Job Description: Research Assistant – Bioinformatics

Educational Background

- Master's degree in Bioinformatics, Computational Biology, or a closely related field.

Professional Experience

- Minimum of 3 years of hands-on experience analyzing real-world biological or clinical datasets.
- Proven track record of working with Metagenomics and large-scale NGS data (e.g., WGS, WES, RNA-seq) in research or clinical contexts.

Technical Skills

- Proficient in building automated and scalable analysis pipelines from scratch.
- Strong programming expertise in:
    - R (biostatistics, visualization)
    - Python (data parsing, pipeline integration)
    - Bash/Linux shell scripting (workflow automation)
    - Perl (legacy script maintenance or data manipulation)

Bioinformatics Knowledge

- Familiarity with core tools such as GATK, STAR, BWA, HISAT2, samtools, VEP, and Annovar.
- Experience with variant annotation, clinical interpretation, and following ACMG/ClinVar guidelines.
- Understanding of genomic and clinical databases (e.g., gnomAD, dbSNP, ENSEMBL, OMIM).
- Basic understanding of structural variant analysis, copy number variation, and expression analysis.

Workflow & Reproducibility

- Experience using workflow management systems (e.g., Snakemake, Nextflow).
- Proficiency with version control systems (e.g., Git).
- Demonstrated ability to maintain reproducible research pipelines with appropriate documentation.
- Familiarity with containerization tools (e.g., Docker, Singularity) is a plus.

Reporting & Visualization

- Ability to generate clear, interpretable reports for non-specialist audiences.
- Experience in scientific visualization tools (e.g., ggplot2, seaborn, plotly).
- Ability to summarize complex datasets for presentations and publications.

Soft Skills

- Excellent communication skills for interdisciplinary teamwork and collaboration.
- Self-motivated with strong time-management and organizational skills.
- Ability to adapt and learn new tools and technologies as required.