **Senior Computational Biologist** to own the multi-omics evidence layer behind our trait discovery platform. This is a senior, hands-on individual-contributor role for a senior scientist who decides which data is worth generating and ingesting, designs the experiments that produce it, and turns the resulting datasets into defensible gene-to-trait evidence.

You will report to the Head of AI and work as a senior peer alongside our AI and plant genomics experts. You will take full ownership of the multi-omics workstream, which both expands what the company can do and creates capacity in a small, fast-moving team.

The role rests on three pillars: selecting and ingesting the datasets that expand our Trait Foundry knowledge graph, leading the experimental design, and running single-cell and other omics analyses across all projects. You are expected to challenge proposed designs, flag confounders before data is generated, and take a critical view of which datasets earn their place in our knowledge graph.



Main Responsibilities

1. Multi-Omics Data Selection and Ingestion for Trait Foundry

- Identify, evaluate, and prioritise internal and external omics datasets for the Trait Foundry knowledge graph, spanning GWAS summary statistics, QTL and eQTL resources, expression atlases, chromatin accessibility, regulatory and TF binding data, co-expression networks, and pangenome resources. You keep a forward view of emerging resources across various crops like maize, sorghum, and rice.
- Define how each omics layer maps onto knowledge graph entities and relationships, working with the AI team on schema design and on which layers become useful model inputs.
- Critically assess and set curation standards for candidate datasets before ingestion for reference genome compatibility, population structure, publication and ascertainment bias, batch effects, statistical power, and licensing constraints.

2. Omics Analysis Across Programs

- Perform bulk RNA-seq differential expression across multi-tissue and multi-timepoint designs, plus variant calling, genotyping, and population genetics analyses where relevant to trait discovery and breeding populations.
- Analyse single-cell RNA-seq and scATAC-seq data, covering quality control, integration, clustering, cell-type annotation, and cell-type-specific regulatory interpretation.
- Analyse ATAC-seq data, including peak calling, differential accessibility, motif enrichment, TF footprinting, and peak-to-gene linking.
- Perform GWAS and QTL / eQTL analyses, including association mapping, population structure and kinship correction, multiple testing control, fine-mapping, and resolution from interval to credible candidate genes.
- Integrate across omics layers to connect regulatory signals to phenotype, and translate results into structured gene-to-trait evidence that feeds our knowledge graph and downstream models.

3. Experimental Design



- Lead the design of omics experiments, including tissue and timepoint selection, replication, randomisation, blocking and batch structure, and control strategy.
- Make and justify design trade-offs such as bulk versus single-cell resolution, breadth versus depth of sampling, and sequencing depth versus sample number, including power and sample size analysis.
- Anticipate confounders specific to plant systems, such as protoplasting and nuclei isolation artefacts, tissue heterogeneity, and developmental staging, and define quality control gates before data generation begins.
- Co-design studies with wet-lab, greenhouse, and phenotyping colleagues and with partners, and act as a peer reviewer on designs proposed within the team and by partners, raising risks early and constructively.

4. Collaboration and Communication

- You are a teamplayer, proactively take up and divide the scientific workloads, and work closely with the Head of AI, the AI and bioinformatics experts, the AI infrastructure engineer, and wet-lab scientists.
- Deliver reproducible, well-documented analyses using workflow managers such as Nextflow and nf-core, and communicate methods, assumptions, and limitations clearly to non-computational colleagues, leadership, and partners.
- Contribute to grant applications, partner deliverables, and publications, and represent Rainbow Crops at scientific conferences.

Key Skills and Personal Attributes

- Scientific Ownership: Wants to shape which experiments happen and which data matters, not only to analyse what arrives.
- Critical and Rigorous: Interrogates data quality, confounders, and statistical assumptions before drawing conclusions, and is comfortable saying a dataset or design is not fit for purpose.
- Multi-Omics Breadth: Moves comfortably between population-scale genetics and single-cell regulatory data, and understands how the layers inform one another.



- Biological Grounding: Interprets results as plant biology, not only as statistics, and connects molecular signals to trait outcomes.
- Design Instinct: Recognises the failure modes of an experiment while it is still on paper.
- Collaborative Peer: Works effectively as an equal alongside other senior scientists, sharing ownership rather than competing for it, and translates between experimental and computational perspectives.
- Startup Mindset: Comfortable with ambiguity, evolving priorities, and building capability that does not yet exist.

Qualifications

- PhD in Bioinformatics, Computational Biology, Plant Genomics, Quantitative Genetics, or a closely related field.
- At least 5 years of relevant experience beyond the PhD in multi-omics analysis, ideally including plant or crop systems.
- Demonstrated hands-on experience with GWAS and QTL or eQTL analysis, including population structure correction and fine-mapping.
- Demonstrated hands-on experience with single-cell or single-nucleus transcriptomics, experience with chromatin accessibility data (ATAC-seq or scATAC-seq) is a plus
- Strong track record in experimental design for omics studies, including replication strategy and power analysis.
- Proficiency in Python and R, with fluency in the relevant tool ecosystems, for example Scanpy, Seurat, Signac or ArchR, DESeq2, PLINK, GEMMA or GCTA, TASSEL, MACS, and motif and footprinting tools.
- Experience with reproducible workflow managers such as Nextflow or Snakemake.
- Working knowledge of plant reference genomes and their practical pitfalls; experience with pangenome or structural variation resources is a strong plus.



- Willingness to work on-site in Ghent and collaborate closely with wet-lab and R&D teams.

Why Join Us?

- Be part of a forward-thinking company shaping the future of sustainable agriculture.
- Own the omics evidence layer of a genuinely novel trait discovery platform, with real influence over what data gets generated, including data from multiplex genome-edited populations that few groups anywhere can access.
- Collaborate with a talented, diverse team on cutting-edge technologies.
- Competitive salary, benefits, and opportunities for professional growth.

Application Process

Interested candidates should submit their CV and cover letter detailing their qualifications and interest in the role to info@rainbowcrops.com.