**John Smith**

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**Summary**

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| Innovative bioinformatician and lead scientist with extensive research experience and a strong track record of international collaboration. Expertise in multi-omics data analysis, uncovering complex life features and diseases, and leading projects with strategic precision and compliance. Versatile background in improving patient health, controlling genetic defects, and ensuring agricultural product quality. Skilled in managing complex projects, validating findings through tailored tests, and integrating diverse disciplines. Proficient communicator, effective in both technical and non-technical realms, resolving issues collaboratively. Strong interface with teams, partners, and executives, leveraging feedback to innovate bioinformatics solutions and drive continuous improvement. Committed to excellence and innovation in bioinformatics.  **Professional Experience** |
| **Senior Bioinformatician, Institute ABC 2018-present**   * Analyze WGS/WES/RNA-Seq/scRNA-Seq/Methylation/Spatial omics/Bioimage data in cancer projects. * Lead projects, collaborating with bioinformaticians, researchers, and lab staff. * Perform genome analysis, including small/large variants and GWAS. * Conduct omics data analyses for drug sensitivity in IVF samples and developmental stages of non-model organisms. * Screen CRISPR targets * Develop tools, workflows, and shiny apps for various projects. * Lead and teach workshops, supervise PhD students, and examine thesis projects. * Provide consultation on study design and validation tests. * Collaborate on grant proposals and contribute to manuscript writing. |
| **Postdoc, University XYZ 2015-2018**   * Conducted advanced research in bioinformatics, focusing on [specific area, e.g., cancer genomics, microbial genomics, etc.]. * Analyzed high-throughput sequencing data, including WGS, RNA-Seq, and ChIP-Seq, to identify genetic and epigenetic alterations.   **Education** |
| * **PhD in Cancer Biology,** University of Medical Sciences (Country) 2010-2014 * **MSc. Immunology,** University of basic science (Country) 2008-2010 * **BSc. Biology,** University of basic science (Country) 2008-2010   **Technical skills** |
| * **Computational:** R, Python, SAS, SQL, Perl, Git, * **Container technology:** Docker, Singularity * **Workflow management:** Snakemake, Nextflow * **Wet lab:** PCR, qPCR, Western blotting, ddPCR, Taqman genotyping, Nanopore sequencing   **Teaching** |
| * Introduction to bioinformatics, PhD Course * Genomics, MSc. course * Introduction to NGS data analysis, MSc. Course   **Honors and Awards** |
| * Research grant from X & Y Foundation 2016 * Science award for best thesis year 2014 * Best poster conference omics 2013 |
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| **Tools/workflows** |
| * **DetectCNV:** A tool for detecting CNV * **ProbeDesignIS:** In situ primer design * **Shiny app:** scRNASeq and Bulk RNASeq data analysis summary * **miRNA nextflow:** A nextflow pipeline for analysing miRNA data   **Recent Publications** |
| * **Smith J.**, Doe J., et al. (2023). "Comprehensive Multi-Omics Analysis Reveals Key Drivers of Drug Resistance in Breast Cancer." Nature Communications. * **Smith J.**, Johnson K., et al. (2022). "Single-Cell RNA-Seq Uncovers Novel Subpopulations in Tumor Microenvironment of Glioblastoma." Cell Reports. * Doe J., **Smith J.**, et al. (2021). "Epigenetic Landscape of Colorectal Cancer: Methylation Patterns and Their Clinical Implications." Genome Biology.   **References** |
| * **Available upon request** |