

**Position:**

Senior Computational Biologist/ Data Scientist, Bioinformatics

**Company Overview:**

Kernal is creating mRNA drugs that instruct specific cells in the body on how to make their own medicine. Messenger RNA technology has proven extremely useful in rapidly developing vaccines against COVID. Kernal is developing the next-generation of mRNA therapy, called mRNA 2.0. It solves a critical problem of cancer cell selectivity that affects mRNA and oncolytic virus-based immuno-oncology drugs. Located in Cambridge, MA, Kernal received three awards from Amgen and NASA. With roots at MIT, Harvard, and Big Pharma, Kernal's interdisciplinary team of MDs and PhDs previously built a successful Biotech company and has deep expertise in mRNA space.

**Job Summary:**

Kernal is seeking a highly motivated bioinformatics scientist to perform analysis of proteomics and next-generation sequencing data (mRNA-seq, ribo-seq). The successful candidate will work collaboratively with wet lab teams and will contribute to identification of cell specific sequence features.

**Responsibilities:**

- Analyze proteomics, transcriptomics data to generate testable hypotheses for wet lab experiments
- Apply relevant statistical methods to cross-validate and evaluate significance of hypotheses
- Lead hypothesis generation for bench scientists
- Present findings in group meetings
- Collaborate with team members
- Work independently and think out of the box to extract meaningful insights from public datasets

**Requirements:**

- BS/MS in Computational Biology/Bioinformatics or related field with 4+ years of industry experience or Ph.D. in Computational Biology/Bioinformatics preferred
  - Experience with NGS data, genomics analysis, samtools, RNAseq, proteomics, bash/shell scripting, public datasets such as TCGA and GTEX
  - Fluency in a programming language such as Python, R, or C++
  - Eagerness to learn new methods
  - Excellent communication and time management skills
  - Ability to manage multiple projects
  - Attention to details
- 
- Preferred: 3 years of relevant experience of which 1+ in industrial experience
  - Preferred: Candidates with 5+ industry experience will be considered for a senior position
  - Preferred: Theoretical understanding of LC/MS and ribosome profiling

- Preferred: Hands on expertise on single-cell transcriptomics, proteomics analyses, massively parallel reporter assays, workflow management, AWS or Google Cloud, RNA folding, pathway analysis, and/or machine learning and data visualization experience on biological datasets

**Benefits:**

- On-site subsidized cafeteria
- Free parking, monthly subway pass or a subsidized commuter rail pass
- Free MIT Athletic Membership
- Free Bluebikes Membership
- Highly competitive healthcare coverage
- Flexible Spending Account
- Paid parental leave, family caregiver leave, medical leave
- Competitive 401k
- Paid insurance coverage
- Competitive vacation and sick days per year

Kernal is dedicated to providing a diverse work environment and is committed to equal employment opportunity for all its employees and qualified applicants. We do not discriminate in employment practices for reasons of race, color, national origin, age, gender, sexual orientation, marital or veteran status, religion, disability, or any other legally protected status. Kernal will make reasonable accommodations for qualified individuals with known disabilities, in accordance with applicable law.

Click Here to Apply: <https://www.kernalbio.com/careers>